



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 01:15 AM GMT

PDB ID : 2C9J  
Title : STRUCTURE OF THE FLUORESCENT PROTEIN CMFP512 AT 1.35Å  
FROM CERIANTHUS MEMBRANACEUS  
Authors : Renzi, F.; Nienhaus, K.; Wiedenmann, J.; Vallone, B.; Nienhaus, G.U.  
Deposited on : 2005-12-12  
Resolution : 1.35 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.  
We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)  
A user guide is available at  
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>  
with specific help available everywhere you see the ⓘ symbol.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.7 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026688  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk26865

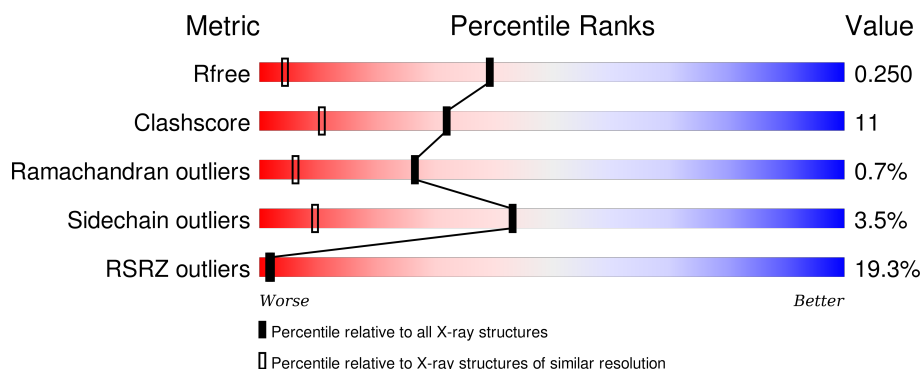
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 1.35 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	91344	2199 (1.40-1.32)
Clashscore	102246	2337 (1.40-1.32)
Ramachandran outliers	100387	2280 (1.40-1.32)
Sidechain outliers	100360	2279 (1.40-1.32)
RSRZ outliers	91569	2199 (1.40-1.32)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	223	<div> <div>28%</div> <div>76%</div> <div>18%</div> <div>• •</div> </div>
1	B	223	<div> <div>15%</div> <div>82%</div> <div>14%</div> <div>• •</div> </div>
1	C	223	<div> <div>19%</div> <div>73%</div> <div>23%</div> <div>• •</div> </div>
1	D	223	<div> <div>21%</div> <div>76%</div> <div>19%</div> <div>• •</div> </div>
1	E	223	<div> <div>17%</div> <div>82%</div> <div>15%</div> <div>• •</div> </div>

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Mol	Chain	Length	Quality of chain
1	F	223	
1	G	223	
1	H	223	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
1	CRQ	A	62	-	-	X	-

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 15518 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called GREEN FLUORESCENT PROTEIN FP512.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	214	Total	C	N	O	S	0	0	0
			1715	1111	282	313	9			
1	B	218	Total	C	N	O	S	0	0	0
			1748	1131	288	320	9			
1	C	218	Total	C	N	O	S	0	2	0
			1760	1141	290	320	9			
1	D	219	Total	C	N	O	S	0	1	0
			1760	1141	289	321	9			
1	E	218	Total	C	N	O	S	0	0	0
			1747	1130	288	320	9			
1	F	216	Total	C	N	O	S	0	2	0
			1743	1132	287	315	9			
1	G	218	Total	C	N	O	S	0	0	0
			1747	1130	288	320	9			
1	H	219	Total	C	N	O	S	0	0	0
			1755	1136	289	321	9			

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	62	CRQ	GLN	CHROMOPHORE	UNP Q5ZQQ5
A	62	CRQ	TYR	CHROMOPHORE	UNP Q5ZQQ5
A	62	CRQ	GLY	CHROMOPHORE	UNP Q5ZQQ5
B	62	CRQ	GLN	CHROMOPHORE	UNP Q5ZQQ5
B	62	CRQ	TYR	CHROMOPHORE	UNP Q5ZQQ5
B	62	CRQ	GLY	CHROMOPHORE	UNP Q5ZQQ5
C	62	CRQ	GLN	CHROMOPHORE	UNP Q5ZQQ5
C	62	CRQ	TYR	CHROMOPHORE	UNP Q5ZQQ5
C	62	CRQ	GLY	CHROMOPHORE	UNP Q5ZQQ5
D	62	CRQ	GLN	CHROMOPHORE	UNP Q5ZQQ5
D	62	CRQ	TYR	CHROMOPHORE	UNP Q5ZQQ5
D	62	CRQ	GLY	CHROMOPHORE	UNP Q5ZQQ5
E	62	CRQ	GLN	CHROMOPHORE	UNP Q5ZQQ5

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Chain	Residue	Modelled	Actual	Comment	Reference
E	62	CRQ	TYR	CHROMOPHORE	UNP Q5ZQQ5
E	62	CRQ	GLY	CHROMOPHORE	UNP Q5ZQQ5
F	62	CRQ	GLN	CHROMOPHORE	UNP Q5ZQQ5
F	62	CRQ	TYR	CHROMOPHORE	UNP Q5ZQQ5
F	62	CRQ	GLY	CHROMOPHORE	UNP Q5ZQQ5
G	62	CRQ	GLN	CHROMOPHORE	UNP Q5ZQQ5
G	62	CRQ	TYR	CHROMOPHORE	UNP Q5ZQQ5
G	62	CRQ	GLY	CHROMOPHORE	UNP Q5ZQQ5
H	62	CRQ	GLN	CHROMOPHORE	UNP Q5ZQQ5
H	62	CRQ	TYR	CHROMOPHORE	UNP Q5ZQQ5
H	62	CRQ	GLY	CHROMOPHORE	UNP Q5ZQQ5

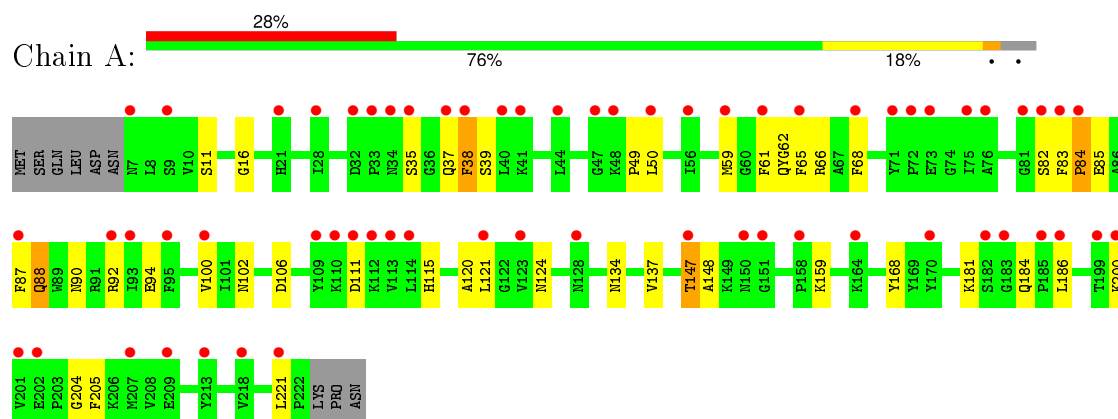
- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	168	Total O 168 168	0	0
2	B	187	Total O 187 187	0	0
2	C	210	Total O 210 210	0	0
2	D	197	Total O 197 197	0	0
2	E	184	Total O 184 184	0	0
2	F	219	Total O 219 219	0	0
2	G	204	Total O 204 204	0	0
2	H	174	Total O 174 174	0	0

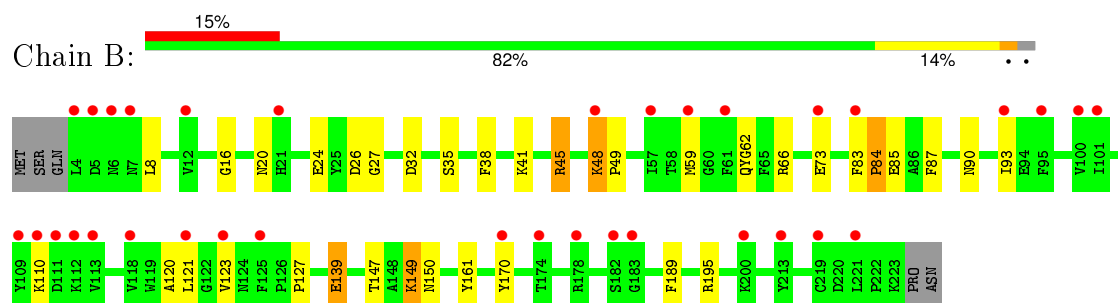
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ( $RSRZ > 2$ ). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

