



Full wwPDB X-ray Structure Validation Report ⓘ

Jul 13, 2016 – 10:34 AM EDT

PDB ID : 5B7O
Title : Crystal structure of proliferating cell nuclear antigen from Leishmania donovani at 2.95 Angstrom resolution
Authors : Yadav, S.P.; Singh, P.K.; Sharma, P.; Kaur, P.; Sharma, S.; Singh, T.P.
Deposited on : 2016-06-08
Resolution : 2.95 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
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : unknown
Xtriage (Phenix) : 1.9-1692
EDS : rb-20027790
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) : rb-20027790

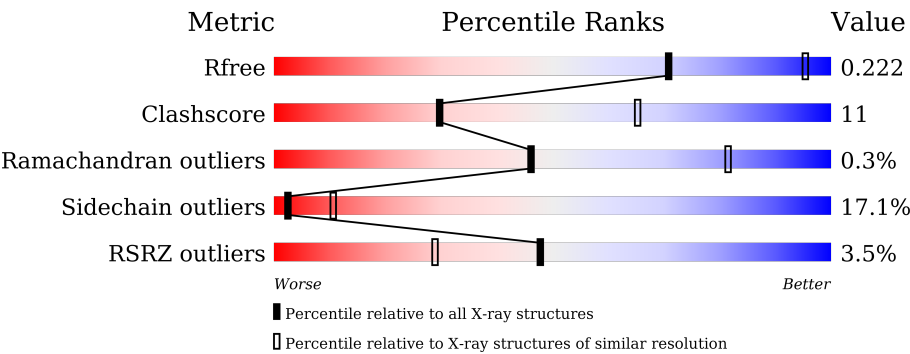
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.95 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	2184 (3.00-2.92)
Clashscore	102246	2552 (3.00-2.92)
Ramachandran outliers	100387	2468 (3.00-2.92)
Sidechain outliers	100360	2471 (3.00-2.92)
RSRZ outliers	91569	2201 (3.00-2.92)

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 ≥ 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	292	<div><div>0%</div><div><div>59%</div><div>21%</div><div>• •</div><div>15%</div></div></div>
1	B	292	<div><div>2%</div><div><div>61%</div><div>20%</div><div>• •</div><div>15%</div></div></div>
1	C	292	<div><div>5%</div><div><div>58%</div><div>20%</div><div>5% •</div><div>15%</div></div></div>
1	D	292	<div><div>2%</div><div><div>58%</div><div>18%</div><div>8% •</div><div>15%</div></div></div>
1	E	292	<div><div>5%</div><div><div>56%</div><div>21%</div><div>8%</div><div>15%</div></div></div>
1	F	292	<div><div>3%</div><div><div>58%</div><div>20%</div><div>6% •</div><div>15%</div></div></div>

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 11525 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 Proliferating cell nuclear antigen.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	248	Total	C	N	O	S	0	0	0
			1919	1210	317	377	15			
1	B	248	Total	C	N	O	S	0	0	0
			1919	1210	317	377	15			
1	C	248	Total	C	N	O	S	0	0	0
			1919	1210	317	377	15			
1	D	248	Total	C	N	O	S	0	0	0
			1919	1210	317	377	15			
1	E	248	Total	C	N	O	S	0	0	0
			1919	1210	317	377	15			
1	F	248	Total	C	N	O	S	0	0	0
			1919	1210	317	377	15			

