



# Full wwPDB X-ray Structure Validation Report

Feb 26, 2014 – 04:37 PM GMT

PDB ID : 1C5F  
Title : CRYSTAL STRUCTURE OF THE CYCLOPHILIN-LIKE DOMAIN FROM  
BRUGIA MALAYI COMPLEXED WITH CYCLOSPORIN A  
Authors : Ellis, P.J.; Carlow, C.K.S.; Ma, D.; Kuhn, P.  
Deposited on : 1999-11-22  
Resolution : 2.47 Å(reported)

This is a full wwPDB 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/ValidationPDFNotes.html>

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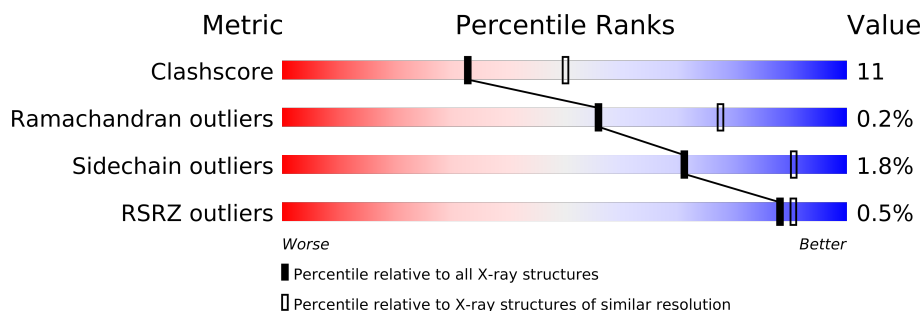
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.15 2013  
Xtriage (Phenix) : dev-1323  
EDS : stable22639  
Percentile statistics : 21963  
Refmac : 5.8.0049  
CCP4 : 6.3.0 (Settle)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)  
Validation Pipeline (wwPDB-VP) : stable22683

# 1 Overall quality at a glance

The reported resolution of this entry is 2.47 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))
Clashscore	79885	4136 (2.50-2.46)
Ramachandran outliers	78287	4052 (2.50-2.46)
Sidechain outliers	78261	4054 (2.50-2.46)
RSRZ outliers	66119	3279 (2.50-2.46)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	177	
1	C	177	
1	E	177	
1	G	177	
1	I	177	
1	K	177	
1	M	177	
1	O	177	
2	B	11	
2	D	11	
2	F	11	
2	H	11	
2	J	11	
2	L	11	
2	N	11	
2	P	11	

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 11774 atoms, of which 0 are hydrogen and 0 are deuterium.

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 PEPTIDYL-PROLYL CIS-TRANS ISOMERASE 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	177	Total	C	N	O	S	9	0	0
			1365	862	237	255	11			
1	C	177	Total	C	N	O	S	6	0	0
			1365	862	237	255	11			
1	E	174	Total	C	N	O	S	5	0	0
			1342	848	233	251	10			
1	G	172	Total	C	N	O	S	3	0	0
			1325	838	230	247	10			
1	I	173	Total	C	N	O	S	10	0	0
			1333	842	231	250	10			
1	K	175	Total	C	N	O	S	3	0	0
			1351	854	235	252	10			
1	M	175	Total	C	N	O	S	4	0	0
			1351	854	235	252	10			
1	O	172	Total	C	N	O	S	5	0	0
			1325	838	230	247	10			

- Molecule 2 is a protein called CYCLOSPORIN A.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	B	11	Total	C	N	O	0	0	0
			85	62	11	12			
2	D	11	Total	C	N	O	0	0	0
			85	62	11	12			
2	F	11	Total	C	N	O	2	0	0
			85	62	11	12			
2	H	11	Total	C	N	O	0	0	0
			85	62	11	12			
2	J	11	Total	C	N	O	2	0	0
			85	62	11	12			
2	L	11	Total	C	N	O	0	0	0
			85	62	11	12			

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	N	11	Total	C	N	O	0	0	0
			85	62	11	12			
2	P	11	Total	C	N	O	0	0	0
			85	62	11	12			

- Molecule 3 is water.

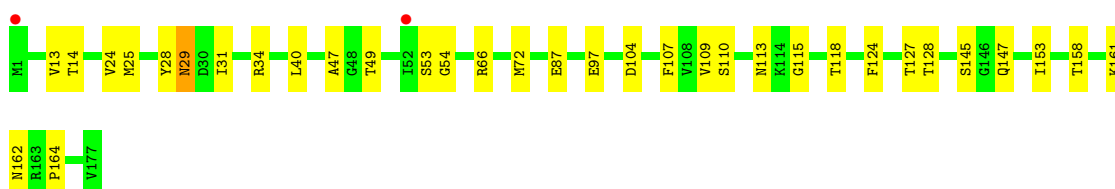
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	40	Total	O	0	0
			40	40		
3	B	1	Total	O	0	0
			1	1		
3	C	49	Total	O	0	0
			49	49		
3	D	3	Total	O	0	0
			3	3		
3	E	44	Total	O	0	0
			44	44		
3	F	1	Total	O	0	0
			1	1		
3	G	30	Total	O	0	0
			30	30		
3	H	2	Total	O	0	0
			2	2		
3	I	24	Total	O	0	0
			24	24		
3	J	2	Total	O	0	0
			2	2		
3	K	51	Total	O	0	0
			51	51		
3	L	3	Total	O	0	0
			3	3		
3	M	45	Total	O	0	0
			45	45		
3	N	1	Total	O	0	0
			1	1		
3	O	41	Total	O	0	0
			41	41		

### 3 Residue-property plots

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: PEPTIDYL-PROLYL CIS-TRANS ISOMERASE 1

Chain A: 



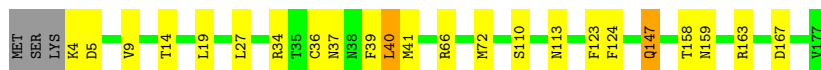
- Molecule 1: PEPTIDYL-PROLYL CIS-TRANS ISOMERASE 1

Chain C: 



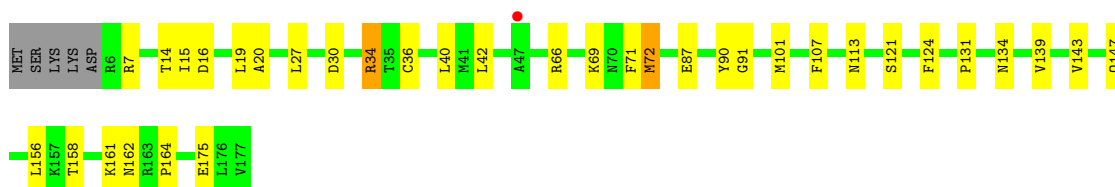
- Molecule 1: PEPTIDYL-PROLYL CIS-TRANS ISOMERASE 1

Chain E: 



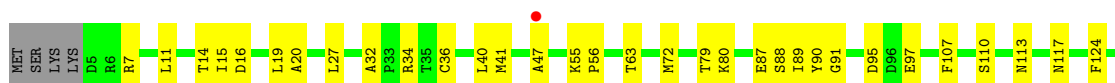
- Molecule 1: PEPTIDYL-PROLYL CIS-TRANS ISOMERASE 1

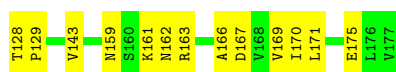
Chain G: 



- Molecule 1: PEPTIDYL-PROLYL CIS-TRANS ISOMERASE 1

Chain I: 





- Molecule 1: PEPTIDYL-PROLYL CIS-TRANS ISOMERASE 1

Chain K:



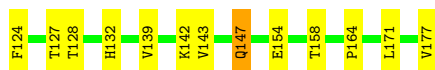
- Molecule 1: PEPTIDYL-PROLYL CIS-TRANS ISOMERASE 1

Chain M:



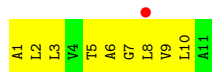
- Molecule 1: PEPTIDYL-PROLYL CIS-TRANS ISOMERASE 1

Chain O:



- Molecule 2: CYCLOSPORIN A

Chain B:



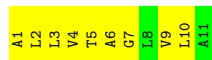
- Molecule 2: CYCLOSPORIN A

Chain D:



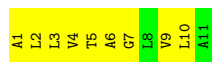
- Molecule 2: CYCLOSPORIN A

Chain F:



- Molecule 2: CYCLOSPORIN A

Chain H:



- Molecule 2: CYCLOSPORIN A

Chain J: 

A1	L2	L3	V4	T5	A6	G7	A11
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- Molecule 2: CYCLOSPORIN A

Chain L: 

A1	L2	L3	V4	T5	A6	G7	A11
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- Molecule 2: CYCLOSPORIN A

Chain N: 

A1	L2	L3	V4	T5	A6	G7	L8	V9	L10	A11
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- Molecule 2: CYCLOSPORIN A

Chain P: 