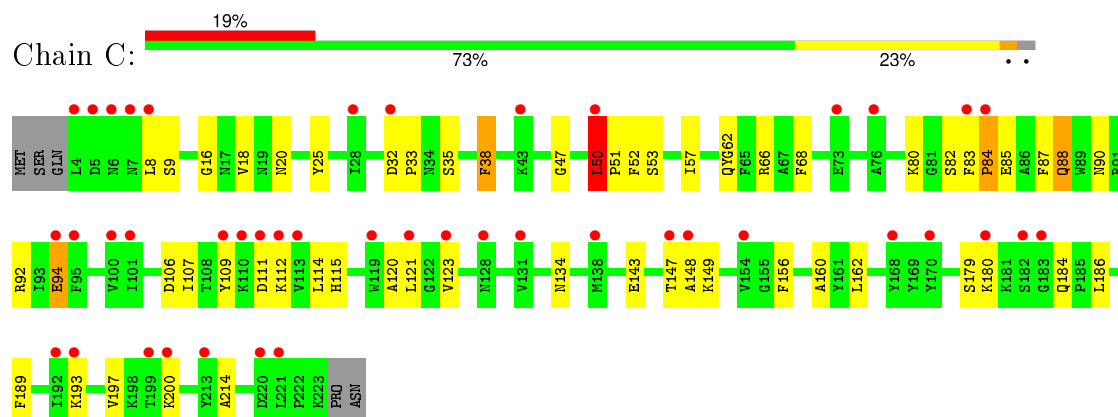
#### • Molecule 1: GREEN FLUORESCENT PROTEIN FP512



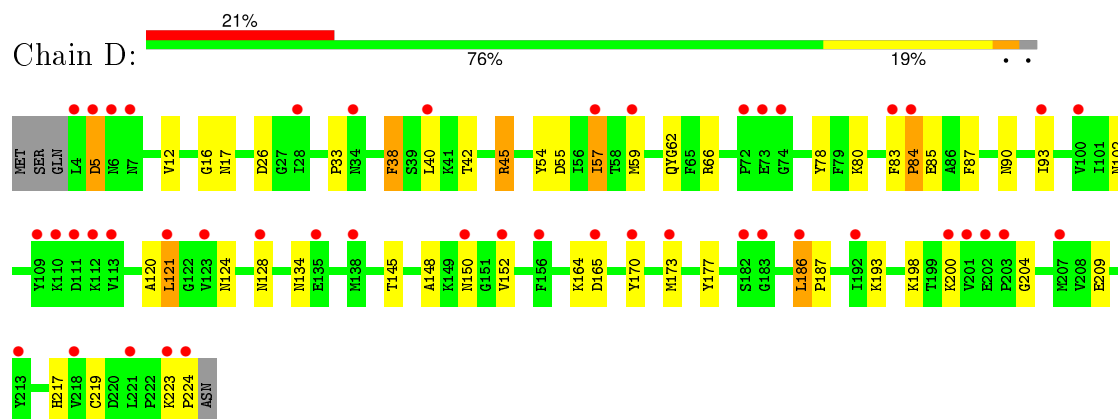
#### • Molecule 1: GREEN FLUORESCENT PROTEIN FP512



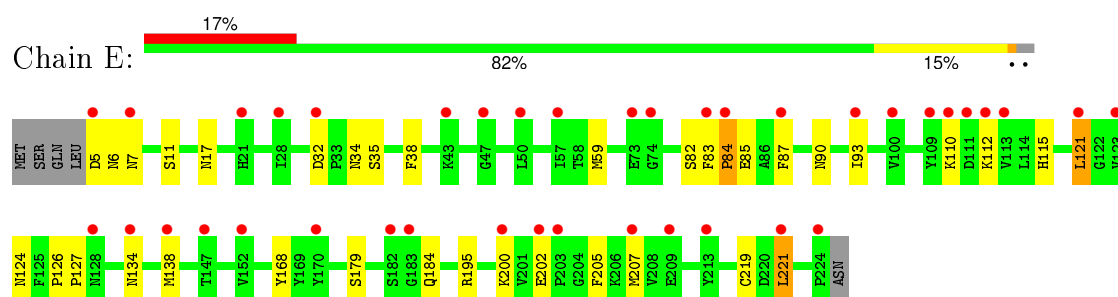
#### • Molecule 1: GREEN FLUORESCENT PROTEIN FP512



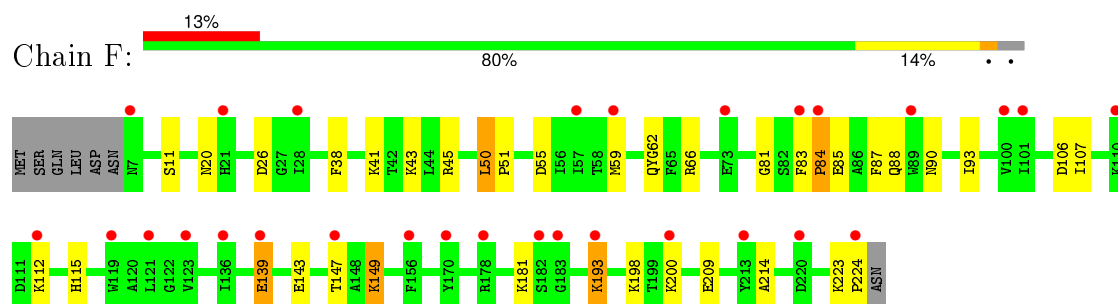
## ● Molecule 1: GREEN FLUORESCENT PROTEIN FP512



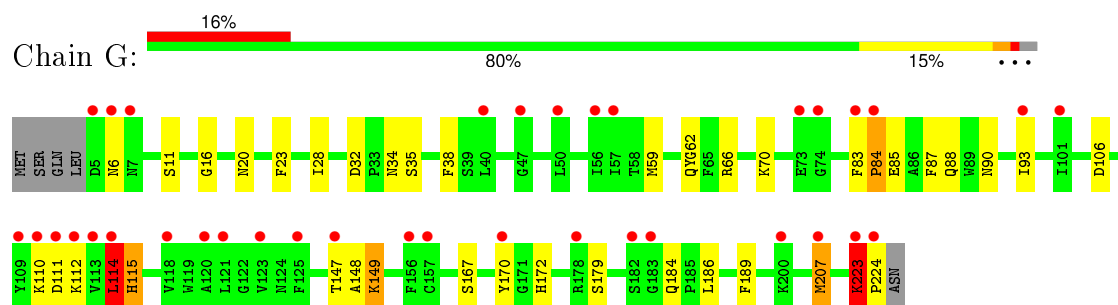
## ● Molecule 1: GREEN FLUORESCENT PROTEIN FP512



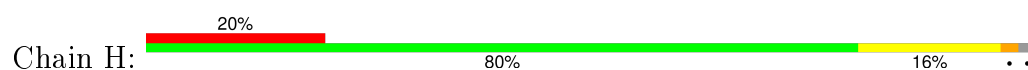
## ● Molecule 1: GREEN FLUORESCENT PROTEIN FP512

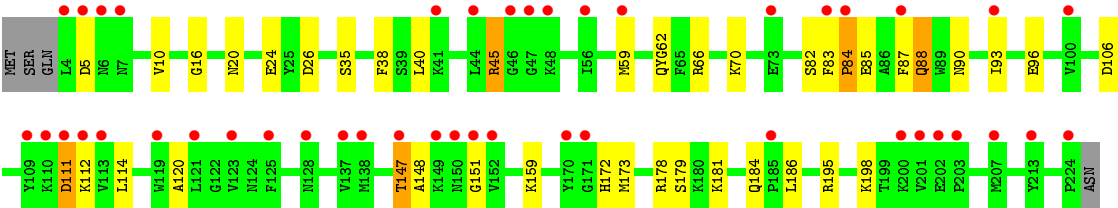


## ● Molecule 1: GREEN FLUORESCENT PROTEIN FP512



## ● Molecule 1: GREEN FLUORESCENT PROTEIN FP512







## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	54.00 Å 60.11 Å 125.40 Å 83.80° 89.98° 73.85°	Depositor
Resolution (Å)	55.00 – 1.35 34.02 – 1.35	Depositor EDS
% Data completeness (in resolution range)	91.0 (55.00-1.35) 87.7 (34.02-1.35)	Depositor EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.30 (at 1.35 Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, $R_{free}$	0.228 , 0.255 0.224 , 0.250	Depositor DCC
$R_{free}$ test set	15172 reflections (5.31%)	DCC
Wilson B-factor (Å <sup>2</sup> )	17.7	Xtriage
Anisotropy	0.133	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.40 , 39.4	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 300979 reflections	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	15518	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	18.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.82% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

## 5 Model quality ⓘ

### 5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: CRQ

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 5$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
1	A	0.39	0/1741	0.60	1/2350 (0.0%)
1	B	0.42	0/1774	0.63	0/2394
1	C	0.43	0/1792	0.67	2/2416 (0.1%)
1	D	0.41	0/1790	0.65	0/2417
1	E	0.41	0/1774	0.63	0/2395
1	F	0.44	0/1776	0.64	0/2395
1	G	0.44	0/1774	0.67	3/2395 (0.1%)
1	H	0.41	0/1782	0.61	1/2406 (0.0%)
All	All	0.42	0/14203	0.64	7/19168 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	2
1	B	0	2
1	C	0	3
1	D	0	3
1	E	0	2
1	F	0	4
1	G	0	4
1	H	0	2
All	All	0	22

There are no bond length outliers.

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	50	LEU	CA-CB-CG	6.40	130.03	115.30
1	G	115	HIS	N-CA-CB	6.34	122.00	110.60
1	G	114	LEU	CA-CB-CG	5.95	128.98	115.30
1	A	88	GLN	N-CA-C	5.91	126.96	111.00
1	H	88	GLN	N-CA-C	5.71	126.42	111.00
1	C	88	GLN	N-CA-C	5.25	125.18	111.00
1	G	115	HIS	N-CA-C	-5.05	97.36	111.00

There are no chirality outliers.