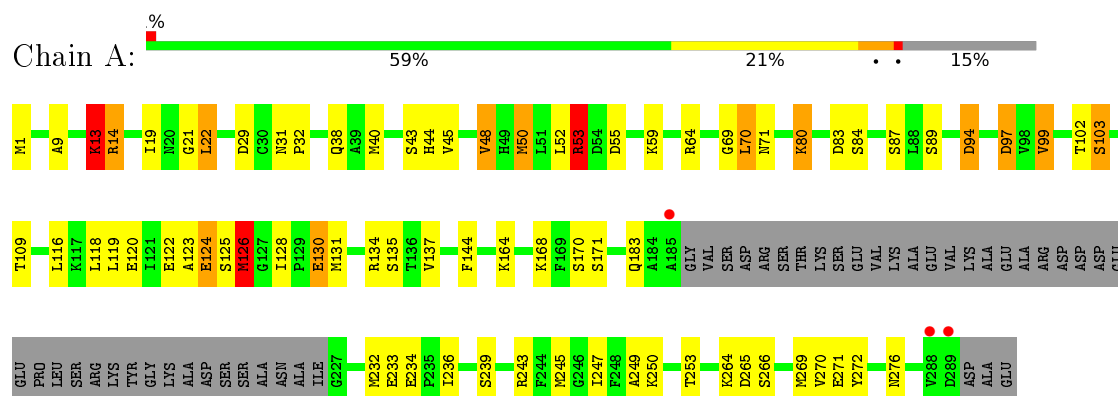
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	4	Total	O	0	0
			4	4		
2	B	1	Total	O	0	0
			1	1		
2	C	1	Total	O	0	0
			1	1		
2	E	1	Total	O	0	0
			1	1		
2	F	4	Total	O	0	0
			4	4		

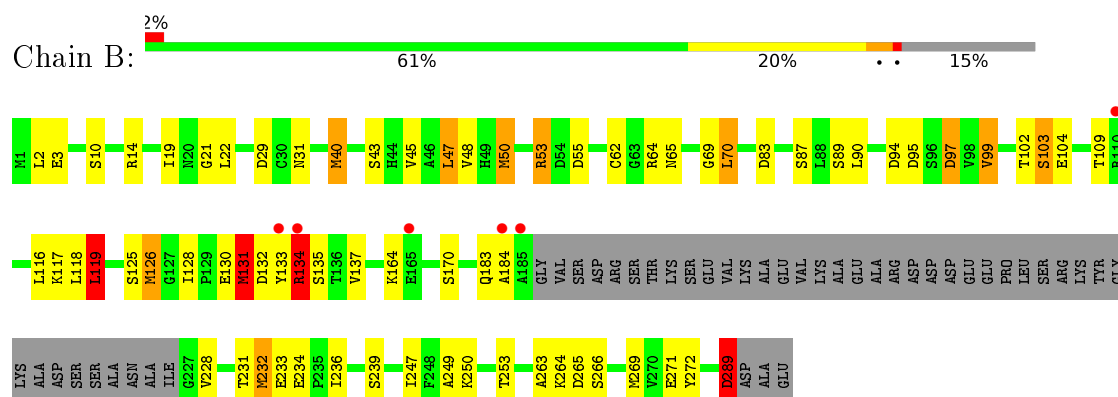
3 Residue-property plots

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.

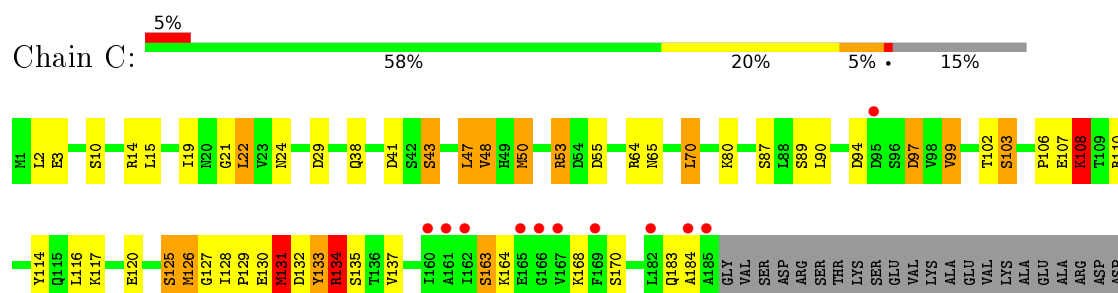
- Molecule 1: Proliferating cell nuclear antigen

