Full wwPDB X-ray Structure Validation Report (i)

Mar 4, 2024 – 07:57 PM EST

PDB ID	:	2AVF
Title	:	Crystal Structure of C-terminal Desundecapeptide Nitrite Reductase from Achromobacter cycloclastes
Authors	:	Li, H.T.; Chang, T.; Chang, W.C.; Chen, C.J.; Liu, M.Y.; Gui, L.L.; Zhang, J.P.; An, X.M.; Chang, W.R.
Deposited on	:	2005-08-30
Resolution	:	2.60 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*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references (1)) were used in the production of this report:

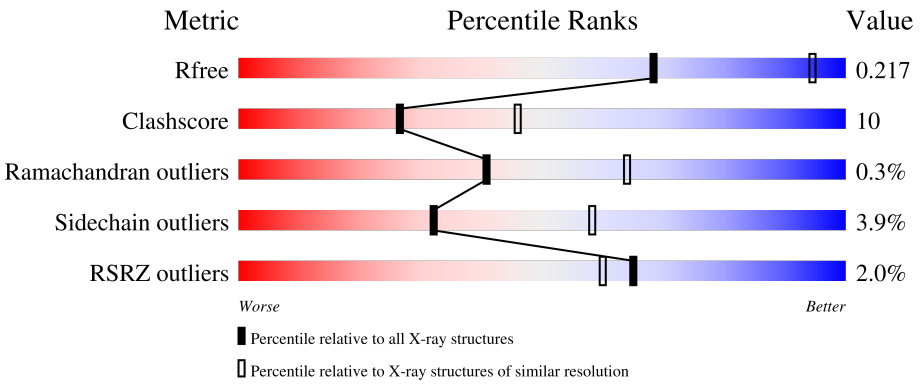
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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}	130704	3163 (2.60-2.60)
Clashscore	141614	3518 (2.60-2.60)
Ramachandran outliers	138981	3455 (2.60-2.60)
Sidechain outliers	138945	3455 (2.60-2.60)
RSRZ outliers	127900	3104 (2.60-2.60)

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 of the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. 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 <=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	329	2%, 72%, 21%, 5%
1	B	329	2%, 70%, 25%
1	C	329	%, 76%, 19%
1	D	329	4%, 74%, 21%
1	E	329	2%, 77%, 17%

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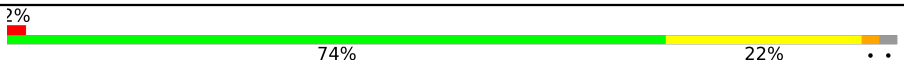
Mol	Chain	Length	Quality of chain
1	F	329	

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 15115 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 Copper-containing nitrite reductase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	314	2429	1550	419	452	8	0	0	0
1	B	316	2450	1565	422	455	8	0	0	0
1	C	316	2442	1557	421	456	8	0	0	0
1	D	320	2468	1575	425	460	8	0	0	0
1	E	315	2433	1552	420	453	8	0	0	0
1	F	323	2499	1595	430	466	8	0	0	0

- Molecule 2 is COPPER (II) ION (three-letter code: CU) (formula: Cu).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Cu		
2	A	2	2	2	0	0
2	B	2	2	2	0	0
2	C	2	2	2	0	0
2	D	2	2	2	0	0
2	E	2	2	2	0	0
2	F	2	2	2	0	0

- Molecule 3 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Cl		
3	B	2	2	2	0	0
			Total	Cl		
3	C	1	1	1	0	0
			Total	Cl		
3	D	1	1	1	0	0
			Total	Cl		
3	F	2	2	2	0	0

- Molecule 4 is water.

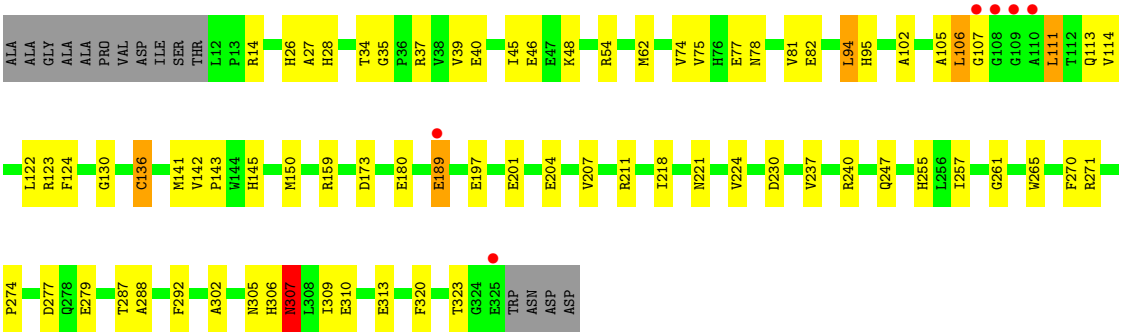
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
4	A	72	72	72	0	0
			Total	O		
4	B	54	54	54	0	0
			Total	O		
4	C	71	71	71	0	0
			Total	O		
4	D	55	55	55	0	0
			Total	O		
4	E	47	47	47	0	0
			Total	O		
4	F	77	77	77	0	0

3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes 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.

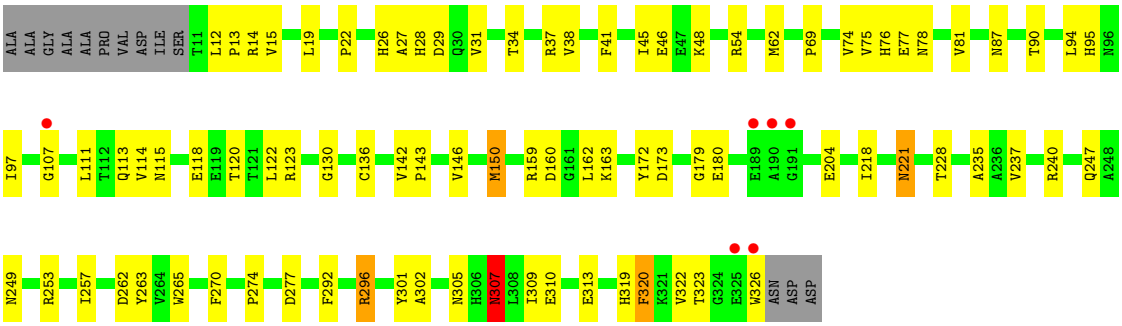
• Molecule 1: Copper-containing nitrite reductase