All (22) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	83	PHE	Peptide
1	A	87	PHE	Peptide
1	B	83	PHE	Peptide
1	B	87	PHE	Peptide
1	C	50	LEU	Peptide
1	C	83	PHE	Peptide
1	C	87	PHE	Peptide
1	D	186	LEU	Peptide
1	D	83	PHE	Peptide
1	D	87	PHE	Peptide
1	E	83	PHE	Peptide
1	E	87	PHE	Peptide
1	F	223	LYS	Peptide
1	F	50	LEU	Peptide
1	F	83	PHE	Peptide
1	F	87	PHE	Peptide
1	G	110	LYS	Peptide
1	G	114	LEU	Peptide
1	G	83	PHE	Peptide
1	G	87	PHE	Peptide
1	H	83	PHE	Peptide
1	H	87	PHE	Peptide

## 5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1715	0	1649	47	0
1	B	1748	0	1682	32	0
1	C	1760	0	1710	57	0
1	D	1760	0	1702	60	0
1	E	1747	0	1678	26	0
1	F	1743	0	1696	37	0
1	G	1747	0	1680	33	0
1	H	1755	0	1691	47	0
2	A	168	0	0	3	0
2	B	187	0	0	3	0
2	C	210	0	0	13	0
2	D	197	0	0	3	0
2	E	184	0	0	1	0
2	F	219	0	0	4	0
2	G	204	0	0	3	0
2	H	174	0	0	2	0
All	All	15518	0	13488	292	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 11.

All (292) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:62:CRQ:C	1:A:65:PHE:N	1.84	1.40
1:E:219:CYS:SG	1:F:193[A]:LYS:HE3	1.62	1.38
1:H:59:MET:CE	1:H:173:MET:HE1	1.53	1.36
1:E:219:CYS:SG	1:F:193[A]:LYS:CE	2.19	1.30
1:A:61:PHE:C	1:A:62:CRQ:N	1.89	1.25
1:A:59:MET:CE	1:A:159:LYS:HE2	1.66	1.24
1:A:59:MET:HE3	1:A:159:LYS:HE2	1.12	1.07
1:H:59:MET:HE3	1:H:173:MET:CE	1.85	1.06
1:H:59:MET:CE	1:H:173:MET:CE	2.33	1.06
1:B:26:ASP:OD1	1:B:45:ARG:HD3	1.61	0.98
1:C:84:PRO:HD2	1:C:85:GLU:OE1	1.64	0.98
1:D:84:PRO:HD2	1:D:85:GLU:OE1	1.63	0.96
1:A:59:MET:CE	1:A:159:LYS:CE	2.46	0.94
1:F:26:ASP:OD1	1:F:45:ARG:HD3	1.68	0.94
1:C:193[A]:LYS:HE2	2:C:2180:HOH:O	1.69	0.91
1:E:84:PRO:HD2	1:E:85:GLU:OE1	1.71	0.91
1:D:26:ASP:OD2	1:D:45:ARG:HD3	1.69	0.90
1:A:148:ALA:HB1	1:A:186:LEU:HD13	1.54	0.90