A1	L2	L3	V4	T5	A6	G7	L8	V9	L10	A11
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## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	62.00Å 100.16Å 133.92Å 90.00° 93.75° 90.00°	Depositor
Resolution (Å)	47.10 – 2.47 46.95 – 2.47	Depositor EDS
% Data completeness (in resolution range)	95.1 (47.10-2.47) 95.8 (46.95-2.47)	Depositor EDS
$R_{merge}$	0.12	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.83 (at 2.48Å)	Xtriage
Refinement program	CNS	Depositor
R, $R_{free}$	0.201 , 0.249 0.201 , (Not available)	Depositor DCC
$R_{free}$ test set	No test flags present.	DCC
Wilson B-factor (Å <sup>2</sup> )	43.0	Xtriage
Anisotropy	0.526	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 27.0	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	1 of 56200 reflections (0.002%)	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	11774	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	43.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 17.12% of the height of the origin peak. No significant pseudotranslation is detected.*

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



## 5 Model quality ⓘ

### 5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: ABA, MLE, DAL, MVA, BMT, SAR

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	0.37	0/1391	0.62	0/1872
1	C	0.39	0/1391	0.64	0/1872
1	E	0.40	0/1368	0.66	0/1843
1	G	0.37	0/1351	0.62	0/1821
1	I	0.36	0/1359	0.61	0/1832
1	K	0.38	0/1377	0.63	0/1854
1	M	0.38	0/1377	0.64	0/1854
1	O	0.37	0/1351	0.62	0/1821
2	B	0.30	0/10	0.58	0/11
2	D	0.23	0/10	0.74	0/11
2	F	0.32	0/10	0.68	0/11
2	H	0.32	0/10	0.63	0/11
2	J	0.24	0/10	0.69	0/11
2	L	0.45	0/10	0.60	0/11
2	N	0.33	0/10	0.68	0/11
2	P	0.25	0/10	0.69	0/11
All	All	0.38	0/11045	0.63	0/14857

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the

chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1365	0	1365	19	0
1	C	1365	0	1365	16	0
1	E	1342	0	1335	18	0
1	G	1325	0	1318	27	0
1	I	1333	0	1322	29	0
1	K	1351	0	1348	18	0
1	M	1351	0	1348	21	0
1	O	1325	0	1318	39	0
2	B	85	0	110	10	0
2	D	85	0	109	9	0
2	F	85	0	109	13	0
2	H	85	0	109	12	0
2	J	85	0	110	10	0
2	L	85	0	110	10	0
2	N	85	0	109	15	0
2	P	85	0	109	18	0
3	A	40	0	0	1	0
3	B	1	0	0	0	0
3	C	49	0	0	0	0
3	D	3	0	0	0	0
3	E	44	0	0	1	0
3	F	1	0	0	0	0
3	G	30	0	0	0	0
3	H	2	0	0	0	0
3	I	24	0	0	1	0
3	J	2	0	0	0	0
3	K	51	0	0	2	0
3	L	3	0	0	0	0
3	M	45	0	0	2	0
3	N	1	0	0	0	0
3	O	41	0	0	8	0
All	All	11774	0	11594	257	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 11.

All (257) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:J:5:BMT:HZ	2:J:5:BMT:HD11	1.59	0.83
1:E:34:ARG:HH12	2:P:8:MLE:HD12	1.45	0.81

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:O:68:ILE:HB	3:O:2018:HOH:O	1.84	0.77
1:M:69:LYS:HA	3:M:2016:HOH:O	1.85	0.75
1:M:51:LYS:H	1:M:51:LYS:HD2	1.50	0.75
1:O:51:LYS:HE2	3:O:2009:HOH:O	1.86	0.74
1:O:104:ASP:HB3	3:O:2028:HOH:O	1.86	0.73
1:G:7:ARG:HD3	1:G:175:GLU:OE1	1.87	0.73
2:D:1:DAL:C	2:D:3:MLE:HN1	2.20	0.72
1:M:161:LYS:O	1:M:162:ASN:HB2	1.90	0.71
1:E:66:ARG:HH22	2:F:3:MLE:HN3	1.55	0.71
2:L:1:DAL:C	2:L:3:MLE:HN1	2.21	0.69
1:E:34:ARG:NH1	2:P:8:MLE:HD12	2.08	0.68
1:O:110:SER:HB3	1:O:124:PHE:CZ	2.29	0.68
1:M:66:ARG:HH22	2:N:3:MLE:HN3	1.59	0.67
1:A:24:VAL:HB	1:A:145:SER:HB3	1.78	0.66
1:A:25:MET:SD	1:A:109:VAL:HG21	2.37	0.65
2:J:5:BMT:HD11	2:J:5:BMT:CZ	2.25	0.65
1:E:14:THR:HG22	1:E:19:LEU:HD23	1.78	0.65
1:O:72:MET:HE3	3:O:2018:HOH:O	1.95	0.65
3:K:2038:HOH:O	2:L:3:MLE:HD23	1.95	0.65
2:J:1:DAL:C	2:J:3:MLE:HN1	2.25	0.65
2:H:1:DAL:C	2:H:3:MLE:HN1	2.27	0.64
1:G:101:MET:HB2	1:G:139:VAL:HB	1.80	0.64
1:E:159:ASN:ND2	1:E:163:ARG:HB3	2.12	0.63
1:I:34:ARG:HB2	1:I:97:GLU:CD	2.19	0.63
1:C:3:LYS:HD3	1:C:3:LYS:O	2.00	0.62
2:P:6:ABA:C	2:P:8:MLE:HN1	2.30	0.61
1:M:124:PHE:CD1	2:N:4:MVA:HG11	2.36	0.61
1:O:40:LEU:HD23	1:O:40:LEU:O	2.00	0.61
1:G:40:LEU:O	1:G:40:LEU:HD23	2.01	0.61
1:M:51:LYS:N	1:M:51:LYS:HD2	2.15	0.61
1:G:7:ARG:HD2	1:G:40:LEU:CD1	2.31	0.60
1:M:51:LYS:H	1:M:51:LYS:CD	2.15	0.60
1:E:9:VAL:CG1	1:E:40:LEU:HD22	2.32	0.60
1:I:107:PHE:HB3	1:I:143:VAL:HB	1.84	0.60
1:I:124:PHE:CD2	2:J:4:MVA:HG11	2.36	0.59
2:H:2:MLE:HD13	1:O:132:HIS:HA	1.84	0.59
1:M:40:LEU:HD23	1:M:40:LEU:C	2.23	0.59
1:E:113:ASN:O	2:F:5:BMT:HA	2.03	0.58
1:O:114:LYS:HG2	1:O:118:THR:HB	1.84	0.58
2:P:7:SAR:N	2:P:8:MLE:HN1	2.18	0.58
1:O:147:GLN:H	1:O:147:GLN:CD	2.07	0.58
2:H:1:DAL:O	2:H:3:MLE:HN1	2.04	0.57

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:K:110:SER:HB3	1:K:124:PHE:CE1	2.39	0.57
1:O:12:ASP:OD1	1:O:22:ARG:HB2	2.04	0.57
1:K:110:SER:HB3	1:K:124:PHE:CZ	2.39	0.57
1:O:72:MET:HG3	3:O:2018:HOH:O	2.04	0.57
1:G:113:ASN:O	2:H:5:BMT:HA	2.05	0.57
1:A:115:GLY:O	1:A:118:THR:OG1	2.22	0.57
1:A:34:ARG:HB2	1:A:97:GLU:CD	2.25	0.57
2:B:1:DAL:C	2:B:3:MLE:HN1	2.34	0.57
2:D:5:BMT:O	2:D:7:SAR:HN1	2.04	0.56
1:O:113:ASN:HB2	1:O:118:THR:OG1	2.05	0.56
1:G:87:GLU:O	1:G:121:SER:HB3	2.04	0.56
1:K:107:PHE:HA	1:K:126:THR:O	2.05	0.56
1:G:66:ARG:HH22	2:H:3:MLE:HN3	1.70	0.56
1:O:70:ASN:O	1:O:128:THR:HG21	2.06	0.56
2:L:1:DAL:O	2:L:3:MLE:HN1	2.06	0.55
1:A:47:ALA:HB3	3:A:2013:HOH:O	2.05	0.55
1:O:38:ASN:HA	1:O:89:ILE:CD1	2.37	0.55
2:P:5:BMT:HD22	2:P:10:MLE:HN2	1.87	0.55
2:D:2:MLE:N	2:D:3:MLE:HN1	2.19	0.55
1:G:158:THR:HG22	1:G:164:PRO:HA	1.88	0.55
2:P:3:MLE:HD13	2:P:10:MLE:HB3	1.87	0.54
1:K:24:VAL:HB	1:K:145:SER:HB3	1.88	0.54
1:I:79:THR:O	1:I:80:LYS:HD3	2.08	0.54
1:E:66:ARG:NH2	2:F:3:MLE:HN3	2.22	0.54
2:F:5:BMT:O	2:F:7:SAR:HN1	2.08	0.54
1:O:177:VAL:O	1:O:177:VAL:HG23	2.08	0.53
1:G:101:MET:CB	1:G:139:VAL:HB	2.39	0.53
1:K:70:ASN:O	1:K:128:THR:HG21	2.08	0.53
1:C:12:ASP:OD1	1:C:22:ARG:HB2	2.08	0.53
1:K:126:THR:HG21	3:K:2033:HOH:O	2.08	0.53
1:I:41:MET:HB2	1:I:89:ILE:HG21	1.91	0.53
1:G:124:PHE:CD2	2:H:4:MVA:HG11	2.43	0.52
1:K:136:ILE:HG13	1:K:137:HIS:CD2	2.44	0.52
1:E:159:ASN:HD21	1:E:163:ARG:HB3	1.74	0.52
1:O:107:PHE:HB3	1:O:143:VAL:HB	1.92	0.52
2:B:2:MLE:N	2:B:3:MLE:HN1	2.23	0.52
1:I:63:THR:HG22	1:I:169:VAL:HG22	1.91	0.52
1:A:49:THR:HG23	1:A:54:GLY:O	2.10	0.52
1:A:28:TYR:HD1	1:A:31:ILE:HD12	1.75	0.52
1:O:40:LEU:C	1:O:40:LEU:HD23	2.31	0.51
1:A:113:ASN:O	2:B:5:BMT:HA	2.11	0.51
1:I:55:LYS:HB3	1:I:56:PRO:HD2	1.91	0.51