Chain A: 2% 72% 21% 5%



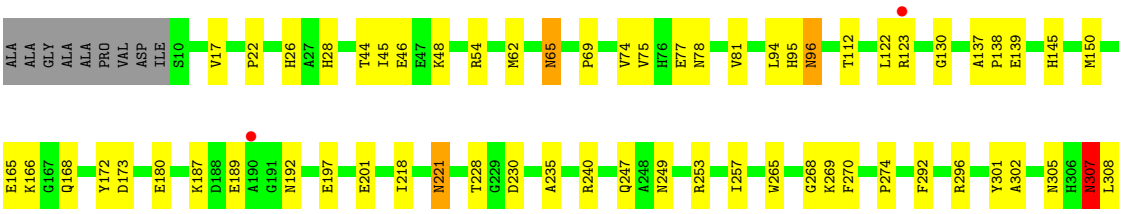
• Molecule 1: Copper-containing nitrite reductase

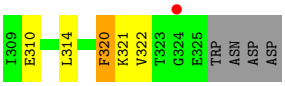
Chain B: 2% 70% 25%



• Molecule 1: Copper-containing nitrite reductase

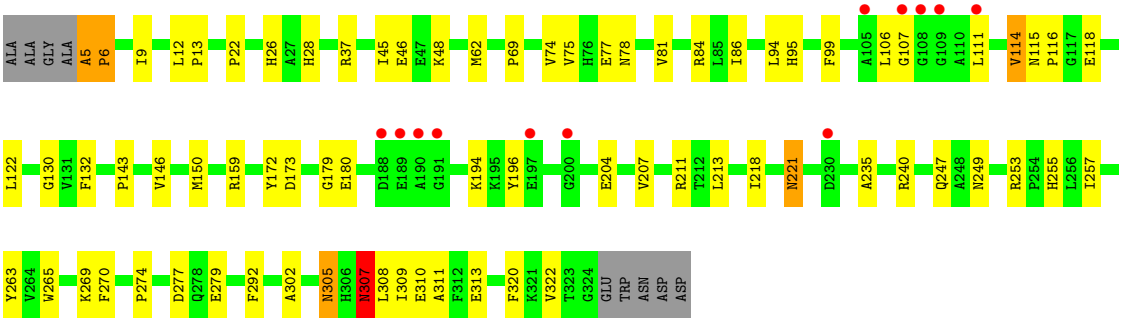
Chain C: % 76% 19%





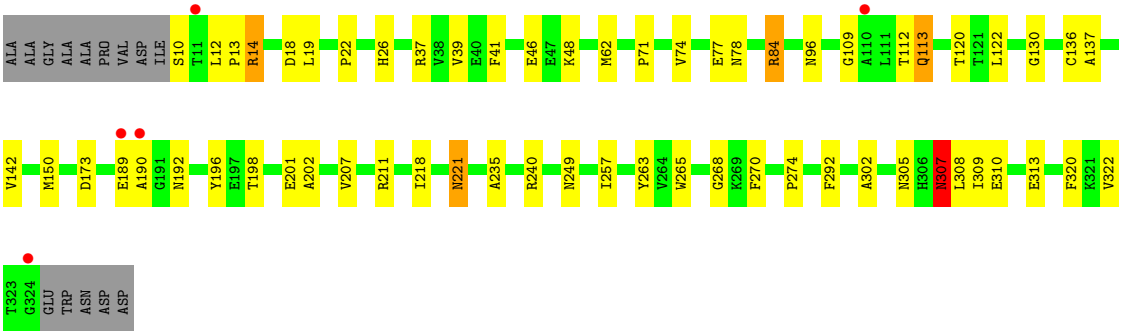
• Molecule 1: Copper-containing nitrite reductase

Chain D:



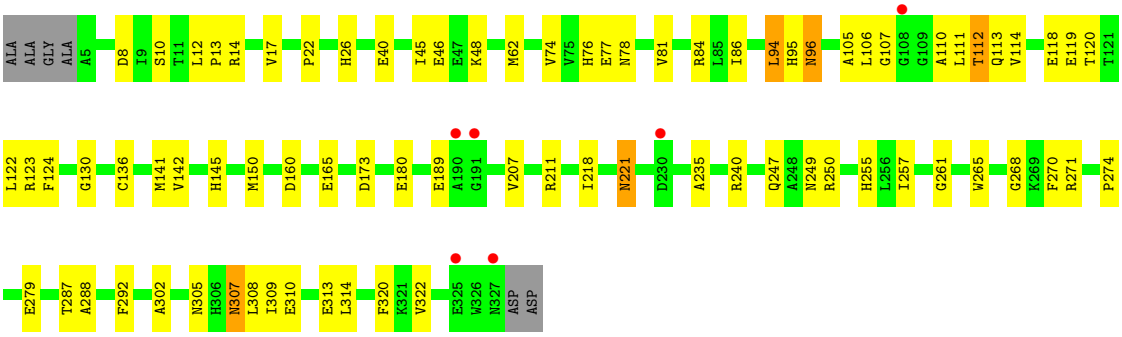
• Molecule 1: Copper-containing nitrite reductase

Chain E:



• Molecule 1: Copper-containing nitrite reductase

Chain F:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	85.78Å 111.07Å 122.88Å 90.00° 101.67° 90.00°	Depositor
Resolution (Å)	20.00 – 2.60 19.92 – 2.59	Depositor EDS
% Data completeness (in resolution range)	95.2 (20.00-2.60) 95.4 (19.92-2.59)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.13	Depositor
$< I/\sigma(I) >$ [1]	3.31 (at 2.59Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.182 , 0.217 0.182 , 0.217	Depositor DCC
R_{free} test set	2806 reflections (4.05%)	wwPDB-VP
Wilson B-factor (Å^2)	31.4	Xtriage
Anisotropy	0.311	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 44.7	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	15115	wwPDB-VP
Average B, all atoms (Å^2)	31.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.45% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality (i)

5.1 Standard geometry (i)

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

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	0/2496	0.71	3/3402 (0.1%)
1	B	0.35	0/2519	0.69	2/3435 (0.1%)
1	C	0.36	0/2509	0.70	2/3420 (0.1%)
1	D	0.35	0/2536	0.70	3/3459 (0.1%)
1	E	0.36	0/2500	0.69	3/3408 (0.1%)
1	F	0.35	0/2569	0.69	4/3505 (0.1%)
All	All	0.36	0/15129	0.70	17/20629 (0.1%)

There are no bond length outliers.