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:10:VAL:CG2	1:H:40:LEU:HD21	2.01	0.90
1:H:26:ASP:OD2	1:H:45:ARG:HD3	1.74	0.88
1:G:147:THR:HG22	1:G:189:PHE:HD1	1.38	0.88
1:E:219:CYS:SG	1:F:193[A]:LYS:HE2	2.13	0.88
1:G:84:PRO:HD2	1:G:85:GLU:OE1	1.72	0.88
1:H:59:MET:HE3	1:H:173:MET:HE1	0.89	0.87
1:H:111:ASP:CG	1:H:112:LYS:H	1.77	0.87
1:F:84:PRO:HD2	1:F:85:GLU:OE1	1.75	0.86
1:D:93:ILE:HG12	1:D:173:MET:HE2	1.58	0.85
1:C:149:LYS:HB2	1:D:170:TYR:OH	1.77	0.85
1:G:223:LYS:HB3	1:G:224:PRO:CD	2.06	0.84
1:B:84:PRO:HD2	1:B:85:GLU:OE1	1.76	0.84
1:A:84:PRO:HD2	1:A:85:GLU:OE1	1.77	0.84
1:H:84:PRO:HD2	1:H:85:GLU:OE1	1.77	0.83
1:D:59:MET:CE	1:D:173:MET:SD	2.67	0.82
1:C:149:LYS:HD2	1:D:170:TYR:CE1	2.15	0.82
1:C:193[A]:LYS:CG	2:C:2180:HOH:O	2.28	0.81
1:C:160:ALA:HB2	2:C:2149:HOH:O	1.81	0.81
1:C:193[A]:LYS:HG2	2:C:2180:HOH:O	1.78	0.80
1:A:59:MET:HE1	1:A:159:LYS:CE	2.10	0.78
1:G:223:LYS:HB3	1:G:224:PRO:HD3	1.63	0.78
1:A:59:MET:HE3	1:A:159:LYS:CE	2.03	0.77
1:H:10:VAL:HG23	1:H:40:LEU:HD21	1.67	0.76
1:H:10:VAL:HG21	1:H:40:LEU:HD21	1.67	0.76
1:C:147:THR:HG22	1:C:189:PHE:HD1	1.51	0.76
1:A:100:VAL:HG23	1:C:92:ARG:HH11	1.52	0.74
1:H:111:ASP:CG	1:H:112:LYS:N	2.40	0.74
1:A:59:MET:HE1	1:A:159:LYS:NZ	2.03	0.73
1:B:48:LYS:HG3	2:B:2052:HOH:O	1.89	0.73
1:D:59:MET:HE1	1:D:173:MET:SD	2.29	0.72
1:C:197:VAL:HG11	1:D:224:PRO:HG3	1.70	0.72
1:G:207:MET:HB3	2:G:2185:HOH:O	1.90	0.72
2:C:2149:HOH:O	1:D:145:THR:HG21	1.89	0.71
1:G:147:THR:HG22	1:G:189:PHE:CD1	2.23	0.71
1:B:90:ASN:ND2	1:D:124:ASN:H	1.89	0.70
1:E:124:ASN:H	1:G:90:ASN:ND2	1.88	0.70
1:D:59:MET:HE2	1:D:173:MET:SD	2.32	0.70
1:A:84:PRO:HD2	1:A:85:GLU:H	1.58	0.69
1:F:139:GLU:OE2	2:F:2134:HOH:O	2.12	0.68
1:D:40[B]:LEU:HD21	1:D:42:THR:HG23	1.73	0.68
1:A:168:TYR:O	1:B:149:LYS:HE2	1.93	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:18:VAL:HG21	2:C:2056:HOH:O	1.94	0.67
1:C:57:ILE:HG23	2:C:2056:HOH:O	1.95	0.67
1:C:109:TYR:CE1	1:C:112:LYS:O	2.49	0.66
1:A:221:LEU:HB2	1:B:195:ARG:NH1	2.11	0.66
1:A:124:ASN:H	1:C:90:ASN:ND2	1.94	0.66
1:E:168:TYR:CG	1:F:147:THR:HG21	2.31	0.65
1:F:88:GLN:HA	2:F:2094:HOH:O	1.97	0.65
1:D:40[B]:LEU:HD21	1:D:42:THR:CG2	2.27	0.65
1:B:147:THR:CG2	1:B:189:PHE:HD1	2.10	0.65
1:D:54:TYR:HA	1:D:57:ILE:HD11	1.77	0.65
1:B:139:GLU:HG2	1:B:161:TYR:CE2	2.32	0.64
1:B:121:LEU:HD22	1:D:102:ASN:HB3	1.79	0.64
1:C:193[A]:LYS:CE	2:C:2180:HOH:O	2.36	0.63
1:F:26:ASP:OD1	1:F:45:ARG:CD	2.44	0.63
1:D:152:VAL:HG13	1:D:177:TYR:O	1.99	0.63
1:A:147:THR:HG21	1:B:170:TYR:CE2	2.34	0.62
1:A:100:VAL:CG2	1:C:92:ARG:HH11	2.11	0.62
1:H:148:ALA:HB1	1:H:186:LEU:HD13	1.82	0.61
1:H:59:MET:HE1	1:H:173:MET:CE	2.30	0.61
1:H:10:VAL:HG23	1:H:40:LEU:CD2	2.30	0.61
1:A:84:PRO:HD2	1:A:85:GLU:CD	2.21	0.61
1:A:62:CRQ:C	1:A:65:PHE:CA	2.76	0.61
1:A:221:LEU:HB2	1:B:195:ARG:HH12	1.66	0.60
1:A:61:PHE:C	1:A:62:CRQ:CA1	2.67	0.60
1:D:59:MET:SD	1:D:173:MET:CE	2.89	0.60
1:H:10:VAL:HG12	1:H:114:LEU:HB3	1.83	0.59
1:F:41:LYS:NZ	1:F:43[B]:LYS:HE2	2.17	0.59
1:H:93:ILE:HG12	1:H:173:MET:HE2	1.84	0.59
1:C:106:ASP:OD1	1:C:180:LYS:HE2	2.03	0.59
1:D:198:LYS:NZ	2:D:2170:HOH:O	2.36	0.59
1:G:223:LYS:CB	1:G:224:PRO:HD3	2.33	0.59
1:H:59:MET:SD	1:H:173:MET:CE	2.91	0.59
1:D:12:VAL:HG11	1:D:40[B]:LEU:HD11	1.85	0.58
1:F:11:SER:OG	1:F:115:HIS:HD2	1.86	0.58
1:G:170:TYR:CE1	1:H:147:THR:HG21	2.37	0.58
1:A:62:CRQ:CA3	1:A:65:PHE:N	2.63	0.58
1:H:151:GLY:C	1:H:186:LEU:HD11	2.24	0.58
1:E:90:ASN:HD22	1:G:20:ASN:ND2	2.01	0.58
1:F:55:ASP:OD1	1:F:198:LYS:CE	2.53	0.57
1:F:90:ASN:HD22	1:H:20:ASN:ND2	2.03	0.57
1:D:223:LYS:HB3	1:D:224:PRO:HD2	1.84	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:90:ASN:HD22	1:C:20:ASN:ND2	2.02	0.56
1:H:59:MET:SD	1:H:173:MET:HE1	2.45	0.56
1:B:20:ASN:ND2	1:D:90:ASN:HD22	2.03	0.56
1:A:84:PRO:CD	1:A:85:GLU:H	2.17	0.56
1:C:143:GLU:CD	1:C:193[A]:LYS:HD2	2.26	0.56
1:D:26:ASP:OD2	1:D:45:ARG:CD	2.50	0.56
1:C:121:LEU:CD2	1:C:123:VAL:HG13	2.35	0.56
1:E:17:ASN:HB3	1:E:121:LEU:HD23	1.87	0.56
1:D:134:ASN:O	1:D:164:LYS:HE2	2.05	0.55
1:A:134:ASN:HD21	1:A:205:PHE:HE1	1.55	0.55
1:D:84:PRO:HD2	1:D:85:GLU:H	1.70	0.55
1:E:82:SER:HA	1:E:184:GLN:HE22	1.73	0.54
1:A:62:CRQ:HB1	2:A:2134:HOH:O	2.07	0.54
1:C:156:PHE:HZ	1:D:170:TYR:CD1	2.25	0.54
1:F:20:ASN:ND2	1:H:90:ASN:HD22	2.06	0.53
1:G:6:ASN:HD22	1:G:34:ASN:HD22	1.56	0.53
1:E:219:CYS:SG	1:F:193[A]:LYS:NZ	2.80	0.53
1:H:88:GLN:OE1	1:H:178:ARG:NH1	2.42	0.53
1:G:84:PRO:HD2	1:G:85:GLU:H	1.74	0.53
1:E:134:ASN:HD21	1:E:205:PHE:HE1	1.57	0.53
1:H:84:PRO:HD2	1:H:85:GLU:H	1.75	0.52
1:D:59:MET:SD	1:D:173:MET:HE1	2.50	0.52
1:C:149:LYS:HD2	1:D:170:TYR:HE1	1.68	0.52
1:C:143:GLU:OE1	1:C:193[A]:LYS:HD3	2.10	0.52
1:F:55:ASP:OD1	1:F:198:LYS:HE3	2.10	0.52
1:D:40[B]:LEU:CD2	1:D:42:THR:HG23	2.40	0.52
1:D:200:LYS:HB2	1:D:209:GLU:HB2	1.92	0.51
1:B:147:THR:HG22	1:B:189:PHE:HD1	1.74	0.51
1:E:32:ASP:HB3	1:E:35:SER:OG	2.10	0.51
2:G:2148:HOH:O	1:H:172:HIS:HE1	1.92	0.51
1:E:202:GLU:HG3	1:E:207:MET:HB2	1.92	0.51
1:E:195:ARG:HD2	1:F:224:PRO:O	2.10	0.51
1:D:54:TYR:HA	1:D:57:ILE:CD1	2.41	0.51
1:B:127:PRO:HD2	1:D:150:ASN:OD1	2.11	0.51
1:D:223:LYS:CB	1:D:224:PRO:HD2	2.41	0.51
1:G:111:ASP:O	1:G:112:LYS:HB2	2.11	0.51
1:E:11:SER:OG	1:E:115:HIS:HD2	1.94	0.51
1:G:223:LYS:CB	1:G:224:PRO:CD	2.84	0.50
1:B:48:LYS:HD2	2:B:2024:HOH:O	2.12	0.50
1:D:59:MET:HE3	1:D:62:CRQ:CG2	2.42	0.50
1:E:219:CYS:HA	1:F:193[A]:LYS:HE2	1.92	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:62:CRQ:HD2	1:H:62:CRQ:N2	2.27	0.50
1:G:111:ASP:C	1:G:112:LYS:HD2	2.32	0.50
1:D:84:PRO:CD	1:D:85:GLU:H	2.23	0.49
1:A:92:ARG:NH1	1:A:94:GLU:OE2	2.44	0.49
1:D:193:LYS:HG3	1:D:217:HIS:CD2	2.48	0.49
1:D:148:ALA:HB1	1:D:186:LEU:HD13	1.93	0.49
1:F:200:LYS:HB2	1:F:209:GLU:HB2	1.93	0.49
1:G:170:TYR:HE1	1:H:147:THR:HG21	1.78	0.49
1:C:32:ASP:HB3	1:C:35:SER:OG	2.12	0.49
1:F:143:GLU:OE2	1:F:193[A]:LYS:HG3	2.12	0.49
1:D:59:MET:HE3	1:D:62:CRQ:CB2	2.43	0.49
1:F:81:GLY:O	1:F:181:LYS:HE3	2.13	0.49
1:C:121:LEU:HD22	1:C:123:VAL:HG13	1.95	0.49
1:G:149:LYS:HE2	1:H:96:GLU:OE1	2.12	0.49
2:A:2069:HOH:O	1:C:94:GLU:HG2	2.12	0.49
1:A:90:ASN:HB2	1:C:123:VAL:HG12	1.95	0.48
1:B:59:MET:HE3	1:B:93:ILE:HD11	1.94	0.48
1:A:88:GLN:HG2	1:A:106:ASP:OD2	2.13	0.48
1:D:62:CRQ:HB1	2:D:2143:HOH:O	2.13	0.48
1:A:62:CRQ:N2	1:A:62:CRQ:HD2	2.28	0.48
1:H:59:MET:HG2	1:H:62:CRQ:CD2	2.43	0.48
1:E:90:ASN:HD22	1:G:20:ASN:HD21	1.60	0.48
1:D:84:PRO:HD2	1:D:85:GLU:CD	2.31	0.47
1:C:57:ILE:CG2	2:C:2056:HOH:O	2.57	0.47
1:A:102:ASN:HB3	1:C:121:LEU:HD22	1.95	0.47
1:C:143:GLU:OE1	1:C:193[A]:LYS:CD	2.63	0.47
1:A:90:ASN:HD22	1:C:20:ASN:HD21	1.62	0.47
1:D:12:VAL:CG1	1:D:40[B]:LEU:HD11	2.44	0.47
1:D:17:ASN:HB3	1:D:121:LEU:HD23	1.95	0.47
1:G:84:PRO:CD	1:G:85:GLU:H	2.27	0.47
1:D:55:ASP:OD1	1:D:198:LYS:HE2	2.15	0.47
1:C:85:GLU:O	1:C:180:LYS:HD3	2.15	0.47
1:C:197:VAL:HG21	1:D:224:PRO:HD3	1.97	0.47
1:F:41:LYS:HZ3	1:F:43[B]:LYS:HE2	1.81	0.46
1:C:162:LEU:HD11	2:C:2151:HOH:O	2.15	0.46
1:C:147:THR:HG22	1:C:189:PHE:CD1	2.40	0.46
1:B:62:CRQ:HB1	2:B:2125:HOH:O	2.14	0.46
1:B:66:ARG:NE	1:B:66:ARG:HA	2.31	0.46
1:H:84:PRO:CD	1:H:85:GLU:H	2.29	0.46
1:B:150:ASN:ND2	1:D:128:ASN:HD21	2.13	0.46
1:B:48:LYS:HD3	1:B:49:PRO:O	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:219:CYS:SG	1:E:221:LEU:HB2	2.56	0.46
1:H:151:GLY:CA	1:H:186:LEU:HD11	2.46	0.46
1:H:88:GLN:HG2	1:H:106:ASP:OD2	2.16	0.46
1:D:78:TYR:HB2	1:D:187:PRO:HD3	1.96	0.46
1:A:84:PRO:CD	1:A:85:GLU:N	2.79	0.45
2:C:2149:HOH:O	1:D:145:THR:CG2	2.57	0.45
1:D:5:ASP:N	1:D:5:ASP:OD1	2.39	0.45
1:A:35:SER:OG	1:A:37:GLN:HG2	2.16	0.45
1:C:82:SER:HA	1:C:184:GLN:NE2	2.31	0.45
1:A:100:VAL:HG23	1:C:92:ARG:NH1	2.26	0.45
1:G:32:ASP:HB3	1:G:35:SER:OG	2.17	0.45
1:E:6:ASN:ND2	1:E:34:ASN:HD22	2.14	0.45
1:F:90:ASN:HD22	1:H:20:ASN:HD21	1.65	0.45
1:A:66:ARG:HA	1:A:66:ARG:NE	2.31	0.45
1:F:59:MET:HE3	1:F:93:ILE:HD11	1.99	0.45
1:B:24:GLU:HB2	1:B:45:ARG:HG3	1.99	0.45
1:B:121:LEU:CD2	1:B:123:VAL:HG13	2.46	0.45
1:H:24:GLU:HB2	1:H:45:ARG:HG3	1.99	0.45
1:C:156:PHE:CZ	1:D:170:TYR:CD1	3.05	0.45
1:B:20:ASN:HD21	1:D:90:ASN:HD22	1.65	0.45
1:D:204:GLY:HA2	2:D:2050:HOH:O	2.17	0.45
1:G:148:ALA:HB1	1:G:186:LEU:HD13	1.98	0.44
1:D:59:MET:CE	1:D:62:CRQ:CD1	2.95	0.44
1:G:62:CRQ:N	1:G:62:CRQ:HA31	2.31	0.44
1:G:11:SER:HB3	1:G:115:HIS:HD2	1.81	0.44
1:A:38:PHE:CZ	1:A:62:CRQ:HB11	2.53	0.44
1:F:41:LYS:HZ2	1:F:43[B]:LYS:HE2	1.81	0.44
1:D:38:PHE:CZ	1:D:62:CRQ:HB11	2.53	0.44
1:B:32:ASP:HB3	1:B:35:SER:OG	2.18	0.44
1:F:50:LEU:HA	1:F:51:PRO:HD3	1.85	0.44
1:A:39:SER:HA	1:A:62:CRQ:HE12	1.82	0.44
1:F:149:LYS:HE2	1:F:149:LYS:HB2	1.60	0.44
1:H:16:GLY:HA2	1:H:120:ALA:O	2.18	0.44
1:H:173:MET:HB2	1:H:173:MET:HE2	1.49	0.44
1:H:179:SER:OG	1:H:184:GLN:NE2	2.51	0.44
1:E:6:ASN:HD22	1:E:34:ASN:HD22	1.66	0.43
1:D:62:CRQ:HD2	1:D:62:CRQ:N2	2.33	0.43
1:B:84:PRO:HD2	1:B:85:GLU:H	1.82	0.43
1:F:20:ASN:HD21	1:H:90:ASN:HD22	1.65	0.43
1:D:193:LYS:CG	1:D:217:HIS:CD2	3.01	0.43
1:C:53:SER:OG	1:C:134:ASN:HA	2.17	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:82:SER:HA	1:C:184:GLN:HE22	1.83	0.43
1:A:11:SER:O	1:A:115:HIS:HA	2.18	0.43
1:A:115:HIS:HE1	2:A:2094:HOH:O	2.02	0.43
1:A:59:MET:HG2	1:A:62:CRQ:CD2	2.49	0.43
1:C:62:CRQ:HD2	1:C:62:CRQ:N2	2.34	0.43
1:C:107:ILE:HA	1:C:115:HIS:O	2.18	0.43
1:H:59:MET:HE1	1:H:159:LYS:HE2	2.00	0.43
1:C:84:PRO:HD2	1:C:85:GLU:H	1.82	0.43
1:E:179:SER:OG	1:E:184:GLN:NE2	2.52	0.43
1:E:115:HIS:HE1	2:E:2098:HOH:O	2.00	0.43
1:C:47:GLY:HA2	1:G:28:ILE:HG12	2.00	0.43
1:E:82:SER:HA	1:E:184:GLN:NE2	2.32	0.42
1:G:66:ARG:HA	1:G:66:ARG:NE	2.33	0.42
1:D:84:PRO:CD	1:D:85:GLU:N	2.81	0.42
1:H:66:ARG:HA	1:H:66:ARG:NE	2.34	0.42
1:C:66:ARG:NE	1:C:66:ARG:HA	2.35	0.42
1:H:198:LYS:HB2	1:H:198:LYS:HE3	1.92	0.42
1:G:179:SER:OG	1:G:184:GLN:NE2	2.51	0.42
1:C:106:ASP:OD1	1:C:180:LYS:CE	2.66	0.42
1:F:139:GLU:OE1	2:F:2132:HOH:O	2.21	0.42
1:G:35:SER:HA	1:G:70:LYS:HE3	2.00	0.42
1:C:33:PRO:HB2	1:C:80:LYS:HE3	2.01	0.42
1:C:51:PRO:HD2	1:C:52:PHE:CD2	2.53	0.42
1:C:148:ALA:HB1	1:C:186:LEU:HD13	2.02	0.42
1:A:49:PRO:HB3	1:A:204:GLY:HA3	2.01	0.42
1:A:38:PHE:HB3	1:A:68:PHE:CD2	2.55	0.42
1:B:84:PRO:CD	1:B:85:GLU:H	2.32	0.42
1:D:33:PRO:HB2	1:D:80:LYS:HE3	2.02	0.42
1:G:172:HIS:HE1	2:H:2133:HOH:O	2.01	0.42
1:B:27:GLY:HA2	1:B:41:LYS:O	2.20	0.42
1:F:62:CRQ:N2	1:F:62:CRQ:HD2	2.35	0.42
2:C:2180:HOH:O	1:D:219:CYS:SG	2.01	0.42
1:D:198:LYS:HB2	1:D:198:LYS:HE3	1.85	0.42
1:C:88:GLN:HG2	1:C:106:ASP:OD1	2.19	0.41
1:F:43[A]:LYS:HD3	2:F:2019:HOH:O	2.19	0.41
1:C:38:PHE:HB3	1:C:68:PHE:CD2	2.55	0.41
1:G:115:HIS:HE1	2:G:2106:HOH:O	2.02	0.41
1:G:88:GLN:HG2	1:G:106:ASP:OD1	2.20	0.41
1:C:84:PRO:CD	1:C:85:GLU:H	2.32	0.41
1:H:84:PRO:HD2	1:H:85:GLU:CD	2.38	0.41
1:E:168:TYR:CD1	1:F:147:THR:HG21	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:59:MET:HE3	1:G:93:ILE:HD11	2.02	0.41
1:E:59:MET:HE3	1:E:93:ILE:HD11	2.01	0.41
1:A:147:THR:CG2	1:B:170:TYR:CE2	3.02	0.41
1:H:35:SER:HA	1:H:70:LYS:HD2	2.01	0.41
1:D:66:ARG:NE	1:D:66:ARG:HA	2.35	0.41
1:F:66:ARG:NE	1:F:66:ARG:HA	2.36	0.41
1:H:10:VAL:CG2	1:H:40:LEU:CD2	2.83	0.41
1:C:25:TYR:OH	1:C:50:LEU:HG	2.20	0.41
1:A:82:SER:HA	1:A:184:GLN:NE2	2.35	0.41
1:F:88:GLN:HG2	1:F:106:ASP:OD2	2.20	0.41
1:C:179:SER:OG	1:C:184:GLN:NE2	2.53	0.41
1:H:62:CRQ:HB1	2:H:2135:HOH:O	2.20	0.41
1:G:224:PRO:HD2	1:H:195:ARG:HD3	2.03	0.41
1:H:82:SER:HA	1:H:184:GLN:NE2	2.36	0.41
1:F:38:PHE:CZ	1:F:62:CRQ:HB11	2.56	0.41
1:F:107:ILE:HA	1:F:115:HIS:O	2.20	0.41
1:C:16:GLY:HA2	1:C:120:ALA:O	2.21	0.40
1:C:193[A]:LYS:CD	2:C:2180:HOH:O	2.57	0.40
1:A:221:LEU:O	1:B:195:ARG:NH1	2.54	0.40
1:D:16:GLY:HA2	1:D:120:ALA:O	2.21	0.40
1:B:147:THR:CG2	1:B:189:PHE:CD1	2.99	0.40
1:G:16:GLY:HA3	1:G:23:PHE:CZ	2.57	0.40
1:A:16:GLY:HA2	1:A:120:ALA:O	2.21	0.40
1:B:147:THR:HG23	1:B:189:PHE:HD1	1.82	0.40
1:B:16:GLY:HA2	1:B:120:ALA:O	2.21	0.40
1:E:126:PRO:HA	1:E:127:PRO:HD3	1.99	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles ⓘ