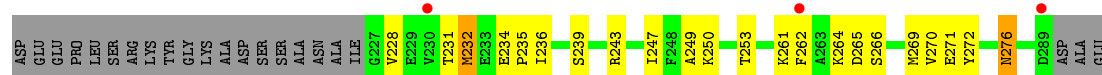


- Molecule 1: Proliferating cell nuclear antigen

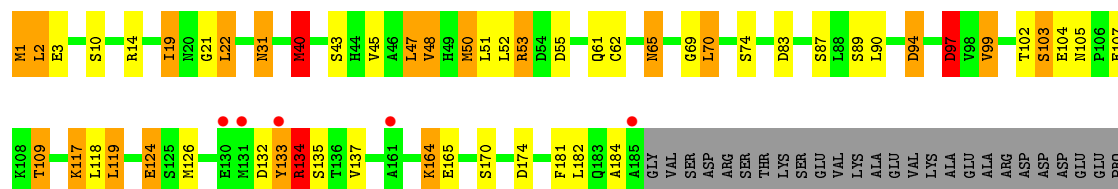


- Molecule 1: Proliferating cell nuclear antigen

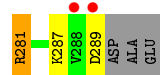
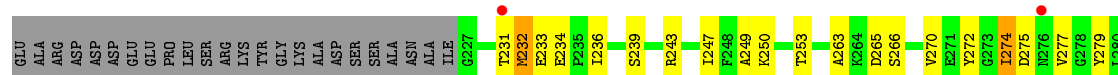
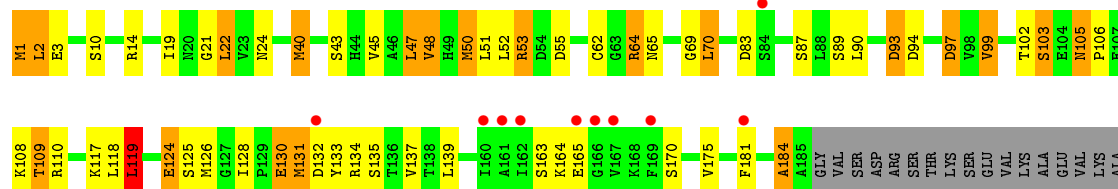




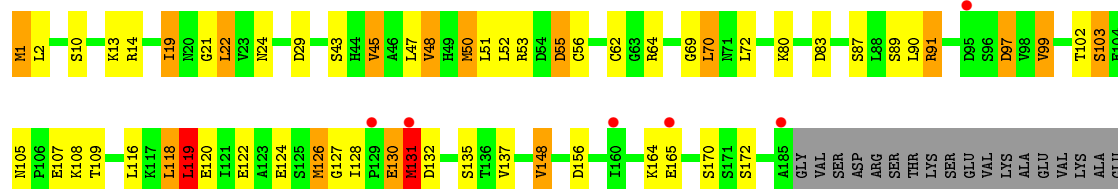
• Molecule 1: Proliferating cell nuclear antigen



• Molecule 1: Proliferating cell nuclear antigen



• Molecule 1: Proliferating cell nuclear antigen



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	135.02Å 150.66Å 170.55Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 2.95 43.49 – 2.95	Depositor EDS
% Data completeness (in resolution range)	98.8 (50.00-2.95) 98.8 (43.49-2.95)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.12	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.08 (at 2.95Å)	Xtrriage
Refinement program	REFMAC 5.8.0151	Depositor
R, R_{free}	0.210 , 0.222 0.214 , 0.222	Depositor DCC
R_{free} test set	1437 reflections (2.02%)	DCC
Wilson B-factor (Å ²)	88.8	Xtrriage
Anisotropy	0.234	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 51.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	11525	wwPDB-VP
Average B, all atoms (Å ²)	99.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.93% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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	0.88	1/1947 (0.1%)	1.15	12/2627 (0.5%)
1	B	0.85	0/1947	1.16	14/2627 (0.5%)
1	C	0.87	0/1947	1.19	14/2627 (0.5%)
1	D	0.85	0/1947	1.11	14/2627 (0.5%)
1	E	0.83	0/1947	1.17	17/2627 (0.6%)
1	F	0.82	1/1947 (0.1%)	1.19	17/2627 (0.6%)
All	All	0.85	2/11682 (0.0%)	1.16	88/15762 (0.6%)

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	B	0	2
1	C	0	3
1	D	0	1
1	E	0	1
All	All	0	7

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	171	SER	CB-OG	-6.02	1.34	1.42
1	F	89	SER	CB-OG	-5.40	1.35	1.42