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	307	ASN	N-CA-C	-7.98	89.45	111.00
1	D	307	ASN	N-CA-C	-7.91	89.66	111.00
1	F	307	ASN	N-CA-C	-7.33	91.20	111.00
1	C	307	ASN	N-CA-C	-7.18	91.63	111.00
1	E	307	ASN	N-CA-C	-7.11	91.79	111.00
1	B	307	ASN	N-CA-C	-6.84	92.52	111.00
1	D	305	ASN	N-CA-C	-5.99	94.82	111.00
1	B	305	ASN	N-CA-C	-5.96	94.89	111.00
1	C	305	ASN	N-CA-C	-5.91	95.04	111.00
1	E	305	ASN	N-CA-C	-5.82	95.29	111.00
1	D	5	ALA	C-N-CD	-5.74	107.97	120.60
1	A	261	GLY	N-CA-C	-5.66	98.95	113.10
1	E	268	GLY	N-CA-C	5.44	126.70	113.10
1	A	305	ASN	N-CA-C	-5.44	96.32	111.00
1	F	305	ASN	N-CA-C	-5.37	96.50	111.00
1	F	261	GLY	N-CA-C	-5.31	99.83	113.10
1	F	268	GLY	N-CA-C	5.10	125.86	113.10

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

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	2429	0	2363	54	0
1	B	2450	0	2380	53	0
1	C	2442	0	2375	50	0
1	D	2468	0	2405	53	0
1	E	2433	0	2369	50	0
1	F	2499	0	2427	53	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
2	C	2	0	0	0	0
2	D	2	0	0	0	0
2	E	2	0	0	0	0
2	F	2	0	0	0	0
3	B	2	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
3	F	2	0	0	0	0
4	A	72	0	0	2	0
4	B	54	0	0	1	0
4	C	71	0	0	1	0
4	D	55	0	0	1	0
4	E	47	0	0	0	0
4	F	77	0	0	1	0
All	All	15115	0	14319	299	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 10.

All (299) 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:E:14:ARG:HG2	1:E:14:ARG:HH11	1.13	1.13