### 5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	211/223 (95%)	205 (97%)	4 (2%)	2 (1%)	21	4
1	B	215/223 (96%)	209 (97%)	5 (2%)	1 (0%)	34	10
1	C	217/223 (97%)	209 (96%)	6 (3%)	2 (1%)	21	4
1	D	217/223 (97%)	211 (97%)	5 (2%)	1 (0%)	34	10
1	E	215/223 (96%)	209 (97%)	4 (2%)	2 (1%)	21	4
1	F	215/223 (96%)	211 (98%)	3 (1%)	1 (0%)	34	10
1	G	215/223 (96%)	209 (97%)	4 (2%)	2 (1%)	21	4
1	H	216/223 (97%)	211 (98%)	4 (2%)	1 (0%)	34	10
All	All	1721/1784 (96%)	1674 (97%)	35 (2%)	12 (1%)	26	6

All (12) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	E	112	LYS
1	G	223	LYS
1	A	84	PRO
1	H	84	PRO
1	B	84	PRO
1	C	84	PRO
1	C	111	ASP
1	D	84	PRO
1	E	84	PRO
1	G	84	PRO
1	A	111	ASP
1	F	84	PRO

### 5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	180/189 (95%)	173 (96%)	7 (4%)	39	7
1	B	184/189 (97%)	176 (96%)	8 (4%)	35	5
1	C	186/189 (98%)	179 (96%)	7 (4%)	40	7