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:I:47:ALA:HB3	3:I:2008:HOH:O	2.10	0.51
1:A:107:PHE:CE1	1:A:127:THR:HG22	2.45	0.51
2:H:3:MLE:HN3	2:H:3:MLE:O	2.11	0.51
1:O:95:ASP:HA	1:O:117:ASN:HB3	1.94	0.50
2:F:1:DAL:C	2:F:3:MLE:HN1	2.41	0.50
2:B:6:ABA:C	2:B:8:MLE:HN1	2.41	0.50
1:G:71:PHE:CD2	1:G:72:MET:HG3	2.47	0.50
1:O:87:GLU:O	1:O:121:SER:HB3	2.11	0.50
2:N:1:DAL:C	2:N:3:MLE:HN1	2.41	0.49
2:L:5:BMT:O	2:L:7:SAR:HN1	2.11	0.49
1:O:38:ASN:HA	1:O:89:ILE:HD13	1.95	0.49
1:M:66:ARG:NH2	2:N:3:MLE:HN3	2.25	0.49
1:I:34:ARG:HB2	1:I:97:GLU:OE2	2.13	0.49
1:K:73:ILE:O	1:K:73:ILE:HG13	2.12	0.49
1:I:95:ASP:HA	1:I:117:ASN:HB3	1.95	0.49
2:B:5:BMT:O	2:B:7:SAR:HN1	2.13	0.49
1:K:100:VAL:O	1:K:102:LYS:HE3	2.13	0.49
2:J:2:MLE:N	2:J:3:MLE:HN1	2.24	0.49
1:I:32:ALA:HB1	1:I:97:GLU:OE1	2.13	0.48
1:I:87:GLU:HG2	1:I:88:SER:N	2.28	0.48
2:F:1:DAL:HA	2:F:2:MLE:HN1	1.49	0.48
2:J:6:ABA:HA	2:J:7:SAR:HN1	1.61	0.48
1:M:159:ASN:HD21	1:M:163:ARG:HB3	1.78	0.48
2:J:5:BMT:CD1	2:J:5:BMT:HZ	2.37	0.48
1:K:113:ASN:O	2:L:5:BMT:HA	2.13	0.48
1:I:40:LEU:HD23	1:I:40:LEU:C	2.34	0.48
1:I:15:ILE:HG13	1:I:20:ALA:HB2	1.95	0.48
1:O:70:ASN:N	1:O:154:GLU:OE2	2.47	0.48
1:I:7:ARG:NH2	1:I:175:GLU:OE2	2.47	0.48
1:C:124:PHE:CD1	2:D:4:MVA:HG11	2.48	0.48
2:L:2:MLE:N	2:L:3:MLE:HN1	2.26	0.47
2:N:1:DAL:O	2:N:2:MLE:HD22	2.14	0.47
1:C:113:ASN:O	2:D:5:BMT:HA	2.13	0.47
1:E:110:SER:HB3	1:E:124:PHE:CZ	2.49	0.47
2:B:9:VAL:HA	2:B:10:MLE:HN1	1.49	0.47
1:G:40:LEU:C	1:G:40:LEU:HD23	2.34	0.47
2:H:9:VAL:HA	2:H:10:MLE:HN1	1.50	0.47
1:I:110:SER:HB3	1:I:124:PHE:CZ	2.49	0.47
1:G:42:LEU:HD13	1:G:121:SER:HB2	1.95	0.47
1:G:15:ILE:O	1:G:16:ASP:HB2	2.13	0.47
2:F:3:MLE:HD13	2:F:10:MLE:HB3	1.97	0.47
2:B:7:SAR:N	2:B:8:MLE:HN1	2.29	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:G:15:ILE:HD13	1:G:20:ALA:CB	2.44	0.47
2:P:1:DAL:HA	2:P:2:MLE:HN1	1.50	0.47
1:O:122:GLN:CD	2:P:6:ABA:HG2	2.35	0.46
2:L:5:BMT:HZ	2:L:5:BMT:HD13	1.96	0.46
1:O:158:THR:HG22	1:O:164:PRO:HA	1.96	0.46
1:I:7:ARG:HH11	1:I:7:ARG:HG3	1.80	0.46
1:O:32:ALA:HB2	3:O:2026:HOH:O	2.14	0.46
2:P:9:VAL:HA	2:P:10:MLE:HN1	1.47	0.46
1:M:40:LEU:O	1:M:40:LEU:HD23	2.15	0.46
1:I:11:LEU:HD22	1:I:170:ILE:HD13	1.97	0.46
2:B:6:ABA:HA	2:B:7:SAR:HN1	1.74	0.46
1:G:15:ILE:HD13	1:G:20:ALA:HB2	1.96	0.46
2:P:3:MLE:O	2:P:3:MLE:HN3	2.16	0.46
2:L:1:DAL:HA	2:L:2:MLE:HN1	1.49	0.46
1:C:81:GLY:O	1:C:163:ARG:NH2	2.43	0.46
2:D:9:VAL:HA	2:D:10:MLE:HN1	1.53	0.46
1:G:27:LEU:HB3	1:G:36:CYS:SG	2.56	0.46
1:M:161:LYS:O	1:M:162:ASN:CB	2.62	0.45
2:H:1:DAL:HB1	3:O:2031:HOH:O	2.15	0.45
2:B:1:DAL:HA	2:B:2:MLE:HN1	1.52	0.45
1:C:40:LEU:C	1:C:40:LEU:HD23	2.37	0.45
2:P:5:BMT:O	2:P:7:SAR:HN1	2.17	0.45
1:G:161:LYS:O	1:G:162:ASN:HB2	2.16	0.45
1:K:128:THR:OG1	1:K:129:PRO:HD2	2.17	0.45
1:C:157:LYS:HD3	1:C:165:LEU:HD12	1.98	0.45
2:N:4:MVA:HA	2:N:5:BMT:HN1	1.69	0.45
1:A:34:ARG:HB2	1:A:97:GLU:OE2	2.16	0.45
1:A:29:ASN:N	1:A:29:ASN:OD1	2.49	0.45
2:P:1:DAL:C	2:P:3:MLE:HN1	2.46	0.45
2:P:6:ABA:HA	2:P:7:SAR:HN1	1.68	0.45
1:K:12:ASP:OD1	1:K:22:ARG:HB2	2.16	0.45
2:F:9:VAL:HA	2:F:10:MLE:HN1	1.48	0.45
2:N:1:DAL:HA	2:N:2:MLE:HN1	1.50	0.45
2:J:1:DAL:HA	2:J:2:MLE:HN1	1.54	0.45
1:O:114:LYS:HG2	1:O:118:THR:CB	2.46	0.45
1:K:55:LYS:HB3	1:K:56:PRO:HD2	1.98	0.45
1:A:158:THR:HG22	1:A:164:PRO:HA	1.98	0.44
1:O:65:HIS:CE1	1:O:74:GLN:HG2	2.51	0.44
1:C:110:SER:HB3	1:C:124:PHE:CZ	2.51	0.44
1:K:40:LEU:C	1:K:40:LEU:HD13	2.38	0.44
1:G:107:PHE:HB3	1:G:143:VAL:HB	1.98	0.44
2:H:3:MLE:HB2	2:H:4:MVA:HN1	1.99	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:N:3:MLE:HA	2:N:4:MVA:HN1	1.82	0.44
1:M:124:PHE:CG	2:N:4:MVA:HG11	2.51	0.44
1:K:136:ILE:HG13	1:K:137:HIS:HD2	1.83	0.44
1:E:158:THR:HA	1:E:163:ARG:O	2.17	0.44
1:M:138:VAL:HG21	3:M:2010:HOH:O	2.18	0.44
1:I:14:THR:HG23	1:I:171:LEU:HB2	1.99	0.44
2:N:9:VAL:HA	2:N:10:MLE:HN1	1.45	0.44
2:F:2:MLE:N	2:F:3:MLE:HN1	2.33	0.43
2:D:5:BMT:C	2:D:7:SAR:HN1	2.48	0.43
1:E:39:PHE:HE1	1:E:123:PHE:CD2	2.36	0.43
2:P:4:MVA:HA	2:P:5:BMT:HN1	1.66	0.43
1:G:30:ASP:N	1:G:30:ASP:OD2	2.51	0.43
1:M:110:SER:HB3	1:M:124:PHE:CZ	2.53	0.43
1:A:66:ARG:HH22	2:B:3:MLE:HN3	1.84	0.43
1:I:27:LEU:HB3	1:I:36:CYS:SG	2.57	0.43
1:A:161:LYS:O	1:A:162:ASN:HB2	2.18	0.43
1:M:53:SER:OG	1:M:55:LYS:HB2	2.18	0.43
1:A:40:LEU:HD23	1:A:40:LEU:C	2.38	0.43
1:I:113:ASN:O	2:J:5:BMT:HA	2.19	0.43
1:G:7:ARG:HD2	1:G:40:LEU:HD11	1.99	0.43
2:L:5:BMT:C	2:L:7:SAR:HN1	2.48	0.43
2:F:3:MLE:O	2:F:3:MLE:HN3	2.19	0.42
1:C:3:LYS:HD3	1:C:3:LYS:C	2.39	0.42
2:F:3:MLE:HA	2:F:4:MVA:HN1	1.84	0.42
2:L:6:ABA:HA	2:L:7:SAR:HN1	1.79	0.42
1:C:101:MET:HB2	1:C:139:VAL:HB	2.02	0.42
1:C:155:TYR:CD1	1:E:147:GLN:HG3	2.54	0.42
1:I:7:ARG:NH1	1:I:7:ARG:HG3	2.35	0.42
1:G:69:LYS:HB3	1:G:69:LYS:HE2	1.76	0.42
2:H:2:MLE:N	2:H:3:MLE:HN1	2.33	0.42
1:O:87:GLU:HG2	1:O:88:SER:N	2.35	0.42
1:G:14:THR:HG22	1:G:19:LEU:HD23	2.02	0.42
1:K:5:ASP:O	1:K:7:ARG:HG2	2.20	0.42
1:I:19:LEU:HD13	1:O:171:LEU:HD23	2.02	0.42
1:G:7:ARG:HD2	1:G:40:LEU:HD13	2.02	0.42
2:N:5:BMT:O	2:N:7:SAR:HN1	2.20	0.42
1:E:14:THR:HG22	1:E:19:LEU:HA	2.02	0.42
1:O:72:MET:SD	1:O:72:MET:C	2.98	0.42
2:H:6:ABA:HA	2:H:7:SAR:HN1	1.74	0.42
1:G:34:ARG:HG3	1:G:90:TYR:OH	2.20	0.42
1:O:49:THR:HG22	1:O:50:GLY:N	2.35	0.42
1:M:114:LYS:HD3	2:N:6:ABA:O	2.19	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:O:67:VAL:HG23	1:O:67:VAL:O	2.20	0.42
1:M:131:PRO:HA	1:M:134:ASN:ND2	2.34	0.42
1:O:38:ASN:O	1:O:42:LEU:HG	2.20	0.41
1:M:52:ILE:HG22	1:M:53:SER:N	2.35	0.41
1:A:13:VAL:HG12	1:A:14:THR:N	2.35	0.41
1:I:161:LYS:O	1:I:162:ASN:HB2	2.19	0.41
2:N:2:MLE:N	2:N:3:MLE:HN1	2.34	0.41
2:N:7:SAR:HA2	2:N:8:MLE:HN1	1.86	0.41
1:K:109:VAL:HG12	1:K:140:PHE:CZ	2.55	0.41
2:D:4:MVA:HA	2:D:5:BMT:HN1	1.78	0.41
1:O:38:ASN:OD1	1:O:89:ILE:HG12	2.20	0.41
1:G:156:LEU:O	1:G:158:THR:HG23	2.21	0.41
1:C:107:PHE:HA	1:C:126:THR:O	2.20	0.41
2:P:2:MLE:N	2:P:3:MLE:HN1	2.36	0.41
1:E:27:LEU:HB3	1:E:36:CYS:SG	2.61	0.41
1:E:4:LYS:HB2	3:E:2002:HOH:O	2.21	0.41
1:C:148:GLU:HG2	1:C:149:VAL:N	2.36	0.41
1:K:57:LEU:HD13	1:K:89:ILE:HA	2.01	0.41
1:O:122:GLN:NE2	2:P:6:ABA:HG2	2.36	0.41
1:C:57:LEU:HD13	1:C:89:ILE:HA	2.01	0.41
1:E:34:ARG:NH1	2:P:8:MLE:HD23	2.36	0.41
2:D:1:DAL:HA	2:D:2:MLE:HN1	1.50	0.41
2:F:6:ABA:HA	2:F:7:SAR:HN1	1.73	0.41
1:A:53:SER:OG	1:A:87:GLU:OE1	2.34	0.41
1:O:101:MET:HB2	1:O:139:VAL:HB	2.02	0.41
2:N:6:ABA:HA	2:N:7:SAR:HN1	1.74	0.41
1:C:77:ASP:OD1	1:C:77:ASP:C	2.59	0.41
1:G:131:PRO:HA	1:G:134:ASN:ND2	2.36	0.41
1:I:16:ASP:HB2	1:I:166:ALA:HB1	2.02	0.41
1:I:95:ASP:HA	1:I:117:ASN:CB	2.52	0.40
1:O:13:VAL:HG12	1:O:14:THR:N	2.35	0.40
1:M:69:LYS:O	1:M:70:ASN:HB2	2.21	0.40
2:F:3:MLE:HD12	2:F:5:BMT:HD23	2.04	0.40
1:I:88:SER:C	1:I:90:TYR:H	2.24	0.40
1:E:37:ASN:O	1:E:41:MET:HG2	2.22	0.40
2:J:3:MLE:HA	2:J:4:MVA:HN1	1.75	0.40
1:I:128:THR:O	1:I:129:PRO:C	2.60	0.40
1:C:134:ASN:O	1:C:135:ASN:HB2	2.22	0.40
1:O:142:LYS:HE3	3:O:2034:HOH:O	2.21	0.40
1:O:124:PHE:CD2	2:P:4:MVA:HG11	2.57	0.40
1:A:13:VAL:HG11	1:A:153:ILE:HD11	2.04	0.40
1:A:110:SER:HB3	1:A:124:PHE:CZ	2.56	0.40