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:106:LEU:HD13	1:A:122:LEU:HD21	1.46	0.97
1:F:106:LEU:HD22	1:F:122:LEU:HD11	1.44	0.95
1:E:112:THR:HG23	1:E:122:LEU:HD13	1.60	0.82
1:C:96:ASN:HD21	1:C:137:ALA:H	1.29	0.81
1:B:14:ARG:HG2	1:B:38:VAL:HB	1.64	0.79
1:F:26:HIS:HE1	1:F:74:VAL:H	1.31	0.76
1:E:257:ILE:HD12	1:E:302:ALA:HB3	1.67	0.76
1:D:26:HIS:HE1	1:D:74:VAL:H	1.34	0.76
1:A:271:ARG:HD2	1:B:277:ASP:OD2	1.86	0.75
1:C:112:THR:HG23	1:C:122:LEU:HD13	1.70	0.74
1:B:37:ARG:HG2	1:B:37:ARG:HH11	1.53	0.73
1:E:14:ARG:HH11	1:E:14:ARG:CG	1.96	0.72
1:C:112:THR:HG21	1:C:122:LEU:HD22	1.70	0.72
1:D:257:ILE:HD12	1:D:302:ALA:HB3	1.69	0.72
1:B:257:ILE:HD12	1:B:302:ALA:HB3	1.70	0.71
1:B:14:ARG:HG3	1:B:14:ARG:HH11	1.56	0.71
1:E:112:THR:HG21	1:E:122:LEU:HD22	1.73	0.70
1:E:14:ARG:HG2	1:E:14:ARG:NH1	1.94	0.70
1:A:26:HIS:HE1	1:A:74:VAL:H	1.39	0.70
1:F:112:THR:HG21	1:F:122:LEU:CD1	2.22	0.69
1:B:204:GLU:HB2	4:B:618:HOH:O	1.93	0.69
1:F:8:ASP:OD1	1:F:10:SER:HB3	1.93	0.68
1:A:257:ILE:HD12	1:A:302:ALA:HB3	1.74	0.68
1:E:84:ARG:HG2	1:E:84:ARG:HH11	1.58	0.68
1:A:111:LEU:HD12	1:A:113:GLN:HG3	1.76	0.66
1:C:218:ILE:HD12	1:C:310:GLU:HG2	1.79	0.65
1:D:180:GLU:HB3	1:D:247:GLN:HG2	1.79	0.65
1:D:173:ASP:OD2	1:D:240:ARG:HD3	1.96	0.65
1:E:46:GLU:OE2	1:E:48:LYS:HD3	1.97	0.64
1:C:96:ASN:ND2	1:C:137:ALA:H	1.95	0.64
1:C:26:HIS:HE1	1:C:74:VAL:H	1.44	0.63
1:E:22:PRO:HB2	1:E:221:ASN:HD21	1.62	0.63
1:A:62:MET:O	1:A:150:MET:HG3	1.98	0.63
1:A:197:GLU:HB2	1:A:201:GLU:OE2	1.99	0.62
1:A:94:LEU:HD12	1:A:94:LEU:C	2.20	0.62
1:B:77:GLU:O	1:B:78:ASN:HB2	1.99	0.61
1:D:307:ASN:HD22	1:D:310:GLU:H	1.47	0.61
1:E:235:ALA:O	1:E:322:VAL:HA	1.99	0.61
1:B:37:ARG:HG2	1:B:37:ARG:NH1	2.15	0.61
1:F:46:GLU:OE2	1:F:48:LYS:HD3	2.00	0.61
1:C:46:GLU:OE2	1:C:48:LYS:HD3	2.01	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:26:HIS:CE1	1:F:74:VAL:H	2.17	0.60
1:A:143:PRO:HG2	4:A:519:HOH:O	2.01	0.60
1:C:28:HIS:HE1	1:C:172:TYR:OH	1.84	0.60
1:B:309:ILE:O	1:B:313:GLU:HB2	2.01	0.60
1:F:96:ASN:OD1	1:F:110:ALA:HA	2.01	0.60
1:D:13:PRO:HB2	1:D:37:ARG:HD3	1.84	0.60
1:D:28:HIS:HE1	1:D:172:TYR:OH	1.85	0.60
1:F:111:LEU:O	1:F:112:THR:HG23	2.01	0.59
1:F:77:GLU:O	1:F:78:ASN:HB2	2.02	0.59
1:D:106:LEU:CD1	1:D:106:LEU:N	2.66	0.59
1:D:106:LEU:N	1:D:106:LEU:HD12	2.17	0.59
1:C:26:HIS:CE1	1:C:74:VAL:H	2.21	0.59
1:D:207:VAL:O	1:D:211:ARG:HG3	2.02	0.59
1:F:173:ASP:OD2	1:F:240:ARG:HD3	2.03	0.59
1:F:106:LEU:HD13	1:F:122:LEU:HG	1.85	0.58
1:B:173:ASP:OD2	1:B:240:ARG:HD3	2.03	0.58
1:D:194:LYS:HE3	1:D:196:TYR:OH	2.03	0.58
1:F:96:ASN:HB2	1:F:113:GLN:HG2	1.85	0.58
1:B:46:GLU:OE2	1:B:48:LYS:HD3	2.03	0.58
1:F:112:THR:HG21	1:F:122:LEU:HD11	1.84	0.58
1:F:45:ILE:HG21	1:F:95:HIS:CD2	2.39	0.58
1:C:257:ILE:HD12	1:C:302:ALA:HB3	1.85	0.57
1:D:26:HIS:CE1	1:D:74:VAL:H	2.21	0.57
1:C:62:MET:O	1:C:150:MET:HG3	2.05	0.57
1:A:105:ALA:O	1:A:107:GLY:N	2.38	0.57
1:D:22:PRO:HB2	1:D:221:ASN:HD21	1.68	0.57
1:E:307:ASN:HD22	1:E:307:ASN:C	2.07	0.57
1:D:235:ALA:O	1:D:322:VAL:HA	2.05	0.56
1:E:62:MET:O	1:E:150:MET:HG3	2.05	0.56
1:D:309:ILE:O	1:D:313:GLU:HB2	2.05	0.56
1:A:218:ILE:HD12	1:A:310:GLU:HG2	1.86	0.56
1:F:106:LEU:HD12	1:F:124:PHE:HB3	1.86	0.56
1:C:22:PRO:HB2	1:C:221:ASN:HD21	1.71	0.56
1:C:301:TYR:O	1:C:320:PHE:HB2	2.05	0.56
1:B:142:VAL:HB	1:B:143:PRO:HD3	1.88	0.56
1:B:62:MET:O	1:B:150:MET:HG3	2.06	0.56
1:A:207:VAL:O	1:A:211:ARG:HG3	2.06	0.55
1:D:46:GLU:OE2	1:D:48:LYS:HD3	2.06	0.55
1:C:307:ASN:C	1:C:307:ASN:HD22	2.08	0.55
1:E:198:THR:OG1	1:E:201:GLU:HB2	2.06	0.55
1:D:277:ASP:OD2	1:F:271:ARG:HD2	2.06	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:77:GLU:O	1:E:78:ASN:HB2	2.07	0.55
1:B:75:VAL:HG11	1:B:81:VAL:HG22	1.88	0.55
1:B:107:GLY:O	1:B:111:LEU:HD12	2.06	0.55
1:B:180:GLU:HB3	1:B:247:GLN:HG2	1.89	0.55
1:F:22:PRO:HB2	1:F:221:ASN:HD21	1.71	0.55
1:F:84:ARG:CZ	1:F:86:ILE:HD11	2.37	0.55
1:F:257:ILE:HD12	1:F:302:ALA:HB3	1.90	0.54
1:A:130:GLY:HA2	1:A:270:PHE:CD2	2.42	0.54
1:A:307:ASN:HA	1:C:249:ASN:O	2.07	0.54
1:D:114:VAL:HG23	1:D:118:GLU:HB2	1.89	0.54
1:E:112:THR:HA	1:E:120:THR:HG21	1.89	0.54
1:F:114:VAL:HG21	1:F:120:THR:HG22	1.90	0.54
1:A:26:HIS:CE1	1:A:74:VAL:H	2.23	0.54
1:C:45:ILE:HG21	1:C:95:HIS:CD2	2.42	0.54
1:E:96:ASN:HD21	1:E:109:GLY:C	2.11	0.54
1:E:173:ASP:OD2	1:E:240:ARG:HD3	2.07	0.54
1:A:62:MET:C	1:A:150:MET:HG3	2.28	0.54