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	D	186/189 (98%)	180 (97%)	6 (3%)	46	11
1	E	184/189 (97%)	176 (96%)	8 (4%)	35	5
1	F	184/189 (97%)	179 (97%)	5 (3%)	52	15
1	G	184/189 (97%)	178 (97%)	6 (3%)	45	10
1	H	185/189 (98%)	179 (97%)	6 (3%)	46	11
All	All	1473/1512 (97%)	1420 (96%)	53 (4%)	43	9

All (53) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	38	PHE
1	A	50	LEU
1	A	121	LEU
1	A	137	VAL
1	A	147	THR
1	A	181	LYS
1	A	200	LYS
1	B	8	LEU
1	B	38	PHE
1	B	45	ARG
1	B	48	LYS
1	B	73	GLU
1	B	110	LYS
1	B	139	GLU
1	B	149	LYS
1	C	8	LEU
1	C	9	SER
1	C	38	PHE
1	C	50	LEU
1	C	94	GLU
1	C	114	LEU
1	C	200	LYS
1	D	5	ASP
1	D	38	PHE
1	D	45	ARG
1	D	57	ILE
1	D	121	LEU
1	D	165	ASP
1	E	5	ASP
1	E	7	ASN

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Mol	Chain	Res	Type
1	E	38	PHE
1	E	110	LYS
1	E	121	LEU
1	E	138	MET
1	E	200	LYS
1	E	221	LEU
1	F	112	LYS
1	F	139	GLU
1	F	149	LYS
1	F	193[A]	LYS
1	F	193[B]	LYS
1	G	38	PHE
1	G	114	LEU
1	G	149	LYS
1	G	167	SER
1	G	207	MET
1	G	223	LYS
1	H	5	ASP
1	H	38	PHE
1	H	45	ARG
1	H	111	ASP
1	H	147	THR
1	H	181	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (39) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	20	ASN
1	A	37	GLN
1	A	115	HIS
1	A	124	ASN
1	A	184	GLN
1	B	20	ASN
1	B	37	GLN
1	B	90	ASN
1	B	150	ASN
1	C	6	ASN
1	C	20	ASN
1	C	37	GLN
1	C	90	ASN
1	C	134	ASN
1	C	150	ASN

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Mol	Chain	Res	Type
1	C	184	GLN
1	D	20	ASN
1	D	37	GLN
1	D	184	GLN
1	E	6	ASN
1	E	20	ASN
1	E	37	GLN
1	E	115	HIS
1	E	150	ASN
1	E	184	GLN
1	F	20	ASN
1	F	115	HIS
1	F	150	ASN
1	G	6	ASN
1	G	20	ASN
1	G	90	ASN
1	G	115	HIS
1	G	134	ASN
1	G	172	HIS
1	G	184	GLN
1	H	20	ASN
1	H	37	GLN
1	H	172	HIS
1	H	184	GLN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

8 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
1	CRQ	A	62	-	24,25,26	2.90	5 (20%)	25,34,36	5.74	9 (36%)
1	CRQ	B	62	1	24,25,26	2.90	6 (25%)	25,34,36	5.53	10 (40%)
1	CRQ	C	62	1	24,25,26	2.93	7 (29%)	25,34,36	5.29	9 (36%)
1	CRQ	D	62	1	24,25,26	2.87	5 (20%)	25,34,36	5.50	9 (36%)
1	CRQ	E	62	1	24,25,26	2.92	5 (20%)	25,34,36	5.48	8 (32%)
1	CRQ	F	62	1	24,25,26	2.92	5 (20%)	25,34,36	5.46	9 (36%)
1	CRQ	G	62	1	24,25,26	2.89	7 (29%)	25,34,36	5.37	9 (36%)
1	CRQ	H	62	1	24,25,26	2.94	5 (20%)	25,34,36	5.67	8 (32%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	CRQ	A	62	-	-	0/10/32/33	0/2/2/2
1	CRQ	B	62	1	-	0/10/32/33	0/2/2/2
1	CRQ	C	62	1	-	0/10/32/33	0/2/2/2
1	CRQ	D	62	1	-	0/10/32/33	0/2/2/2
1	CRQ	E	62	1	-	0/10/32/33	0/2/2/2
1	CRQ	F	62	1	-	0/10/32/33	0/2/2/2
1	CRQ	G	62	1	-	0/10/32/33	0/2/2/2
1	CRQ	H	62	1	-	0/10/32/33	0/2/2/2

All (45) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	G	62	CRQ	CA2-C2	-6.56	1.41	1.48
1	F	62	CRQ	CA2-C2	-6.37	1.41	1.48
1	H	62	CRQ	CA2-C2	-6.29	1.41	1.48
1	A	62	CRQ	CA2-C2	-6.16	1.41	1.48
1	B	62	CRQ	CA2-C2	-6.14	1.41	1.48
1	H	62	CRQ	OH-CZ	-6.06	1.22	1.37
1	D	62	CRQ	CA2-C2	-6.04	1.42	1.48
1	A	62	CRQ	OH-CZ	-5.97	1.22	1.37
1	C	62	CRQ	OH-CZ	-5.96	1.22	1.37
1	F	62	CRQ	OH-CZ	-5.94	1.22	1.37
1	D	62	CRQ	OH-CZ	-5.92	1.22	1.37
1	C	62	CRQ	CA2-C2	-5.89	1.42	1.48
1	B	62	CRQ	OH-CZ	-5.85	1.23	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	62	CRQ	OH-CZ	-5.84	1.23	1.37
1	G	62	CRQ	OH-CZ	-5.78	1.23	1.37
1	E	62	CRQ	CA2-C2	-5.73	1.42	1.48
1	C	62	CRQ	CG1-CB1	-2.39	1.45	1.52
1	C	62	CRQ	CG1-CD3	-2.15	1.42	1.51
1	G	62	CRQ	CE1-CD1	-2.07	1.35	1.38
1	G	62	CRQ	CG1-CB1	-2.06	1.45	1.52
1	B	62	CRQ	CG1-CB1	-2.00	1.46	1.52
1	G	62	CRQ	C1-N2	3.11	1.39	1.33
1	C	62	CRQ	C1-N2	3.22	1.39	1.33
1	D	62	CRQ	C1-N2	3.22	1.39	1.33
1	F	62	CRQ	C1-N2	3.28	1.40	1.33
1	E	62	CRQ	C1-N2	3.29	1.40	1.33
1	G	62	CRQ	CD3-NE1	3.35	1.43	1.32
1	H	62	CRQ	C1-N2	3.36	1.40	1.33
1	B	62	CRQ	CD3-NE1	3.38	1.43	1.32
1	A	62	CRQ	C1-N2	3.43	1.40	1.33
1	F	62	CRQ	CD3-NE1	3.44	1.43	1.32
1	C	62	CRQ	CD3-NE1	3.47	1.43	1.32
1	B	62	CRQ	C1-N2	3.48	1.40	1.33
1	E	62	CRQ	CD3-NE1	3.50	1.44	1.32
1	H	62	CRQ	CD3-NE1	3.58	1.44	1.32
1	D	62	CRQ	CD3-NE1	3.62	1.44	1.32
1	A	62	CRQ	CD3-NE1	3.78	1.44	1.32
1	G	62	CRQ	CB2-CA2	8.50	1.42	1.35
1	F	62	CRQ	CB2-CA2	8.84	1.42	1.35
1	B	62	CRQ	CB2-CA2	8.95	1.43	1.35
1	C	62	CRQ	CB2-CA2	8.97	1.43	1.35
1	D	62	CRQ	CB2-CA2	9.11	1.43	1.35
1	H	62	CRQ	CB2-CA2	9.16	1.43	1.35
1	A	62	CRQ	CB2-CA2	9.28	1.43	1.35
1	E	62	CRQ	CB2-CA2	9.63	1.43	1.35

All (71) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	62	CRQ	O2-C2-CA2	-11.28	124.85	130.95
1	H	62	CRQ	O2-C2-CA2	-10.46	125.30	130.95
1	E	62	CRQ	O2-C2-CA2	-8.88	126.15	130.95
1	D	62	CRQ	O2-C2-CA2	-8.86	126.16	130.95
1	F	62	CRQ	O2-C2-CA2	-8.77	126.21	130.95
1	G	62	CRQ	O2-C2-CA2	-7.99	126.63	130.95