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:O:106:PRO:HB3	1:O:127:THR:O	2.21	0.40
1:M:12:ASP:OD2	1:M:22:ARG:HB2	2.21	0.40
1:I:159:ASN:OD1	1:I:163:ARG:HB3	2.22	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	175/177 (99%)	163 (93%)	12 (7%)	0	100	100
1	C	175/177 (99%)	163 (93%)	12 (7%)	0	100	100
1	E	172/177 (97%)	159 (92%)	13 (8%)	0	100	100
1	G	170/177 (96%)	157 (92%)	12 (7%)	1 (1%)	33	53
1	I	171/177 (97%)	158 (92%)	12 (7%)	1 (1%)	33	53
1	K	173/177 (98%)	161 (93%)	12 (7%)	0	100	100
1	M	173/177 (98%)	157 (91%)	15 (9%)	1 (1%)	33	53
1	O	170/177 (96%)	158 (93%)	12 (7%)	0	100	100
2	B	1/11 (9%)	1 (100%)	0	0	100	100
2	D	1/11 (9%)	1 (100%)	0	0	100	100
2	F	1/11 (9%)	1 (100%)	0	0	100	100
2	H	1/11 (9%)	1 (100%)	0	0	100	100
2	J	1/11 (9%)	1 (100%)	0	0	100	100
2	L	1/11 (9%)	1 (100%)	0	0	100	100
2	N	1/11 (9%)	1 (100%)	0	0	100	100
2	P	1/11 (9%)	1 (100%)	0	0	100	100
All	All	1387/1504 (92%)	1284 (93%)	100 (7%)	3 (0%)	56	77

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	I	91	GLY
1	M	52	ILE
1	G	91	GLY

### 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	151/151 (100%)	146 (97%)	5 (3%)	50	75
1	C	151/151 (100%)	150 (99%)	1 (1%)	91	98
1	E	148/151 (98%)	143 (97%)	5 (3%)	49	74
1	G	146/151 (97%)	143 (98%)	3 (2%)	66	88
1	I	147/151 (97%)	145 (99%)	2 (1%)	78	93
1	K	149/151 (99%)	147 (99%)	2 (1%)	80	94
1	M	149/151 (99%)	147 (99%)	2 (1%)	80	94
1	O	146/151 (97%)	144 (99%)	2 (1%)	78	93
2	B	1/1 (100%)	1 (100%)	0	100	100
2	D	1/1 (100%)	1 (100%)	0	100	100
2	F	1/1 (100%)	1 (100%)	0	100	100
2	H	1/1 (100%)	1 (100%)	0	100	100
2	J	1/1 (100%)	1 (100%)	0	100	100
2	L	1/1 (100%)	1 (100%)	0	100	100
2	N	1/1 (100%)	1 (100%)	0	100	100
2	P	1/1 (100%)	1 (100%)	0	100	100
All	All	1195/1216 (98%)	1173 (98%)	22 (2%)	71	90

All (22) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	29	ASN
1	A	72	MET
1	A	104	ASP
1	A	128	THR

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Mol	Chain	Res	Type
1	A	147	GLN
1	C	72	MET
1	E	5	ASP
1	E	40	LEU
1	E	72	MET
1	E	147	GLN
1	E	167	ASP
1	G	34	ARG
1	G	72	MET
1	G	147	GLN
1	I	72	MET
1	I	167	ASP
1	K	16	ASP
1	K	72	MET
1	M	72	MET
1	M	147	GLN
1	O	72	MET
1	O	147	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	E	58	HIS
1	M	58	HIS
1	M	162	ASN

### 5.3.3 RNA ⓘ

There are no RNA chains in this entry.