1:A:46:GLU:OE2	1:A:48:LYS:HD3	2.06	0.54
1:C:130:GLY:HA2	1:C:270:PHE:CD2	2.42	0.54
1:C:165:GLU:OE2	1:C:166:LYS:HG3	2.09	0.53
1:D:9:ILE:O	1:D:9:ILE:HG22	2.08	0.53
1:B:228:THR:HB	1:B:319:HIS:CD2	2.43	0.53
1:C:77:GLU:O	1:C:78:ASN:HB2	2.08	0.53
1:C:240:ARG:HB3	1:C:292:PHE:CZ	2.43	0.53
1:C:166:LYS:CB	1:C:168:GLN:NE2	2.72	0.53
1:A:77:GLU:O	1:A:78:ASN:HB2	2.09	0.53
1:F:310:GLU:HA	1:F:314:LEU:HB2	1.89	0.53
1:B:14:ARG:HG3	1:B:14:ARG:NH1	2.22	0.53
1:E:207:VAL:O	1:E:211:ARG:HG3	2.09	0.53
1:B:22:PRO:HB2	1:B:221:ASN:HD21	1.74	0.52
1:F:240:ARG:HB3	1:F:292:PHE:CZ	2.44	0.52
1:B:28:HIS:HE1	1:B:172:TYR:OH	1.93	0.52
1:C:44:THR:H	1:C:65:ASN:ND2	2.06	0.52
1:B:26:HIS:HD2	1:B:27:ALA:O	1.92	0.52
1:A:111:LEU:CD1	1:A:113:GLN:HG3	2.39	0.52
1:B:162:LEU:O	1:B:163:LYS:HD3	2.09	0.52
1:B:19:LEU:HD21	1:B:41:PHE:CD1	2.45	0.52
1:B:94:LEU:C	1:B:94:LEU:HD23	2.30	0.51
1:F:309:ILE:O	1:F:313:GLU:HB2	2.10	0.51
1:C:173:ASP:OD2	1:C:240:ARG:HD3	2.11	0.51
1:F:235:ALA:O	1:F:322:VAL:HA	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:106:LEU:CD1	1:A:122:LEU:HD21	2.29	0.51
1:F:62:MET:O	1:F:150:MET:HG3	2.10	0.51
1:F:106:LEU:HD22	1:F:122:LEU:CD1	2.31	0.51
1:A:307:ASN:C	1:A:307:ASN:HD22	2.14	0.51
1:D:143:PRO:HG2	4:D:648:HOH:O	2.09	0.51
1:B:130:GLY:HA2	1:B:270:PHE:CD2	2.45	0.51
1:C:268:GLY:C	1:C:269:LYS:HE3	2.31	0.51
1:F:287:THR:HG22	1:F:288:ALA:N	2.26	0.51
1:F:130:GLY:HA2	1:F:270:PHE:CD2	2.45	0.51
1:C:187:LYS:HA	1:C:192:ASN:O	2.11	0.50
1:E:19:LEU:HD13	1:E:71:PRO:CG	2.40	0.50
1:B:87:ASN:HB3	1:B:114:VAL:HG12	1.93	0.50
1:F:84:ARG:HD3	1:F:119:GLU:OE1	2.11	0.50
1:A:211:ARG:NH2	4:A:539:HOH:O	2.45	0.50
1:B:26:HIS:HE1	1:B:74:VAL:H	1.60	0.50
1:C:112:THR:CG2	1:C:122:LEU:HD13	2.38	0.50
1:C:138:PRO:HG2	1:C:145:HIS:CE1	2.47	0.50
1:E:265:TRP:CE2	1:E:274:PRO:HB3	2.46	0.50
1:C:166:LYS:HB2	1:C:168:GLN:NE2	2.27	0.50
1:D:218:ILE:HD12	1:D:310:GLU:HG2	1.94	0.50
1:B:13:PRO:HG2	1:B:37:ARG:NH1	2.26	0.49
1:E:112:THR:CG2	1:E:122:LEU:HD13	2.35	0.49
1:B:262:ASP:OD2	1:B:296:ARG:NH2	2.46	0.49
1:D:130:GLY:HA2	1:D:270:PHE:CD2	2.48	0.49
1:E:84:ARG:HH11	1:E:84:ARG:CG	2.26	0.49
1:C:228:THR:HG21	4:C:646:HOH:O	2.13	0.49
1:B:45:ILE:HG21	1:B:95:HIS:CD2	2.47	0.49
1:E:190:ALA:HB3	1:E:192:ASN:ND2	2.28	0.49
1:B:249:ASN:O	1:C:307:ASN:HA	2.13	0.49
1:D:62:MET:O	1:D:150:MET:HG3	2.13	0.48
1:A:54:ARG:HH21	1:A:224:VAL:HG12	1.79	0.48
1:A:173:ASP:OD2	1:A:240:ARG:HD3	2.13	0.48
1:F:26:HIS:HE1	1:F:74:VAL:N	2.06	0.48
1:A:94:LEU:HD12	1:A:95:HIS:N	2.27	0.48
1:D:114:VAL:O	1:D:114:VAL:HG13	2.13	0.48
1:A:265:TRP:CE2	1:A:274:PRO:HB3	2.49	0.48
1:C:235:ALA:O	1:C:322:VAL:HA	2.13	0.48
1:D:99:PHE:HD1	1:D:106:LEU:HD23	1.79	0.48
1:E:14:ARG:CG	1:E:14:ARG:NH1	2.63	0.48
1:E:240:ARG:HB3	1:E:292:PHE:CZ	2.49	0.48
1:F:207:VAL:O	1:F:211:ARG:HG3	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:94:LEU:HD23	1:C:95:HIS:N	2.28	0.48
1:B:263:TYR:HB2	1:B:292:PHE:HB3	1.94	0.47
1:A:114:VAL:HG23	1:A:114:VAL:O	2.14	0.47
1:A:106:LEU:HD13	1:A:122:LEU:CD2	2.30	0.47
1:A:39:VAL:HG21	1:A:75:VAL:HG12	1.95	0.47
1:B:114:VAL:HG13	1:B:118:GLU:HB2	1.96	0.47
1:D:77:GLU:O	1:D:78:ASN:HB2	2.14	0.47
1:F:114:VAL:HG13	1:F:118:GLU:HB2	1.96	0.47
1:A:240:ARG:HB3	1:A:292:PHE:CZ	2.49	0.47
1:D:305:ASN:O	1:D:311:ALA:HB2	2.15	0.47
1:E:196:TYR:CG	1:E:202:ALA:HB2	2.49	0.47
1:B:81:VAL:O	1:B:123:ARG:HA	2.15	0.47
1:B:26:HIS:O	1:B:28:HIS:HD2	1.98	0.47
1:B:31:VAL:HG13	1:B:160:ASP:HA	1.97	0.47
1:E:19:LEU:HD21	1:E:41:PHE:HD2	1.80	0.47
1:B:97:ILE:CG2	1:B:122:LEU:HD21	2.45	0.47
1:B:69:PRO:HG3	1:B:179:GLY:HA3	1.96	0.46
1:F:265:TRP:CE2	1:F:274:PRO:HB3	2.50	0.46
1:B:301:TYR:O	1:B:320:PHE:HB2	2.15	0.46
1:A:102:ALA:HB2	1:A:124:PHE:CG	2.51	0.46
1:A:287:THR:HG22	1:A:288:ALA:N	2.31	0.46
1:F:180:GLU:HB3	1:F:247:GLN:HG2	1.96	0.46
1:F:218:ILE:HD12	1:F:310:GLU:HB3	1.96	0.46
1:E:249:ASN:O	1:F:307:ASN:HA	2.15	0.46
1:C:218:ILE:CD1	1:C:310:GLU:HG2	2.46	0.46
1:D:240:ARG:HB3	1:D:292:PHE:CZ	2.50	0.46
1:E:142:VAL:CG1	1:F:308:LEU:HD13	2.45	0.46
1:D:13:PRO:HB2	1:D:37:ARG:CD	2.45	0.46
1:E:137:ALA:HA	1:E:142:VAL:HG22	1.98	0.46
1:B:228:THR:HB	1:B:319:HIS:HD2	1.79	0.45
1:B:307:ASN:C	1:B:307:ASN:HD22	2.20	0.45
1:A:142:VAL:HB	1:A:143:PRO:CD	2.46	0.45
1:A:180:GLU:HB3	1:A:247:GLN:HG2	1.98	0.45
1:D:263:TYR:HB2	1:D:292:PHE:HB3	1.97	0.45
1:F:62:MET:C	1:F:150:MET:HG3	2.37	0.45