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	62	CRQ	O2-C2-CA2	-7.92	126.67	130.95
1	F	62	CRQ	CB1-CA1-N	-7.18	111.74	124.94
1	C	62	CRQ	CB1-CA1-N	-7.06	111.97	124.94
1	D	62	CRQ	CB1-CA1-N	-6.93	112.20	124.94
1	B	62	CRQ	CB1-CA1-N	-6.91	112.24	124.94
1	A	62	CRQ	CB1-CA1-N	-6.56	112.89	124.94
1	A	62	CRQ	CG2-CB2-CA2	-6.49	121.80	130.22
1	E	62	CRQ	CB1-CA1-N	-6.39	113.19	124.94
1	H	62	CRQ	CG2-CB2-CA2	-6.37	121.95	130.22
1	D	62	CRQ	CG2-CB2-CA2	-6.11	122.29	130.22
1	C	62	CRQ	O2-C2-CA2	-6.11	127.65	130.95
1	A	62	CRQ	C2-CA2-N2	-6.10	104.05	108.91
1	H	62	CRQ	CB1-CA1-N	-5.99	113.93	124.94
1	C	62	CRQ	CG2-CB2-CA2	-5.80	122.68	130.22
1	B	62	CRQ	C2-CA2-N2	-5.80	104.28	108.91
1	G	62	CRQ	C2-CA2-N2	-5.77	104.30	108.91
1	B	62	CRQ	CG2-CB2-CA2	-5.71	122.81	130.22
1	G	62	CRQ	CB1-CA1-N	-5.66	114.53	124.94
1	G	62	CRQ	CG2-CB2-CA2	-5.57	122.98	130.22
1	F	62	CRQ	CG2-CB2-CA2	-5.55	123.01	130.22
1	D	62	CRQ	C2-CA2-N2	-5.52	104.51	108.91
1	F	62	CRQ	C2-CA2-N2	-5.43	104.58	108.91
1	E	62	CRQ	C2-CA2-N2	-5.38	104.61	108.91
1	E	62	CRQ	CG2-CB2-CA2	-5.26	123.39	130.22
1	H	62	CRQ	C2-CA2-N2	-5.24	104.73	108.91
1	C	62	CRQ	C2-CA2-N2	-5.18	104.78	108.91
1	F	62	CRQ	OE1-CD3-CG1	-4.10	109.10	121.05
1	C	62	CRQ	OE1-CD3-CG1	-3.62	110.50	121.05
1	G	62	CRQ	OE1-CD3-CG1	-3.51	110.83	121.05
1	E	62	CRQ	OE1-CD3-CG1	-3.50	110.86	121.05
1	H	62	CRQ	OE1-CD3-CG1	-3.17	111.80	121.05
1	D	62	CRQ	OE1-CD3-CG1	-3.05	112.15	121.05
1	B	62	CRQ	OE1-CD3-CG1	-2.66	113.30	121.05
1	A	62	CRQ	OE1-CD3-CG1	-2.52	113.69	121.05
1	C	62	CRQ	O2-C2-N3	-2.30	119.53	124.50
1	B	62	CRQ	O2-C2-N3	-2.09	119.99	124.50
1	B	62	CRQ	CG1-CD3-NE1	-2.06	110.07	116.53
1	G	62	CRQ	CD2-CG2-CB2	2.00	128.07	121.23
1	D	62	CRQ	CB2-CA2-C2	2.09	125.41	122.36
1	F	62	CRQ	C-CA3-N3	2.14	117.68	113.00
1	A	62	CRQ	CB2-CA2-C2	2.65	126.25	122.36
1	B	62	CRQ	CA3-N3-C2	2.74	128.46	123.99

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	G	62	CRQ	CA3-N3-C2	2.86	128.64	123.99
1	F	62	CRQ	CA3-N3-C2	3.03	128.92	123.99
1	C	62	CRQ	CA3-N3-C2	3.32	129.40	123.99
1	H	62	CRQ	CA3-N3-C2	4.04	130.57	123.99
1	A	62	CRQ	CA3-N3-C2	4.14	130.73	123.99
1	D	62	CRQ	CA3-N3-C2	4.20	130.83	123.99
1	E	62	CRQ	CA3-N3-C2	4.30	130.99	123.99
1	F	62	CRQ	CB1-CG1-CD3	11.64	166.46	113.86
1	A	62	CRQ	CB1-CG1-CD3	11.71	166.78	113.86
1	D	62	CRQ	CB1-CG1-CD3	11.93	167.79	113.86
1	E	62	CRQ	CB1-CG1-CD3	11.96	167.90	113.86
1	G	62	CRQ	CB1-CG1-CD3	11.99	168.02	113.86
1	C	62	CRQ	CB1-CG1-CD3	12.13	168.65	113.86
1	H	62	CRQ	CB1-CG1-CD3	12.24	169.17	113.86
1	B	62	CRQ	CB1-CG1-CD3	12.28	169.36	113.86
1	C	62	CRQ	CA2-C2-N3	18.74	112.80	103.40
1	F	62	CRQ	CA2-C2-N3	19.12	112.98	103.40
1	G	62	CRQ	CA2-C2-N3	19.15	113.00	103.40
1	D	62	CRQ	CA2-C2-N3	19.16	113.00	103.40
1	E	62	CRQ	CA2-C2-N3	19.40	113.13	103.40
1	B	62	CRQ	CA2-C2-N3	19.81	113.33	103.40
1	A	62	CRQ	CA2-C2-N3	19.81	113.33	103.40
1	H	62	CRQ	CA2-C2-N3	19.83	113.34	103.40

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

7 monomers are involved in 24 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	62	CRQ	10	0
1	B	62	CRQ	1	0
1	C	62	CRQ	1	0
1	D	62	CRQ	6	0
1	F	62	CRQ	2	0
1	G	62	CRQ	1	0
1	H	62	CRQ	3	0

## 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry

There are no ligands in this entry.

## 5.7 Other polymers

There are no such residues in this entry.

## 5.8 Polymer linkage issues

There are no chain breaks in this entry.

## 6 Fit of model and data ⓘ

### 6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
1	A	213/223 (95%)	1.75	63 (29%) 1 1	12, 20, 29, 35	3 (1%)
1	B	217/223 (97%)	1.28	34 (15%) 3 3	10, 16, 25, 36	1 (0%)
1	C	217/223 (97%)	1.31	43 (19%) 1 2	12, 16, 25, 40	0
1	D	218/223 (97%)	1.42	46 (21%) 1 1	10, 17, 25, 36	2 (0%)
1	E	217/223 (97%)	1.26	39 (17%) 2 2	11, 16, 24, 32	3 (1%)
1	F	215/223 (96%)	1.11	29 (13%) 4 4	11, 15, 21, 27	1 (0%)
1	G	217/223 (97%)	1.22	36 (16%) 2 2	10, 15, 23, 33	1 (0%)
1	H	218/223 (97%)	1.43	44 (20%) 1 2	11, 18, 27, 34	0
All	All	1732/1784 (97%)	1.35	334 (19%) 2 2	10, 16, 27, 40	11 (0%)

All (334) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	H	4	LEU	11.9
1	D	224	PRO	10.8
1	A	112	LYS	10.1
1	C	4	LEU	9.8
1	D	170	TYR	9.1
1	G	224	PRO	9.1
1	H	112	LYS	9.0
1	A	111	ASP	8.7
1	E	111	ASP	8.4
1	B	182	SER	7.6
1	B	112	LYS	7.5
1	C	111	ASP	7.2
1	H	113	VAL	7.2
1	A	109	TYR	6.9
1	A	7	ASN	6.7
1	B	111	ASP	6.6

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Mol	Chain	Res	Type	RSRZ
1	A	113	VAL	6.6
1	G	111	ASP	6.6
1	H	111	ASP	6.5
1	D	111	ASP	6.3
1	E	5	ASP	6.3
1	E	109	TYR	6.2
1	F	224	PRO	6.0
1	C	5	ASP	5.9
1	A	110	LYS	5.8
1	H	5	ASP	5.7
1	H	109	TYR	5.7
1	C	183	GLY	5.6
1	A	151	GLY	5.5
1	C	73	GLU	5.5
1	G	110	LYS	5.5
1	E	170	TYR	5.5
1	A	150	ASN	5.4
1	B	5	ASP	5.4
1	G	83	PHE	5.4
1	G	112	LYS	5.4
1	B	4	LEU	5.4
1	A	73	GLU	5.3
1	B	73	GLU	5.3
1	A	182	SER	5.2
1	G	5	ASP	5.2
1	E	7	ASN	5.2
1	D	112	LYS	5.0
1	E	110	LYS	5.0
1	G	170	TYR	4.9
1	G	73	GLU	4.8
1	B	170	TYR	4.8
1	C	112	LYS	4.7
1	A	83	PHE	4.7
1	G	47	GLY	4.6
1	B	6	ASN	4.6
1	H	7	ASN	4.6
1	D	213	TYR	4.6
1	E	74	GLY	4.6
1	A	28	ILE	4.6
1	H	128	ASN	4.6
1	B	83	PHE	4.5
1	E	83	PHE	4.5

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Mol	Chain	Res	Type	RSRZ
1	D	109	TYR	4.5
1	A	121	LEU	4.5
1	B	7	ASN	4.5
1	G	6	ASN	4.4
1	A	207	MET	4.4
1	B	110	LYS	4.4
1	D	40[A]	LEU	4.4
1	G	109	TYR	4.3
1	H	151	GLY	4.3
1	H	110	LYS	4.2
1	H	83	PHE	4.2
1	D	7	ASN	4.2
1	E	183	GLY	4.2
1	D	4	LEU	4.2
1	C	220	ASP	4.1
1	A	200	LYS	4.0
1	F	100	VAL	4.0
1	E	112	LYS	4.0
1	E	84	PRO	4.0
1	C	100	VAL	4.0
1	A	183	GLY	4.0
1	B	93	ILE	4.0
1	B	213	TYR	3.9
1	C	6	ASN	3.9
1	C	7	ASN	3.9
1	H	150	ASN	3.9
1	D	165	ASP	3.9
1	D	186	LEU	3.9
1	D	6	ASN	3.9
1	A	213	TYR	3.9
1	H	213	TYR	3.9
1	A	37	GLN	3.9
1	D	100	VAL	3.8
1	B	48	LYS	3.8
1	D	74	GLY	3.8
1	D	203	PRO	3.8
1	F	83	PHE	3.8
1	C	121	LEU	3.8
1	D	83	PHE	3.8
1	G	223	LYS	3.7
1	F	200	LYS	3.7
1	H	170	TYR	3.7