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

72 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
2	DAL	B	1	2	4,4,5	9.06	2 (50%)	3,4,6	5.75	1 (33%)
2	MLE	B	10	2	8,8,9	6.18	2 (25%)	6,9,11	0.82	0
2	MLE	B	2	2	8,8,9	6.37	2 (25%)	6,9,11	0.99	1 (16%)
2	MLE	B	3	2	8,8,9	6.57	2 (25%)	6,9,11	0.98	1 (16%)
2	MVA	B	4	2	7,7,8	6.72	2 (28%)	5,8,10	0.98	0
2	BMT	B	5	2	12,12,13	5.44	2 (16%)	11,14,16	0.96	1 (9%)
2	ABA	B	6	2	5,5,6	8.20	2 (40%)	3,5,7	0.83	0
2	SAR	B	7	2	4,4,5	9.20	2 (50%)	1,3,5	3.74	1 (100%)
2	MLE	B	8	2	8,8,9	6.43	2 (25%)	6,9,11	0.94	1 (16%)
2	DAL	D	1	2	4,4,5	9.08	2 (50%)	3,4,6	2.48	1 (33%)
2	MLE	D	10	2	8,8,9	6.45	2 (25%)	6,9,11	0.84	0
2	MLE	D	2	2	8,8,9	5.97	2 (25%)	6,9,11	0.94	1 (16%)
2	MLE	D	3	2	8,8,9	6.86	2 (25%)	6,9,11	1.03	0
2	MVA	D	4	2	7,7,8	6.73	2 (28%)	5,8,10	0.95	0
2	BMT	D	5	2	12,12,13	5.27	2 (16%)	11,14,16	1.27	2 (18%)
2	ABA	D	6	2	5,5,6	7.93	2 (40%)	3,5,7	0.93	0
2	SAR	D	7	2	4,4,5	9.19	2 (50%)	1,3,5	3.90	1 (100%)
2	MLE	D	8	2	8,8,9	6.14	2 (25%)	6,9,11	0.96	0
2	DAL	F	1	2	4,4,5	8.72	2 (50%)	3,4,6	10.15	1 (33%)
2	MLE	F	10	2	8,8,9	6.22	2 (25%)	6,9,11	0.95	1 (16%)
2	MLE	F	2	2	8,8,9	6.35	2 (25%)	6,9,11	0.91	1 (16%)
2	MLE	F	3	2	8,8,9	6.85	2 (25%)	6,9,11	1.17	0
2	MVA	F	4	2	7,7,8	6.75	2 (28%)	5,8,10	0.95	0
2	BMT	F	5	2	12,12,13	5.31	2 (16%)	11,14,16	1.23	1 (9%)
2	ABA	F	6	2	5,5,6	7.88	2 (40%)	3,5,7	1.08	0
2	SAR	F	7	2	4,4,5	8.44	2 (50%)	1,3,5	4.11	1 (100%)
2	MLE	F	8	2	8,8,9	6.38	2 (25%)	6,9,11	0.91	1 (16%)
2	DAL	H	1	2	4,4,5	9.01	2 (50%)	3,4,6	13.59	2 (66%)
2	MLE	H	10	2	8,8,9	6.66	2 (25%)	6,9,11	0.90	1 (16%)
2	MLE	H	2	2	8,8,9	6.24	2 (25%)	6,9,11	0.92	1 (16%)
2	MLE	H	3	2	8,8,9	6.73	2 (25%)	6,9,11	1.11	1 (16%)
2	MVA	H	4	2	7,7,8	6.86	2 (28%)	5,8,10	0.83	0
2	BMT	H	5	2	12,12,13	5.00	3 (25%)	11,14,16	0.94	0
2	ABA	H	6	2	5,5,6	7.72	2 (40%)	3,5,7	1.78	1 (33%)
2	SAR	H	7	2	4,4,5	9.23	2 (50%)	1,3,5	4.03	1 (100%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	MLE	H	8	2	8,8,9	6.44	2 (25%)	6,9,11	1.05	1 (16%)
2	DAL	J	1	2	4,4,5	8.68	2 (50%)	3,4,6	10.17	1 (33%)
2	MLE	J	10	2	8,8,9	5.96	2 (25%)	6,9,11	0.93	1 (16%)
2	MLE	J	2	2	8,8,9	6.36	2 (25%)	6,9,11	0.98	1 (16%)
2	MLE	J	3	2	8,8,9	6.61	2 (25%)	6,9,11	0.92	1 (16%)
2	MVA	J	4	2	7,7,8	6.86	2 (28%)	5,8,10	0.98	0
2	BMT	J	5	2	12,12,13	5.41	4 (33%)	11,14,16	0.97	0
2	ABA	J	6	2	5,5,6	8.26	2 (40%)	3,5,7	2.02	1 (33%)
2	SAR	J	7	2	4,4,5	9.06	2 (50%)	1,3,5	3.88	1 (100%)
2	MLE	J	8	2	8,8,9	6.35	2 (25%)	6,9,11	0.91	1 (16%)
2	DAL	L	1	2	4,4,5	8.83	2 (50%)	3,4,6	6.03	1 (33%)
2	MLE	L	10	2	8,8,9	6.53	2 (25%)	6,9,11	1.02	1 (16%)
2	MLE	L	2	2	8,8,9	6.59	2 (25%)	6,9,11	1.05	1 (16%)
2	MLE	L	3	2	8,8,9	6.65	2 (25%)	6,9,11	0.98	1 (16%)
2	MVA	L	4	2	7,7,8	6.71	2 (28%)	5,8,10	0.90	0
2	BMT	L	5	2	12,12,13	5.26	2 (16%)	11,14,16	1.04	0
2	ABA	L	6	2	5,5,6	7.91	2 (40%)	3,5,7	0.98	0
2	SAR	L	7	2	4,4,5	9.52	2 (50%)	1,3,5	3.73	1 (100%)
2	MLE	L	8	2	8,8,9	6.62	2 (25%)	6,9,11	0.93	1 (16%)
2	DAL	N	1	2	4,4,5	9.02	2 (50%)	3,4,6	22.05	2 (66%)
2	MLE	N	10	2	8,8,9	6.54	2 (25%)	6,9,11	0.96	1 (16%)
2	MLE	N	2	2	8,8,9	6.39	2 (25%)	6,9,11	1.02	1 (16%)
2	MLE	N	3	2	8,8,9	6.62	2 (25%)	6,9,11	0.88	1 (16%)
2	MVA	N	4	2	7,7,8	6.83	2 (28%)	5,8,10	0.89	0
2	BMT	N	5	2	12,12,13	5.28	2 (16%)	11,14,16	1.16	1 (9%)
2	ABA	N	6	2	5,5,6	7.94	2 (40%)	3,5,7	1.99	1 (33%)
2	SAR	N	7	2	4,4,5	9.32	2 (50%)	1,3,5	4.24	1 (100%)
2	MLE	N	8	2	8,8,9	6.31	2 (25%)	6,9,11	0.83	0
2	DAL	P	1	2	4,4,5	8.62	1 (25%)	3,4,6	17.00	2 (66%)
2	MLE	P	10	2	8,8,9	6.24	2 (25%)	6,9,11	0.87	1 (16%)
2	MLE	P	2	2	8,8,9	6.31	2 (25%)	6,9,11	1.06	1 (16%)
2	MLE	P	3	2	8,8,9	6.50	2 (25%)	6,9,11	0.87	1 (16%)
2	MVA	P	4	2	7,7,8	6.84	2 (28%)	5,8,10	0.85	0
2	BMT	P	5	2	12,12,13	5.19	2 (16%)	11,14,16	1.12	1 (9%)
2	ABA	P	6	2	5,5,6	7.88	2 (40%)	3,5,7	1.53	1 (33%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	SAR	P	7	2	4,4,5	9.09	2 (50%)	1,3,5	4.15	1 (100%)
2	MLE	P	8	2	8,8,9	6.45	2 (25%)	6,9,11	0.84	0