1:D:249:ASN:O	1:E:307:ASN:HA	2.15	0.45
1:C:166:LYS:HB3	1:C:168:GLN:NE2	2.31	0.45
1:D:75:VAL:HG11	1:D:81:VAL:HG22	1.99	0.45
1:D:265:TRP:CE2	1:D:274:PRO:HB3	2.52	0.45
1:E:19:LEU:HD13	1:E:71:PRO:HG3	1.98	0.45
1:F:76:HIS:HD2	4:F:625:HOH:O	2.00	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:5:ALA:HA	1:D:6:PRO:HD3	1.52	0.45
1:D:45:ILE:HG21	1:D:95:HIS:CD2	2.51	0.45
1:D:62:MET:C	1:D:150:MET:HG3	2.37	0.45
1:A:309:ILE:O	1:A:313:GLU:HB2	2.17	0.45
1:B:13:PRO:HG2	1:B:37:ARG:HH12	1.82	0.45
1:B:237:VAL:HG23	1:B:323:THR:O	2.17	0.45
1:F:94:LEU:C	1:F:94:LEU:HD23	2.37	0.45
1:A:237:VAL:HG23	1:A:323:THR:O	2.17	0.44
1:D:99:PHE:H	1:D:106:LEU:HD21	1.81	0.44
1:C:265:TRP:CE2	1:C:274:PRO:HB3	2.53	0.44
1:C:268:GLY:O	1:C:269:LYS:HE3	2.17	0.44
1:E:309:ILE:O	1:E:313:GLU:HB2	2.17	0.44
1:A:189:GLU:HA	1:A:189:GLU:OE1	2.17	0.44
1:E:196:TYR:CD2	1:E:202:ALA:HB2	2.52	0.44
1:A:14:ARG:NH1	1:A:40:GLU:OE2	2.51	0.44
1:A:277:ASP:O	1:C:269:LYS:HD2	2.17	0.44
1:C:94:LEU:HD23	1:C:94:LEU:C	2.38	0.44
1:F:81:VAL:O	1:F:123:ARG:HA	2.17	0.44
1:A:141:MET:HE3	1:A:145:HIS:NE2	2.33	0.44
1:E:263:TYR:HB2	1:E:292:PHE:HB3	1.99	0.44
1:F:255:HIS:ND1	1:F:279:GLU:O	2.51	0.44
1:A:111:LEU:HD12	1:A:113:GLN:H	1.83	0.44
1:B:235:ALA:O	1:B:322:VAL:HA	2.18	0.44
1:C:197:GLU:HB2	1:C:201:GLU:OE1	2.17	0.44
1:F:105:ALA:C	1:F:107:GLY:H	2.21	0.44
1:D:255:HIS:ND1	1:D:279:GLU:O	2.51	0.43
1:F:12:LEU:HA	1:F:13:PRO:HD3	1.83	0.43
1:E:130:GLY:HA2	1:E:270:PHE:CD2	2.54	0.43
1:B:29:ASP:O	1:B:76:HIS:CE1	2.70	0.43
1:D:84:ARG:CZ	1:D:86:ILE:HD11	2.49	0.43
1:A:34:THR:O	1:A:159:ARG:NH2	2.52	0.43
1:D:307:ASN:HA	1:F:249:ASN:O	2.19	0.43
1:E:26:HIS:HE1	1:E:74:VAL:H	1.66	0.43
1:E:62:MET:C	1:E:150:MET:HG3	2.39	0.43
1:B:142:VAL:HG12	1:C:308:LEU:HD13	2.00	0.43
1:A:106:LEU:HD23	1:A:124:PHE:HB3	1.99	0.43
1:C:180:GLU:HB3	1:C:247:GLN:HG2	1.99	0.43
1:A:35:GLY:O	1:A:37:ARG:HG3	2.18	0.43
1:B:113:GLN:HE21	1:B:115:ASN:HD21	1.64	0.43
1:D:26:HIS:HE1	1:D:74:VAL:N	2.10	0.43
1:A:81:VAL:O	1:A:123:ARG:HA	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:306:HIS:O	1:A:306:HIS:ND1	2.52	0.42
1:E:112:THR:CA	1:E:120:THR:HG21	2.49	0.42
1:A:45:ILE:HG21	1:A:95:HIS:CD2	2.54	0.42
1:A:255:HIS:ND1	1:A:279:GLU:O	2.48	0.42
1:A:136:CYS:HB2	1:A:150:MET:HB3	2.02	0.42
1:C:45:ILE:HD13	1:C:95:HIS:HB2	2.02	0.42
1:E:113:GLN:HE21	1:E:113:GLN:HB2	1.57	0.42
1:C:65:ASN:HD22	1:C:65:ASN:HA	1.61	0.42
1:B:146:VAL:HG21	1:C:308:LEU:CD1	2.49	0.42
1:C:96:ASN:C	1:C:96:ASN:HD22	2.23	0.42
1:B:265:TRP:CE2	1:B:274:PRO:HB3	2.55	0.42
1:D:106:LEU:HD23	1:D:122:LEU:HD21	2.02	0.42
1:D:146:VAL:HG21	1:E:308:LEU:HD12	2.01	0.42
1:D:204:GLU:OE1	1:D:204:GLU:HA	2.19	0.42
1:E:189:GLU:OE1	1:E:189:GLU:HA	2.20	0.42
1:C:62:MET:C	1:C:150:MET:HG3	2.40	0.42
1:C:75:VAL:HG11	1:C:81:VAL:HG22	2.01	0.42
1:E:12:LEU:HA	1:E:13:PRO:HD3	1.80	0.42
1:E:112:THR:CG2	1:E:122:LEU:HD22	2.46	0.42
1:E:218:ILE:HD12	1:E:310:GLU:HG2	2.02	0.42
1:F:173:ASP:OD1	1:F:240:ARG:NH1	2.52	0.42
1:A:106:LEU:CD2	1:A:124:PHE:HB3	2.50	0.42
1:D:114:VAL:HG23	1:D:118:GLU:CB	2.50	0.41
1:B:12:LEU:O	1:B:14:ARG:NH1	2.53	0.41
1:D:99:PHE:HD1	1:D:106:LEU:CD2	2.33	0.41
1:D:12:LEU:HA	1:D:13:PRO:HD3	1.93	0.41
1:A:106:LEU:HB3	1:A:122:LEU:HD11	2.02	0.41
1:C:81:VAL:O	1:C:123:ARG:HA	2.20	0.41
1:D:115:ASN:HB3	1:D:116:PRO:CD	2.50	0.41
1:D:77:GLU:O	1:D:159:ARG:NH1	2.51	0.41
1:E:19:LEU:HD21	1:E:41:PHE:CD2	2.55	0.41
1:F:250:ARG:NH2	1:F:310:GLU:OE2	2.48	0.41
1:A:26:HIS:HD2	1:A:27:ALA:O	2.03	0.41
1:E:39:VAL:HG12	1:E:41:PHE:CE1	2.55	0.41
1:A:82:GLU:HA	1:A:122:LEU:O	2.20	0.41
1:B:34:THR:HB	1:B:37:ARG:NH2	2.36	0.41
1:B:218:ILE:HD12	1:B:310:GLU:HG2	2.01	0.41
1:D:132:PHE:CE2	1:D:269:LYS:HE3	2.55	0.41
1:D:257:ILE:HD12	1:D:302:ALA:CB	2.44	0.41
1:A:28:HIS:CD2	1:A:74:VAL:HG11	2.56	0.40
1:C:69:PRO:HD2	1:C:221:ASN:HD22	1.86	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:308:LEU:HD13	1:F:142:VAL:HG12	2.03	0.40
1:D:69:PRO:HG3	1:D:179:GLY:HA3	2.03	0.40
1:F:14:ARG:NH1	1:F:40:GLU:OE2	2.54	0.40
1:F:141:MET:HE3	1:F:145:HIS:HE2	1.86	0.40
1:B:114:VAL:HG21	1:B:120:THR:HG22	2.02	0.40
1:C:138:PRO:HG2	1:C:145:HIS:ND1	2.37	0.40
1:E:84:ARG:CG	1:E:84:ARG:NH1	2.82	0.40
1:E:142:VAL:HG12	1:F:308:LEU:HD13	2.03	0.40
1:F:165:GLU:OE1	1:F:165:GLU:N	2.55	0.40
1:F:307:ASN:CG	1:F:310:GLU:HG3	2.42	0.40
1:E:84:ARG:HG2	1:E:84:ARG:NH1	2.31	0.40