All (88) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	29	ASP	CB-CG-OD1	16.16	132.84	118.30
1	B	97	ASP	CB-CG-OD1	14.63	131.47	118.30
1	C	97	ASP	CB-CG-OD1	13.64	130.57	118.30
1	A	97	ASP	CB-CG-OD1	13.22	130.19	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	97	ASP	CB-CG-OD2	10.70	127.93	118.30
1	E	2	LEU	CB-CG-CD2	10.61	129.03	111.00
1	F	29	ASP	CB-CG-OD2	-10.44	108.91	118.30
1	F	1	MET	CG-SD-CE	10.01	116.22	100.20
1	D	132	ASP	CB-CG-OD1	-9.73	109.55	118.30
1	B	289	ASP	CB-CG-OD1	9.29	126.66	118.30
1	D	40	MET	CA-CB-CG	9.24	129.01	113.30
1	C	126	MET	CG-SD-CE	8.63	114.00	100.20
1	C	133	TYR	N-CA-C	8.29	133.37	111.00
1	F	13	LYS	CD-CE-NZ	8.18	130.52	111.70
1	B	97	ASP	CB-CG-OD2	-7.97	111.12	118.30
1	F	83	ASP	CB-CG-OD1	7.54	125.09	118.30
1	E	97	ASP	CB-CG-OD1	-7.51	111.54	118.30
1	A	126	MET	CG-SD-CE	7.50	112.20	100.20
1	E	131	MET	CB-CG-SD	7.47	134.83	112.40
1	C	53	ARG	NE-CZ-NH2	-7.43	116.59	120.30
1	F	156	ASP	CB-CG-OD1	7.09	124.68	118.30
1	F	91	ARG	NE-CZ-NH2	-6.89	116.85	120.30
1	E	93	ASP	CB-CG-OD2	6.75	124.38	118.30
1	C	55	ASP	CB-CG-OD2	6.67	124.30	118.30
1	E	83	ASP	CB-CG-OD1	6.35	124.02	118.30
1	E	53	ARG	NE-CZ-NH1	6.33	123.46	120.30
1	A	97	ASP	CB-CG-OD2	-6.30	112.63	118.30
1	F	119	LEU	C-N-CA	6.09	136.92	121.70
1	D	232	MET	CA-CB-CG	6.05	123.59	113.30
1	C	134	ARG	CB-CA-C	-6.05	98.30	110.40
1	A	53	ARG	NE-CZ-NH2	-6.03	117.28	120.30
1	D	48	VAL	CB-CA-C	-6.01	99.98	111.40
1	B	119	LEU	C-N-CA	5.95	136.56	121.70
1	A	14	ARG	NE-CZ-NH1	-5.92	117.34	120.30
1	B	48	VAL	CB-CA-C	-5.91	100.17	111.40
1	E	119	LEU	O-C-N	-5.91	113.25	122.70
1	E	48	VAL	CB-CA-C	-5.87	100.24	111.40
1	F	48	VAL	CB-CA-C	-5.85	100.29	111.40
1	A	70	LEU	CB-CA-C	-5.84	99.10	110.20
1	E	131	MET	CG-SD-CE	-5.84	90.86	100.20
1	C	48	VAL	CB-CA-C	-5.83	100.32	111.40
1	C	43	SER	CB-CA-C	-5.83	99.02	110.10
1	B	134	ARG	NE-CZ-NH1	5.82	123.21	120.30