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
2	DAL	B	1	2	-	0/0/2/4	0/0/0/0
2	MLE	B	10	2	-	0/6/8/10	0/0/0/0
2	MLE	B	2	2	-	0/6/8/10	0/0/0/0
2	MLE	B	3	2	-	0/6/8/10	0/0/0/0
2	MVA	B	4	2	-	0/6/8/10	0/0/0/0
2	BMT	B	5	2	-	0/14/16/18	0/0/0/0
2	ABA	B	6	2	-	0/2/4/6	0/0/0/0
2	SAR	B	7	2	-	0/1/2/3	0/0/0/0
2	MLE	B	8	2	-	0/6/8/10	0/0/0/0
2	DAL	D	1	2	-	0/0/2/4	0/0/0/0
2	MLE	D	10	2	-	0/6/8/10	0/0/0/0
2	MLE	D	2	2	-	0/6/8/10	0/0/0/0
2	MLE	D	3	2	-	0/6/8/10	0/0/0/0
2	MVA	D	4	2	-	0/6/8/10	0/0/0/0
2	BMT	D	5	2	-	0/14/16/18	0/0/0/0
2	ABA	D	6	2	-	0/2/4/6	0/0/0/0
2	SAR	D	7	2	-	0/1/2/3	0/0/0/0
2	MLE	D	8	2	-	0/6/8/10	0/0/0/0
2	DAL	F	1	2	-	0/0/2/4	0/0/0/0
2	MLE	F	10	2	-	0/6/8/10	0/0/0/0
2	MLE	F	2	2	-	0/6/8/10	0/0/0/0
2	MLE	F	3	2	-	0/6/8/10	0/0/0/0
2	MVA	F	4	2	-	0/6/8/10	0/0/0/0
2	BMT	F	5	2	-	0/14/16/18	0/0/0/0
2	ABA	F	6	2	-	0/2/4/6	0/0/0/0
2	SAR	F	7	2	-	0/1/2/3	0/0/0/0
2	MLE	F	8	2	-	0/6/8/10	0/0/0/0
2	DAL	H	1	2	-	0/0/2/4	0/0/0/0
2	MLE	H	10	2	-	0/6/8/10	0/0/0/0
2	MLE	H	2	2	-	0/6/8/10	0/0/0/0
2	MLE	H	3	2	-	0/6/8/10	0/0/0/0
2	MVA	H	4	2	-	0/6/8/10	0/0/0/0
2	BMT	H	5	2	-	0/14/16/18	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	ABA	H	6	2	-	0/2/4/6	0/0/0/0
2	SAR	H	7	2	-	0/1/2/3	0/0/0/0
2	MLE	H	8	2	-	0/6/8/10	0/0/0/0
2	DAL	J	1	2	-	0/0/2/4	0/0/0/0
2	MLE	J	10	2	-	0/6/8/10	0/0/0/0
2	MLE	J	2	2	-	0/6/8/10	0/0/0/0
2	MLE	J	3	2	-	0/6/8/10	0/0/0/0
2	MVA	J	4	2	-	0/6/8/10	0/0/0/0
2	BMT	J	5	2	-	0/14/16/18	0/0/0/0
2	ABA	J	6	2	-	0/2/4/6	0/0/0/0
2	SAR	J	7	2	-	0/1/2/3	0/0/0/0
2	MLE	J	8	2	-	0/6/8/10	0/0/0/0
2	DAL	L	1	2	-	0/0/2/4	0/0/0/0
2	MLE	L	10	2	-	0/6/8/10	0/0/0/0
2	MLE	L	2	2	-	0/6/8/10	0/0/0/0
2	MLE	L	3	2	-	0/6/8/10	0/0/0/0
2	MVA	L	4	2	-	0/6/8/10	0/0/0/0
2	BMT	L	5	2	-	0/14/16/18	0/0/0/0
2	ABA	L	6	2	-	0/2/4/6	0/0/0/0
2	SAR	L	7	2	-	0/1/2/3	0/0/0/0
2	MLE	L	8	2	-	0/6/8/10	0/0/0/0
2	DAL	N	1	2	-	0/0/2/4	0/0/0/0
2	MLE	N	10	2	-	0/6/8/10	0/0/0/0
2	MLE	N	2	2	-	0/6/8/10	0/0/0/0
2	MLE	N	3	2	-	0/6/8/10	0/0/0/0
2	MVA	N	4	2	-	0/6/8/10	0/0/0/0
2	BMT	N	5	2	-	0/14/16/18	0/0/0/0
2	ABA	N	6	2	-	0/2/4/6	0/0/0/0
2	SAR	N	7	2	-	0/1/2/3	0/0/0/0
2	MLE	N	8	2	-	0/6/8/10	0/0/0/0
2	DAL	P	1	2	-	0/0/2/4	0/0/0/0
2	MLE	P	10	2	-	0/6/8/10	0/0/0/0
2	MLE	P	2	2	-	0/6/8/10	0/0/0/0
2	MLE	P	3	2	-	0/6/8/10	0/0/0/0
2	MVA	P	4	2	-	0/6/8/10	0/0/0/0
2	BMT	P	5	2	-	0/14/16/18	0/0/0/0
2	ABA	P	6	2	-	0/2/4/6	0/0/0/0
2	SAR	P	7	2	-	0/1/2/3	0/0/0/0
2	MLE	P	8	2	-	0/6/8/10	0/0/0/0

All (146) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	3	MLE	O-C	19.05	1.24	1.11
2	F	3	MLE	O-C	19.01	1.24	1.11
2	H	3	MLE	O-C	18.72	1.24	1.11
2	L	7	SAR	O-C	18.69	1.24	1.11
2	H	10	MLE	O-C	18.65	1.24	1.11
2	L	8	MLE	O-C	18.46	1.24	1.11
2	L	3	MLE	O-C	18.46	1.24	1.11
2	N	3	MLE	O-C	18.42	1.24	1.11
2	B	5	BMT	O-C	18.41	1.24	1.11
2	L	2	MLE	O-C	18.41	1.24	1.11
2	J	3	MLE	O-C	18.35	1.24	1.11
2	N	7	SAR	O-C	18.31	1.24	1.11
2	B	3	MLE	O-C	18.29	1.24	1.11
2	J	6	ABA	O-C	18.26	1.24	1.11
2	N	10	MLE	O-C	18.26	1.24	1.11
2	L	10	MLE	O-C	18.18	1.23	1.11
2	H	7	SAR	O-C	18.12	1.23	1.11
2	B	6	ABA	O-C	18.12	1.23	1.11
2	J	5	BMT	O-C	18.08	1.23	1.11
2	D	7	SAR	O-C	18.06	1.23	1.11
2	P	3	MLE	O-C	18.04	1.23	1.11
2	B	7	SAR	O-C	18.01	1.23	1.11
2	B	8	MLE	O-C	18.01	1.23	1.11
2	P	8	MLE	O-C	17.99	1.23	1.11
2	F	5	BMT	O-C	17.99	1.23	1.11
2	D	10	MLE	O-C	17.98	1.23	1.11
2	H	8	MLE	O-C	17.96	1.23	1.11
2	P	7	SAR	O-C	17.90	1.23	1.11
2	N	1	DAL	O-C	17.87	1.23	1.11
2	D	5	BMT	O-C	17.87	1.23	1.11
2	B	1	DAL	O-C	17.86	1.23	1.11
2	D	1	DAL	O-C	17.86	1.23	1.11
2	H	4	MVA	O-C	17.85	1.23	1.11
2	H	1	DAL	O-C	17.83	1.23	1.11
2	J	7	SAR	O-C	17.82	1.23	1.11
2	N	4	MVA	O-C	17.81	1.23	1.11
2	F	8	MLE	O-C	17.80	1.23	1.11
2	P	4	MVA	O-C	17.79	1.23	1.11
2	J	4	MVA	O-C	17.78	1.23	1.11
2	N	2	MLE	O-C	17.75	1.23	1.11
2	J	8	MLE	O-C	17.73	1.23	1.11
2	J	2	MLE	O-C	17.71	1.23	1.11
2	B	2	MLE	O-C	17.71	1.23	1.11