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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	312/329 (95%)	297 (95%)	14 (4%)	1 (0%)	41	64
1	B	314/329 (95%)	301 (96%)	13 (4%)	0	100	100
1	C	314/329 (95%)	307 (98%)	7 (2%)	0	100	100
1	D	318/329 (97%)	305 (96%)	10 (3%)	3 (1%)	17	35
1	E	313/329 (95%)	297 (95%)	16 (5%)	0	100	100
1	F	321/329 (98%)	302 (94%)	18 (6%)	1 (0%)	41	64
All	All	1892/1974 (96%)	1809 (96%)	78 (4%)	5 (0%)	41	64

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	106	LEU

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Mol	Chain	Res	Type
1	D	6	PRO
1	D	114	VAL
1	F	112	THR
1	D	107	GLY

5.3.2 Protein sidechains (i)

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	253/263 (96%)	244 (96%)	9 (4%)	35	61
1	B	255/263 (97%)	243 (95%)	12 (5%)	26	50
1	C	255/263 (97%)	241 (94%)	14 (6%)	21	43
1	D	258/263 (98%)	251 (97%)	7 (3%)	44	71
1	E	254/263 (97%)	244 (96%)	10 (4%)	32	58
1	F	261/263 (99%)	253 (97%)	8 (3%)	40	66
All	All	1536/1578 (97%)	1476 (96%)	60 (4%)	32	58

All (60) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	94	LEU
1	A	111	LEU
1	A	136	CYS
1	A	189	GLU
1	A	204	GLU
1	A	221	ASN
1	A	230	ASP
1	A	307	ASN
1	A	320	PHE
1	B	15	VAL
1	B	54	ARG
1	B	90	THR
1	B	136	CYS
1	B	150	MET