1	D	90	LEU	CB-CG-CD1	-5.80	101.13	111.00
1	B	126	MET	CG-SD-CE	5.79	109.47	100.20
1	C	110	ARG	NE-CZ-NH2	-5.79	117.41	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	94	ASP	CB-CG-OD2	5.76	123.49	118.30
1	D	133	TYR	CB-CG-CD1	5.75	124.45	121.00
1	F	116	LEU	CB-CG-CD1	5.74	120.76	111.00
1	F	126	MET	CG-SD-CE	5.71	109.33	100.20
1	D	2	LEU	CB-CG-CD2	-5.68	101.34	111.00
1	C	117	LYS	CA-CB-CG	-5.68	100.91	113.40
1	E	119	LEU	C-N-CA	5.68	135.89	121.70
1	B	95	ASP	CB-CG-OD2	-5.67	113.20	118.30
1	E	64	ARG	CA-CB-CG	5.65	125.83	113.40
1	B	94	ASP	CB-CG-OD1	5.65	123.38	118.30
1	A	83	ASP	CB-CG-OD1	5.64	123.38	118.30
1	B	126	MET	CB-CG-SD	5.63	129.31	112.40
1	D	289	ASP	CB-CG-OD2	5.60	123.34	118.30
1	D	1	MET	CG-SD-CE	5.59	109.14	100.20
1	F	45	VAL	CG1-CB-CG2	-5.55	102.03	110.90
1	F	1	MET	CA-CB-CG	5.54	122.71	113.30
1	D	133	TYR	CB-CG-CD2	-5.52	117.69	121.00
1	F	148	VAL	CA-CB-CG1	5.51	119.17	110.90
1	D	83	ASP	CB-CG-OD1	5.49	123.24	118.30
1	B	83	ASP	CB-CG-OD1	5.46	123.21	118.30
1	A	80	LYS	CD-CE-NZ	5.44	124.21	111.70
1	A	48	VAL	CB-CA-C	-5.43	101.08	111.40
1	C	117	LYS	CB-CG-CD	5.43	125.72	111.60
1	E	181	PHE	CB-CG-CD2	-5.40	117.02	120.80
1	E	110	ARG	NE-CZ-NH1	5.39	122.99	120.30
1	F	119	LEU	O-C-N	-5.39	114.08	122.70
1	F	55	ASP	CB-CA-C	-5.36	99.68	110.40
1	E	83	ASP	CB-CG-OD2	-5.35	113.48	118.30
1	C	108	LYS	N-CA-C	5.31	125.33	111.00
1	D	97	ASP	CB-CG-OD1	5.27	123.04	118.30
1	A	13	LYS	CB-CG-CD	5.25	125.25	111.60
1	B	131	MET	CA-CB-CG	5.20	122.14	113.30
1	D	117	LYS	CA-CB-CG	5.20	124.84	113.40
1	F	131	MET	CG-SD-CE	5.19	108.51	100.20
1	E	289	ASP	CB-CA-C	5.19	120.78	110.40
1	A	164	LYS	CD-CE-NZ	-5.16	99.83	111.70
1	C	50	MET	CG-SD-CE	5.14	108.42	100.20
1	B	134	ARG	CA-CB-CG	5.08	124.57	113.40
1	C	47	LEU	CB-CG-CD2	5.06	119.61	111.00
1	E	275	ASP	CB-CG-OD1	5.06	122.85	118.30
1	B	50	MET	CG-SD-CE	5.04	108.27	100.20
1	A	164	LYS	N-CA-CB	5.02	119.64	110.60