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	N	5	BMT	O-C	17.70	1.23	1.11
2	L	5	BMT	O-C	17.70	1.23	1.11
2	F	2	MLE	O-C	17.69	1.23	1.11
2	P	2	MLE	O-C	17.62	1.23	1.11
2	F	4	MVA	O-C	17.62	1.23	1.11
2	N	8	MLE	O-C	17.59	1.23	1.11
2	D	4	MVA	O-C	17.58	1.23	1.11
2	B	4	MVA	O-C	17.55	1.23	1.11
2	P	5	BMT	O-C	17.54	1.23	1.11
2	N	6	ABA	O-C	17.53	1.23	1.11
2	D	6	ABA	O-C	17.52	1.23	1.11
2	L	4	MVA	O-C	17.49	1.23	1.11
2	P	6	ABA	O-C	17.48	1.23	1.11
2	L	1	DAL	O-C	17.46	1.23	1.11
2	H	2	MLE	O-C	17.43	1.23	1.11
2	F	6	ABA	O-C	17.42	1.23	1.11
2	L	6	ABA	O-C	17.41	1.23	1.11
2	F	10	MLE	O-C	17.41	1.23	1.11
2	P	10	MLE	O-C	17.33	1.23	1.11
2	B	10	MLE	O-C	17.25	1.23	1.11
2	F	1	DAL	O-C	17.20	1.23	1.11
2	J	1	DAL	O-C	17.19	1.23	1.11
2	D	8	MLE	O-C	17.17	1.23	1.11
2	P	1	DAL	O-C	17.12	1.23	1.11
2	H	6	ABA	O-C	16.99	1.23	1.11
2	H	5	BMT	O-C	16.78	1.22	1.11
2	F	7	SAR	O-C	16.69	1.22	1.11
2	J	10	MLE	O-C	16.64	1.22	1.11
2	D	2	MLE	O-C	16.62	1.22	1.11
2	B	7	SAR	CA-C	3.51	1.52	1.48
2	L	7	SAR	CA-C	3.31	1.52	1.48
2	L	3	MLE	CA-C	3.30	1.54	1.48
2	D	3	MLE	CA-C	3.29	1.54	1.48
2	P	3	MLE	CA-C	3.27	1.54	1.48
2	N	7	SAR	CA-C	3.23	1.52	1.48
2	J	3	MLE	CA-C	3.21	1.54	1.48
2	F	3	MLE	CA-C	3.21	1.54	1.48
2	D	1	DAL	CA-C	3.20	1.54	1.48
2	N	5	BMT	CA-C	3.18	1.54	1.48
2	N	2	MLE	CA-C	3.17	1.54	1.48
2	D	7	SAR	CA-C	3.17	1.52	1.48
2	H	7	SAR	CA-C	3.16	1.52	1.48

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	J	4	MVA	CA-C	3.09	1.54	1.48
2	J	7	SAR	CA-C	3.06	1.52	1.48
2	H	3	MLE	CA-C	3.03	1.54	1.48
2	L	6	ABA	CA-C	3.01	1.54	1.48
2	N	3	MLE	CA-C	2.99	1.53	1.48
2	B	1	DAL	CA-C	2.99	1.53	1.48
2	B	3	MLE	CA-C	2.95	1.53	1.48
2	L	10	MLE	CA-C	2.95	1.53	1.48
2	B	2	MLE	CA-C	2.92	1.53	1.48
2	P	7	SAR	CA-C	2.92	1.52	1.48
2	P	4	MVA	CA-C	2.91	1.53	1.48
2	H	6	ABA	CA-C	2.91	1.53	1.48
2	F	1	DAL	CA-C	2.89	1.53	1.48
2	J	5	BMT	CB-CA	2.88	1.58	1.53
2	P	10	MLE	CA-C	2.87	1.53	1.48
2	H	4	MVA	CA-C	2.84	1.53	1.48
2	F	2	MLE	CA-C	2.81	1.53	1.48
2	D	10	MLE	CA-C	2.80	1.53	1.48
2	B	6	ABA	CA-C	2.74	1.53	1.48
2	J	2	MLE	CA-C	2.69	1.53	1.48
2	N	6	ABA	CA-C	2.69	1.53	1.48
2	J	6	ABA	CA-C	2.68	1.53	1.48
2	B	5	BMT	CA-C	2.66	1.53	1.48
2	P	8	MLE	CA-C	2.65	1.53	1.48
2	N	4	MVA	CA-C	2.63	1.53	1.48
2	L	8	MLE	CA-C	2.63	1.53	1.48
2	N	8	MLE	CA-C	2.62	1.53	1.48
2	D	2	MLE	CA-C	2.62	1.53	1.48
2	F	6	ABA	CA-C	2.62	1.53	1.48
2	P	5	BMT	CA-C	2.62	1.53	1.48
2	N	10	MLE	CA-C	2.61	1.53	1.48
2	F	4	MVA	CA-C	2.58	1.53	1.48
2	H	1	DAL	CA-C	2.57	1.53	1.48
2	D	6	ABA	CA-C	2.57	1.53	1.48
2	L	1	DAL	CA-C	2.56	1.53	1.48
2	B	4	MVA	CA-C	2.56	1.53	1.48
2	H	5	BMT	CA-C	2.53	1.53	1.48
2	L	2	MLE	CA-C	2.53	1.53	1.48
2	H	8	MLE	CA-C	2.47	1.52	1.48
2	J	8	MLE	CA-C	2.45	1.52	1.48
2	L	4	MVA	CA-C	2.45	1.52	1.48
2	L	5	BMT	CA-C	2.43	1.52	1.48

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	5	BMT	CA-C	2.41	1.52	1.48
2	F	8	MLE	CA-C	2.41	1.52	1.48
2	P	2	MLE	CA-C	2.40	1.52	1.48
2	H	2	MLE	CA-C	2.39	1.52	1.48
2	J	1	DAL	CA-C	2.35	1.52	1.48
2	D	8	MLE	CA-C	2.33	1.52	1.48
2	N	1	DAL	CA-C	2.33	1.52	1.48
2	D	4	MVA	CA-C	2.32	1.52	1.48
2	H	10	MLE	CA-C	2.32	1.52	1.48
2	F	10	MLE	CA-C	2.31	1.52	1.48
2	J	10	MLE	CA-C	2.29	1.52	1.48
2	H	5	BMT	CB-CA	2.28	1.57	1.53
2	B	10	MLE	CA-C	2.28	1.52	1.48
2	F	7	SAR	CA-C	2.26	1.51	1.48
2	F	5	BMT	CA-C	2.25	1.52	1.48
2	P	6	ABA	CA-C	2.23	1.52	1.48
2	J	5	BMT	CA-C	2.16	1.52	1.48
2	J	5	BMT	CE-CZ	2.07	1.44	1.29
2	B	8	MLE	CA-C	2.04	1.52	1.48

All (54) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	N	1	DAL	C-CA-N	-37.93	108.97	113.27
2	P	1	DAL	C-CA-N	-29.32	109.95	113.27
2	H	1	DAL	C-CA-N	-23.36	110.62	113.27
2	J	1	DAL	C-CA-N	-17.49	111.29	113.27
2	F	1	DAL	C-CA-N	-17.45	111.29	113.27
2	L	1	DAL	C-CA-N	10.40	114.44	113.27
2	B	1	DAL	C-CA-N	-9.82	112.16	113.27
2	N	1	DAL	CB-CA-C	4.38	110.41	108.46
2	N	7	SAR	CN-N-CA	4.24	120.25	112.36
2	P	7	SAR	CN-N-CA	4.15	120.09	112.36
2	F	7	SAR	CN-N-CA	4.11	120.01	112.36
2	H	7	SAR	CN-N-CA	4.03	119.86	112.36
2	D	7	SAR	CN-N-CA	3.90	119.63	112.36
2	J	7	SAR	CN-N-CA	3.88	119.59	112.36
2	B	7	SAR	CN-N-CA	3.74	119.32	112.36
2	L	7	SAR	CN-N-CA	3.73	119.30	112.36
2	D	1	DAL	C-CA-N	-3.73	112.84	113.27
2	N	6	ABA	C-CA-N	-3.37	110.47	113.83
2	J	6	ABA	C-CA-N	-3.34	110.49	113.83

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	H	6	ABA	C-CA-N	-2.90	110.94	113.83
2	D	5	BMT	CG2-CD2-CE	2.84	118.09	113.84
2	H	1	DAL	CB-CA-C	2.73	109.67	108.46
2	P	1	DAL	CB-CA-C	2.55	109.60	108.46
2	N	5	BMT	CG2-CD2-CE	2.54	117.63	113.84
2	P	6	ABA	C-CA-N	-2.41	111.42	113.83
2	H	8	MLE	CN-N-CA	2.33	120.23	113.11
2	P	5	BMT	CG2-CD2-CE	2.33	117.32	113.84
2	H	3	MLE	CN-N-CA	2.31	120.17	113.11
2	F	5	BMT	CG2-CD2-CE	2.25	117.20	113.84
2	N	2	MLE	CN-N-CA	2.23	119.91	113.11
2	B	3	MLE	CN-N-CA	2.20	119.83	113.11
2	L	8	MLE	CN-N-CA	2.20	119.81	113.11
2	B	8	MLE	CN-N-CA	2.19	119.78	113.11
2	J	8	MLE	CN-N-CA	2.17	119.73	113.11
2	L	10	MLE	CN-N-CA	2.16	119.69	113.11
2	P	2	MLE	CN-N-CA	2.16	119.69	113.11
2	J	2	MLE	CN-N-CA	2.16	119.69	113.11
2	J	3	MLE	CN-N-CA	2.15	119.67	113.11
2	B	5	BMT	CN-N-CA	2.15	120.61	114.34
2	J	10	MLE	CN-N-CA	2.14	119.64	113.11
2	F	10	MLE	CN-N-CA	2.13	119.61	113.11
2	D	2	MLE	CN-N-CA	2.13	119.61	113.11
2	B	2	MLE	CN-N-CA	2.11	119.54	113.11
2	N	10	MLE	CN-N-CA	2.10	119.53	113.11
2	H	2	MLE	CN-N-CA	2.10	119.53	113.11
2	H	10	MLE	CN-N-CA	2.10	119.53	113.11
2	N	3	MLE	CN-N-CA	2.08	119.46	113.11
2	L	2	MLE	CN-N-CA	2.08	119.45	113.11
2	D	5	BMT	CN-N-CA	2.06	120.35	114.34
2	F	8	MLE	CN-N-CA	2.06	119.39	113.11
2	P	3	MLE	CN-N-CA	2.04	119.33	113.11
2	F	2	MLE	CN-N-CA	2.03	119.30	113.11
2	P	10	MLE	CN-N-CA	2.01	119.25	113.11
2	L	3	MLE	CN-N-CA	2.00	119.22	113.11