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Mol	Chain	Res	Type
1	B	159	ARG
1	B	221	ASN
1	B	253	ARG
1	B	296	ARG
1	B	307	ASN
1	B	320	PHE
1	B	326	TRP
1	C	17	VAL
1	C	54	ARG
1	C	65	ASN
1	C	96	ASN
1	C	139	GLU
1	C	189	GLU
1	C	221	ASN
1	C	230	ASP
1	C	253	ARG
1	C	296	ARG
1	C	307	ASN
1	C	314	LEU
1	C	320	PHE
1	C	321	LYS
1	D	94	LEU
1	D	111	LEU
1	D	213	LEU
1	D	221	ASN
1	D	253	ARG
1	D	307	ASN
1	D	320	PHE
1	E	10	SER
1	E	14	ARG
1	E	18	ASP
1	E	37	ARG
1	E	84	ARG
1	E	113	GLN
1	E	136	CYS
1	E	221	ASN
1	E	307	ASN
1	E	320	PHE
1	F	17	VAL
1	F	94	LEU
1	F	96	ASN
1	F	136	CYS

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Mol	Chain	Res	Type
1	F	160	ASP
1	F	189	GLU
1	F	221	ASN
1	F	320	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (41) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	26	HIS
1	A	78	ASN
1	A	221	ASN
1	A	307	ASN
1	B	26	HIS
1	B	28	HIS
1	B	78	ASN
1	B	115	ASN
1	B	192	ASN
1	B	221	ASN
1	B	307	ASN
1	B	319	HIS
1	C	26	HIS
1	C	28	HIS
1	C	65	ASN
1	C	78	ASN
1	C	96	ASN
1	C	168	GLN
1	C	221	ASN
1	C	307	ASN
1	C	319	HIS
1	D	26	HIS
1	D	28	HIS
1	D	78	ASN
1	D	221	ASN
1	D	307	ASN
1	E	26	HIS
1	E	78	ASN
1	E	96	ASN
1	E	113	GLN
1	E	192	ASN
1	E	221	ASN
1	E	297	GLN
1	E	307	ASN

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Mol	Chain	Res	Type
1	F	26	HIS
1	F	76	HIS
1	F	78	ASN
1	F	96	ASN
1	F	113	GLN
1	F	221	ASN
1	F	327	ASN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 18 ligands modelled in this entry, 18 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

6 Fit of model and data (i)

6.1 Protein, DNA and RNA chains (i)

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, 95th 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^2)	Q<0.9
1	A	314/329 (95%)	-0.55	6 (1%)	66	62	11, 26, 51, 79	0
1	B	316/329 (96%)	-0.47	6 (1%)	66	62	15, 31, 56, 75	0
1	C	316/329 (96%)	-0.54	3 (0%)	84	82	13, 27, 55, 66	0
1	D	320/329 (97%)	-0.39	12 (3%)	40	33	16, 31, 63, 74	0
1	E	315/329 (95%)	-0.44	5 (1%)	72	68	15, 31, 58, 68	0
1	F	323/329 (98%)	-0.53	6 (1%)	66	62	12, 26, 58, 71	0
All	All	1904/1974 (96%)	-0.49	38 (1%)	65	60	11, 29, 57, 79	0

All (38) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	108	GLY	6.3
1	A	109	GLY	6.0
1	A	110	ALA	5.6
1	B	326	TRP	5.2
1	D	111	LEU	4.0
1	D	109	GLY	4.0
1	B	107	GLY	3.9
1	A	107	GLY	3.6
1	E	189	GLU	3.6
1	F	190	ALA	3.6
1	D	190	ALA	3.6
1	B	325	GLU	3.3
1	D	108	GLY	3.2
1	C	190	ALA	3.0
1	C	324	GLY	2.9
1	D	105	ALA	2.9
1	A	325	GLU	2.8
1	D	230	ASP	2.7
1	B	189	GLU	2.7

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Mol	Chain	Res	Type	RSRZ
1	E	190	ALA	2.6
1	D	189	GLU	2.4
1	D	188	ASP	2.4
1	D	107	GLY	2.4
1	D	197	GLU	2.3
1	F	191	GLY	2.3
1	E	11	THR	2.3
1	F	108	GLY	2.2
1	D	200	GLY	2.2
1	E	324	GLY	2.2
1	A	189	GLU	2.2
1	C	123	ARG	2.2
1	B	190	ALA	2.2
1	D	191	GLY	2.1
1	F	327	ASN	2.1
1	F	230	ASP	2.1
1	E	110	ALA	2.0
1	F	325	GLU	2.0
1	B	191	GLY	2.0

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

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates (i)

There are no monosaccharides in this entry.

6.4 Ligands (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. The B-factors column lists the minimum, median, 95th 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	B-factors(Å^2)	Q<0.9
2	CU	D	501	1/1	0.98	0.07	37,37,37,37	0
2	CU	C	501	1/1	0.99	0.04	32,32,32,32	0
2	CU	A	501	1/1	0.99	0.03	19,19,19,19	0
2	CU	F	501	1/1	0.99	0.07	26,26,26,26	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
3	CL	B	602	1/1	0.99	0.07	29,29,29,29	0
3	CL	C	603	1/1	0.99	0.06	26,26,26,26	0
3	CL	F	605	1/1	0.99	0.05	22,22,22,22	0
2	CU	B	502	1/1	1.00	0.03	14,14,14,14	0
2	CU	E	502	1/1	1.00	0.03	16,16,16,16	0
2	CU	E	501	1/1	1.00	0.06	29,29,29,29	0
2	CU	F	502	1/1	1.00	0.03	12,12,12,12	0
2	CU	B	501	1/1	1.00	0.06	25,25,25,25	0
3	CL	B	601	1/1	1.00	0.05	26,26,26,26	0
2	CU	C	502	1/1	1.00	0.03	16,16,16,16	0
2	CU	A	502	1/1	1.00	0.05	16,16,16,16	0
3	CL	D	604	1/1	1.00	0.03	31,31,31,31	0
2	CU	D	502	1/1	1.00	0.02	17,17,17,17	0
3	CL	F	606	1/1	1.00	0.04	28,28,28,28	0

6.5 Other polymers (i)

There are no such residues in this entry.