There are no chirality outliers.

All (7) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	131	MET	Peptide
1	B	134	ARG	Peptide
1	C	125	SER	Peptide
1	C	131	MET	Peptide
1	C	134	ARG	Mainchain
1	D	134	ARG	Peptide
1	E	274	ILE	Peptide

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	1919	0	1914	36	0
1	B	1919	0	1914	43	0
1	C	1919	0	1914	47	0
1	D	1919	0	1914	45	0
1	E	1919	0	1914	52	0
1	F	1919	0	1914	40	0
2	A	4	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	1	0
2	E	1	0	0	0	0
2	F	4	0	0	0	0
All	All	11525	0	11484	258	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 (258) 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:C:38:GLN:OE1	1:C:128:ILE:CD1	1.72	1.36
1:C:38:GLN:OE1	1:C:128:ILE:HD11	1.19	1.32
1:D:184:ALA:CB	1:D:228:VAL:O	1.79	1.30

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:106:PRO:O	1:C:107:GLU:HG2	1.30	1.26
1:B:184:ALA:CB	1:B:228:VAL:O	1.84	1.24
1:B:184:ALA:HB1	1:B:228:VAL:O	1.40	1.18
1:E:1:MET:CE	1:E:93:ASP:OD1	1.96	1.13
1:C:106:PRO:O	1:C:107:GLU:CG	1.99	1.11
1:E:124:GLU:OE2	1:E:126:MET:O	1.70	1.09
1:D:184:ALA:HB3	1:D:228:VAL:O	1.49	1.08
1:E:1:MET:HE2	1:E:93:ASP:OD1	1.58	1.03
1:E:132:ASP:OD1	1:E:263:ALA:HB2	1.16	1.02
1:E:124:GLU:CD	1:E:126:MET:O	1.96	1.01
1:C:133:TYR:O	1:C:262:PHE:O	1.84	0.94
1:D:184:ALA:HB1	1:D:228:VAL:O	1.69	0.93
1:E:124:GLU:OE1	1:E:126:MET:O	1.87	0.92
1:A:1:MET:CE	1:A:94:ASP:HA	2.00	0.92
1:E:1:MET:HE3	1:E:93:ASP:OD1	1.69	0.91
1:C:38:GLN:OE1	1:C:128:ILE:HD13	1.73	0.88
1:C:108:LYS:HB3	1:C:108:LYS:NZ	1.89	0.88
1:B:134:ARG:HD3	1:B:234:GLU:HB2	1.52	0.87
1:E:2:LEU:HD23	1:E:3:GLU:N	1.89	0.86
1:B:131:MET:HG2	1:B:132:ASP:HA	1.59	0.85
1:B:131:MET:CG	1:B:132:ASP:HA	2.07	0.84
1:A:1:MET:HE2	1:A:94:ASP:HA	1.60	0.82
1:C:106:PRO:C	1:C:107:GLU:HG2	2.00	0.80
1:C:130:GLU:CA	1:C:131:MET:SD	2.69	0.80
1:F:130:GLU:HB3	1:F:131:MET:HG2	1.61	0.80
1:C:130:GLU:C	1:C:131:MET:SD	2.60	0.80
1:E:132:ASP:OD1	1:E:263:ALA:CB	2.04	0.80
1:C:130:GLU:HA	1:C:131:MET:SD	2.24	0.77
1:C:41:ASP:OD2	1:C:43:SER:HB2	1.84	0.77
1:B:184:ALA:HB2	1:B:228:VAL:O	1.84	0.76
1:A:183:GLN:NE2	1:E:109:THR:HA	2.01	0.76
1:C:128:ILE:HG22	1:C:131:MET:HE1	1.67	0.76
1:E:130:GLU:CB	1:E:131:MET:HB2	2.17	0.73
1:F:128:ILE:HD12	1:F:128:ILE:N	2.03	0.73
1:C:276:ASN:HD22	1:C:276:ASN:N	1.87	0.72
1:B:184:ALA:HB2	1:B:228:VAL:HB	1.69	0.72
1:C:131:MET:SD	1:C:131:MET:N	2.62	0.72
1:C:114:TYR:OH	2:C:301:HOH:O	2.07	0.72
1:F:122:GLU:OE2	1:F:122:GLU:N	2.24	0.71
1:C:108:LYS:HB3	1:C:108:LYS:HZ3	1.54	0.71
1:A:50:MET:CE	1:A:52:LEU:HG	2.21	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:2:LEU:HD12	1:C:3:GLU:N	2.06	0.71