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

## 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	177/177 (100%)	-0.35	2 (1%) 77 78	28, 42, 59, 86	4 (2%)
1	C	177/177 (100%)	-0.43	0 100 100	28, 39, 53, 67	2 (1%)
1	E	174/177 (98%)	-0.47	0 100 100	24, 38, 51, 72	2 (1%)
1	G	172/177 (97%)	-0.15	1 (0%) 86 88	29, 44, 61, 68	1 (0%)
1	I	173/177 (97%)	-0.16	1 (0%) 86 88	29, 49, 69, 79	4 (2%)
1	K	175/177 (98%)	-0.30	2 (1%) 77 78	28, 39, 57, 80	2 (1%)
1	M	175/177 (98%)	-0.32	1 (0%) 86 88	28, 42, 60, 84	3 (1%)
1	O	172/177 (97%)	-0.34	0 100 100	31, 44, 60, 63	2 (1%)
2	B	11/11 (100%)	0.26	1 (9%) 9 8	38, 42, 44, 47	0
2	D	11/11 (100%)	-0.24	0 100 100	31, 37, 42, 43	0
2	F	11/11 (100%)	-0.39	0 100 100	37, 39, 43, 44	1 (9%)
2	H	11/11 (100%)	-0.48	0 100 100	31, 36, 40, 40	0
2	J	11/11 (100%)	-0.27	0 100 100	40, 44, 53, 54	1 (9%)
2	L	11/11 (100%)	-0.27	0 100 100	34, 35, 38, 38	0
2	N	11/11 (100%)	0.04	0 100 100	37, 39, 41, 44	0
2	P	11/11 (100%)	0.35	0 100 100	37, 43, 51, 53	0
All	All	1483/1504 (98%)	-0.30	8 (0%) 88 90	24, 42, 61, 86	22 (1%)

All (8) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	8	MLE	5.6
1	K	177	VAL	3.2
1	A	52	ILE	3.2
1	K	5	ASP	2.7
1	M	4	LYS	2.5

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Mol	Chain	Res	Type	RSRZ
1	G	47	ALA	2.4
1	A	1	MET	2.3
1	I	47	ALA	2.1

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

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	RSR	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
2	MLE	B	8	9/10	0.29	7.41	42,44,51,52	0
2	MLE	L	10	9/10	0.13	7.37	32,34,37,38	0
2	SAR	J	7	5/6	0.16	2.99	51,52,54,55	0
2	SAR	D	7	5/6	0.12	2.81	39,40,42,43	0
2	MVA	B	4	8/9	0.14	2.68	38,39,40,41	0
2	BMT	F	5	13/14	0.15	2.42	34,38,42,43	0
2	MLE	D	10	9/10	0.14	2.32	39,40,41,41	0
2	BMT	L	5	13/14	0.14	2.10	31,34,37,38	0
2	MLE	B	10	9/10	0.16	2.03	41,42,44,45	0
2	BMT	D	5	13/14	0.15	2.02	33,35,37,37	0
2	SAR	N	7	5/6	0.15	1.93	37,39,39,41	0
2	ABA	P	6	6/7	0.14	1.83	43,47,48,49	0
2	MLE	D	8	9/10	0.17	1.61	40,42,44,45	0
2	MVA	F	4	8/9	0.14	1.43	36,39,39,40	0
2	MLE	F	3	9/10	0.14	1.15	36,39,41,43	0
2	MLE	L	8	9/10	0.17	1.11	35,37,40,40	0
2	MLE	F	2	9/10	0.14	0.99	34,37,39,39	0
2	BMT	P	5	13/14	0.17	0.98	41,43,50,50	0
2	ABA	N	6	6/7	0.14	0.96	42,43,43,45	0
2	MLE	J	10	9/10	0.14	0.85	45,46,47,47	0
2	MLE	D	2	9/10	0.14	0.84	28,31,34,35	0
2	BMT	N	5	13/14	0.14	0.83	34,39,45,46	0
2	DAL	P	1	5/6	0.16	0.83	40,41,41,42	0
2	MLE	L	2	9/10	0.16	0.81	28,34,36,36	0
2	BMT	B	5	13/14	0.14	0.78	36,41,45,46	0
2	BMT	H	5	13/14	0.14	0.77	27,29,36,40	0
2	MLE	P	10	9/10	0.14	0.73	43,43,44,44	0
2	MLE	H	8	9/10	0.16	0.66	32,36,37,38	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
2	MLE	J	3	9/10	0.13	0.54	39,40,41,42	0
2	ABA	D	6	6/7	0.13	0.53	39,40,41,42	0
2	MLE	P	8	9/10	0.18	0.51	49,52,55,55	0
2	SAR	B	7	5/6	0.13	0.50	43,44,44,44	0
2	SAR	P	7	5/6	0.15	0.38	48,48,52,54	0
2	MLE	H	10	9/10	0.12	0.38	36,39,42,43	0
2	MLE	L	3	9/10	0.14	0.37	33,34,35,36	0
2	ABA	J	6	6/7	0.14	0.33	48,52,52,53	0
2	MVA	D	4	8/9	0.12	0.32	33,34,36,38	0
2	MLE	B	3	9/10	0.12	0.26	40,41,44,44	0
2	MVA	L	4	8/9	0.13	0.11	31,36,38,38	0
2	MLE	H	2	9/10	0.14	-0.07	32,35,37,38	0
2	MVA	P	4	8/9	0.12	-0.09	37,40,42,42	0
2	DAL	H	1	5/6	0.12	-0.09	38,39,40,40	0
2	BMT	J	5	13/14	0.12	-0.14	41,43,48,49	0
2	MVA	J	4	8/9	0.11	-0.14	38,40,41,41	0
2	MVA	N	4	8/9	0.13	-0.21	36,38,40,40	0
2	MLE	N	10	9/10	0.14	-0.30	33,35,38,39	0
2	ABA	F	6	6/7	0.11	-0.31	34,37,38,40	0
2	MLE	F	10	9/10	0.11	-0.41	40,43,46,47	0
2	MLE	H	3	9/10	0.13	-0.43	33,35,36,36	0
2	MLE	J	8	9/10	0.13	-0.53	50,53,55,56	2
2	DAL	L	1	5/6	0.12	-0.75	36,36,37,38	0
2	MLE	D	3	9/10	0.11	-0.83	28,30,32,32	0
2	MLE	P	2	9/10	0.13	-0.85	34,35,38,38	0
2	MLE	B	2	9/10	0.11	-0.85	36,40,40,41	0
2	MLE	J	2	9/10	0.10	-0.87	36,39,41,41	0
2	SAR	L	7	5/6	0.10	-0.95	33,35,36,36	0
2	ABA	B	6	6/7	0.09	-0.97	41,42,43,44	0
2	ABA	H	6	6/7	0.10	-1.08	33,35,36,37	0
2	MVA	H	4	8/9	0.12	-1.18	28,31,32,33	0
2	MLE	N	3	9/10	0.13	-1.19	34,37,38,39	0
2	SAR	H	7	5/6	0.09	-1.25	34,35,36,36	0
2	DAL	F	1	5/6	0.09	-1.39	40,40,41,41	0
2	DAL	B	1	5/6	0.09	-1.64	37,37,40,41	0
2	MLE	N	2	9/10	0.12	-1.66	38,39,40,40	0
2	MLE	N	8	9/10	0.12	-1.71	37,38,40,40	0
2	ABA	L	6	6/7	0.08	-1.77	33,35,35,36	0
2	DAL	J	1	5/6	0.10	-1.80	42,42,43,44	0
2	SAR	F	7	5/6	0.09	-2.02	35,38,40,42	0
2	DAL	D	1	5/6	0.08	-2.38	35,37,38,38	0
2	DAL	N	1	5/6	0.10	-2.57	39,40,40,41	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
2	MLE	P	3	9/10	0.12	-2.75	37,40,40,41	0
2	MLE	F	8	9/10	0.10	-18.00	41,42,43,43	2

### 6.3 Carbohydrates

There are no carbohydrates in this entry.

### 6.4 Ligands

There are no ligands in this entry.

### 6.5 Other polymers

There are no such residues in this entry.