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Mol	Chain	Res	Type	RSRZ
1	H	73	GLU	3.7
1	G	93	ILE	3.7
1	E	100	VAL	3.7
1	D	5	ASP	3.6
1	A	201	VAL	3.6
1	D	110	LYS	3.6
1	D	113	VAL	3.6
1	D	207	MET	3.6
1	A	84	PRO	3.6
1	A	170	TYR	3.6
1	A	128	ASN	3.6
1	A	21	HIS	3.5
1	D	57	ILE	3.5
1	G	183	GLY	3.5
1	A	202	GLU	3.5
1	D	121	LEU	3.5
1	E	121	LEU	3.5
1	H	93	ILE	3.5
1	A	32	ASP	3.5
1	C	213	TYR	3.4
1	B	200	LYS	3.4
1	F	73	GLU	3.4
1	A	48	LYS	3.4
1	D	150	ASN	3.4
1	B	21	HIS	3.4
1	E	134	ASN	3.4
1	H	6	ASN	3.4
1	C	110	LYS	3.3
1	F	101	ILE	3.3
1	E	21	HIS	3.3
1	A	123	VAL	3.3
1	F	121	LEU	3.3
1	C	94	GLU	3.3
1	D	28	ILE	3.3
1	H	202	GLU	3.2
1	E	182	SER	3.2
1	B	121	LEU	3.2
1	D	202	GLU	3.2
1	B	183	GLY	3.2
1	A	186	LEU	3.1
1	H	47	GLY	3.1
1	H	121	LEU	3.1

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Mol	Chain	Res	Type	RSRZ
1	D	59	MET	3.1
1	D	84	PRO	3.1
1	F	28	ILE	3.1
1	C	170	TYR	3.1
1	E	221	LEU	3.1
1	E	207	MET	3.1
1	D	73	GLU	3.1
1	H	100	VAL	3.1
1	C	50	LEU	3.1
1	H	84	PRO	3.1
1	A	47	GLY	3.1
1	A	93	ILE	3.0
1	F	110	LYS	3.0
1	B	109	TYR	3.0
1	F	21	HIS	3.0
1	G	101	ILE	3.0
1	B	57	ILE	3.0
1	F	220	ASP	3.0
1	A	50	LEU	2.9
1	F	183	GLY	2.9
1	H	224	PRO	2.9
1	G	207	MET	2.9
1	F	178	ARG	2.9
1	H	200	LYS	2.9
1	G	7	ASN	2.9
1	E	203	PRO	2.9
1	A	34	ASN	2.9
1	A	68	PHE	2.9
1	F	147	THR	2.9
1	B	113	VAL	2.9
1	E	147	THR	2.8
1	H	87	PHE	2.8
1	E	200	LYS	2.8
1	C	28	ILE	2.8
1	A	164	LYS	2.8
1	E	73	GLU	2.8
1	B	123	VAL	2.8
1	D	218	VAL	2.8
1	E	213	TYR	2.8
1	C	84	PRO	2.8
1	A	59	MET	2.7
1	A	33	PRO	2.7

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Mol	Chain	Res	Type	RSRZ
1	B	101	ILE	2.7
1	E	28	ILE	2.7
1	F	7	ASN	2.7
1	H	207	MET	2.7
1	D	93	ILE	2.7
1	D	192	ILE	2.7
1	C	123	VAL	2.7
1	E	152	VAL	2.7
1	F	123	VAL	2.7
1	C	128	ASN	2.7
1	C	138	MET	2.7
1	H	147	THR	2.7
1	A	41	LYS	2.7
1	F	112	LYS	2.7
1	G	123	VAL	2.7
1	D	200	LYS	2.6
1	H	149	LYS	2.6
1	G	118	VAL	2.6
1	G	178	ARG	2.6
1	H	123	VAL	2.6
1	H	56	ILE	2.6
1	D	156	PHE	2.6
1	D	138	MET	2.6
1	F	213	TYR	2.6
1	B	118	VAL	2.6
1	E	138	MET	2.6
1	B	125	PHE	2.5
1	C	200	LYS	2.5
1	F	170	TYR	2.5
1	E	113	VAL	2.5
1	A	35	SER	2.5
1	G	182	SER	2.5
1	H	203	PRO	2.5
1	A	221	LEU	2.5
1	B	221	LEU	2.5
1	F	57	ILE	2.5
1	F	156	PHE	2.5
1	G	120	ALA	2.5
1	A	81	GLY	2.5
1	F	119	TRP	2.5
1	A	100	VAL	2.5
1	C	147	THR	2.5

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Mol	Chain	Res	Type	RSRZ
1	C	95	PHE	2.5
1	A	72	PRO	2.5
1	F	59	MET	2.5
1	F	193[A]	LYS	2.5
1	C	8	LEU	2.4
1	E	128	ASN	2.4
1	D	183	GLY	2.4
1	H	46	GLY	2.4
1	C	148	ALA	2.4
1	C	101	ILE	2.4
1	E	47	GLY	2.4
1	H	48	LYS	2.4
1	H	185	PRO	2.4
1	G	157	CYS	2.4
1	C	109	TYR	2.4
1	A	82	SER	2.4
1	H	201	VAL	2.4
1	A	40	LEU	2.4
1	F	89	TRP	2.4
1	A	38	PHE	2.4
1	A	87	PHE	2.4
1	C	113	VAL	2.4
1	E	123	VAL	2.4
1	A	147	THR	2.4
1	C	199	THR	2.4
1	G	147	THR	2.4
1	G	114	LEU	2.3
1	H	44	LEU	2.3
1	A	158	PRO	2.3
1	D	152	VAL	2.3
1	E	87	PHE	2.3
1	E	93	ILE	2.3
1	C	43[A]	LYS	2.3
1	A	92	ARG	2.3
1	B	219	CYS	2.3
1	A	44	LEU	2.3
1	E	50	LEU	2.3
1	G	121	LEU	2.3
1	E	202	GLU	2.3
1	C	192	ILE	2.3
1	E	43	LYS	2.3
1	B	100	VAL	2.3

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Mol	Chain	Res	Type	RSRZ
1	D	123	VAL	2.3
1	D	128	ASN	2.3
1	G	40	LEU	2.3
1	A	199	THR	2.2
1	F	182	SER	2.2
1	H	138	MET	2.2
1	A	95	PHE	2.2
1	C	83	PHE	2.2
1	G	156	PHE	2.2
1	F	84	PRO	2.2
1	C	193[A]	LYS	2.2
1	G	57	ILE	2.2
1	A	71	TYR	2.2
1	D	182	SER	2.2
1	A	209	GLU	2.2
1	G	84	PRO	2.2
1	H	59	MET	2.2
1	C	131	VAL	2.2
1	C	154	VAL	2.2
1	F	136	ILE	2.2
1	C	168	TYR	2.2
1	H	41	LYS	2.2
1	A	65	PHE	2.2
1	B	95	PHE	2.2
1	G	125	PHE	2.2
1	H	125	PHE	2.2
1	E	32	ASP	2.2
1	A	9	SER	2.2
1	C	182	SER	2.2
1	D	201	VAL	2.2
1	D	223	LYS	2.2
1	H	119	TRP	2.2
1	D	135	GLU	2.2
1	C	180	LYS	2.1
1	E	224	PRO	2.1
1	A	61	PHE	2.1
1	A	218	VAL	2.1
1	H	137	VAL	2.1
1	B	59	MET	2.1
1	C	119	TRP	2.1
1	B	178	ARG	2.1
1	A	185	PRO	2.1

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Mol	Chain	Res	Type	RSRZ
1	D	173	MET	2.1
1	H	171	GLY	2.1
1	C	32	ASP	2.1
1	G	200	LYS	2.1
1	A	114	LEU	2.1
1	G	50	LEU	2.1
1	D	34	ASN	2.1
1	G	74	GLY	2.1
1	B	61	PHE	2.1
1	G	113	VAL	2.1
1	A	56	ILE	2.1
1	A	75	ILE	2.1
1	D	221	LEU	2.1
1	E	57	ILE	2.1
1	D	72	PRO	2.0
1	F	139	GLU	2.0
1	B	12	VAL	2.0
1	H	152	VAL	2.0
1	C	221	LEU	2.0
1	A	76	ALA	2.0
1	C	76	ALA	2.0
1	G	56	ILE	2.0
1	B	174	THR	2.0
1	E	209	GLU	2.0

## 6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
1	CRQ	D	62	24/25	0.85	0.14	-	14,17,18,19	0
1	CRQ	G	62	24/25	0.90	0.14	-	11,14,16,17	0
1	CRQ	F	62	24/25	0.91	0.13	-	12,16,17,18	0
1	CRQ	C	62	24/25	0.87	0.14	-	12,15,16,17	0
1	CRQ	B	62	24/25	0.88	0.15	-	11,15,17,18	0
1	CRQ	E	62	24/25	0.86	0.14	-	14,16,17,18	0
1	CRQ	A	62	24/25	0.86	0.15	-	18,20,22,23	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
1	CRQ	H	62	24/25	0.87	0.13	-	15,17,18,19	0

### 6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

### 6.4 Ligands [i](#)

There are no ligands in this entry.

### 6.5 Other polymers [i](#)

There are no such residues in this entry.