1:F:50:MET:HE3	1:F:52:LEU:HG	1.72	0.71
1:D:50:MET:CE	1:D:52:LEU:HG	2.22	0.69
1:E:50:MET:CE	1:E:52:LEU:HG	2.23	0.69
1:F:50:MET:CE	1:F:52:LEU:HG	2.24	0.67
1:D:181:PHE:C	1:D:182:LEU:HD23	2.16	0.66
1:D:184:ALA:HB2	1:D:228:VAL:HB	1.76	0.66
1:F:99:VAL:HG12	1:F:118:LEU:HD22	1.78	0.66
1:E:10:SER:HB2	1:E:14:ARG:NH1	2.10	0.66
1:D:14:ARG:HD2	1:D:253:THR:HB	1.79	0.65
1:C:128:ILE:HG22	1:C:131:MET:CE	2.27	0.65
1:A:14:ARG:HD2	1:A:253:THR:HB	1.78	0.65
1:B:14:ARG:HD2	1:B:253:THR:HB	1.79	0.65
1:E:124:GLU:OE1	1:E:125:SER:C	2.35	0.65
1:D:107:GLU:HG2	1:D:109:THR:HG22	1.79	0.64
1:A:44:HIS:CE1	1:C:120:GLU:HB2	2.33	0.64
1:E:2:LEU:HD23	1:E:3:GLU:CA	2.27	0.64
1:A:144:PHE:HZ	1:A:245:MET:HE3	1.63	0.64
1:B:134:ARG:HA	1:B:233:GLU:HB3	1.80	0.64
1:E:130:GLU:HB2	1:E:131:MET:HB2	1.80	0.63
1:A:50:MET:HE3	1:A:52:LEU:HG	1.81	0.63
1:C:134:ARG:O	1:C:135:SER:OG	2.15	0.62
1:B:131:MET:HB3	1:B:132:ASP:HB3	1.81	0.62
1:F:14:ARG:HD2	1:F:253:THR:HB	1.81	0.62
1:D:124:GLU:OE1	1:D:124:GLU:HA	1.98	0.62
1:C:269:MET:HE3	1:C:271:GLU:HB2	1.81	0.61
1:F:130:GLU:HB3	1:F:131:MET:CG	2.30	0.61
1:B:134:ARG:HD3	1:B:234:GLU:CB	2.27	0.60
1:C:14:ARG:HD2	1:C:253:THR:HB	1.83	0.60
1:B:2:LEU:HD12	1:B:3:GLU:N	2.17	0.60
1:A:130:GLU:HB2	1:A:131:MET:CB	2.32	0.59
1:E:14:ARG:HD2	1:E:253:THR:HB	1.82	0.59
1:E:128:ILE:HG22	1:E:128:ILE:O	2.01	0.59
1:F:43:SER:OG	1:F:45:VAL:HG23	2.03	0.59
1:B:131:MET:CB	1:B:132:ASP:HA	2.32	0.59
1:D:134:ARG:HB3	1:D:233:GLU:HB2	1.85	0.59
1:A:183:GLN:HE21	1:E:109:THR:HB	1.68	0.59
1:F:105:ASN:OD1	1:F:107:GLU:N	2.36	0.58
1:F:128:ILE:HG22	1:F:128:ILE:O	2.02	0.58
1:F:107:GLU:HG3	1:F:109:THR:HG23	1.85	0.58
1:F:269:MET:HE3	1:F:271:GLU:HB2	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:269:MET:HE3	1:A:271:GLU:HB2	1.86	0.57
1:D:40:MET:HG2	1:D:47:LEU:CD2	2.34	0.57
1:C:106:PRO:O	1:C:107:GLU:HG3	2.02	0.56
1:A:144:PHE:HZ	1:A:245:MET:CE	2.19	0.56
1:B:269:MET:HE3	1:B:271:GLU:HB2	1.88	0.56
1:C:128:ILE:CG2	1:C:131:MET:CE	2.83	0.56
1:B:131:MET:HG2	1:B:132:ASP:CA	2.32	0.56
1:B:134:ARG:NH1	1:B:234:GLU:HG3	2.20	0.56
1:D:105:ASN:ND2	1:D:109:THR:HG23	2.21	0.56
1:E:50:MET:HE3	1:E:52:LEU:HG	1.87	0.56
1:D:43:SER:OG	1:D:45:VAL:HG23	2.06	0.56
1:A:130:GLU:HB2	1:A:131:MET:CA	2.37	0.55
1:E:124:GLU:OE1	1:E:126:MET:N	2.39	0.55
1:E:43:SER:OG	1:E:45:VAL:HG23	2.07	0.55
1:E:105:ASN:HD22	1:E:106:PRO:HD2	1.72	0.55
1:B:40:MET:HG3	1:B:47:LEU:HD23	1.89	0.55
1:A:38:GLN:HG2	1:A:126:MET:HG3	1.90	0.54
1:C:129:PRO:N	1:C:131:MET:HE1	2.23	0.54
1:D:50:MET:HE3	1:D:52:LEU:HG	1.87	0.54
1:F:56:CYS:HB2	1:F:277:VAL:HB	1.88	0.54
1:B:2:LEU:HD12	1:B:3:GLU:H	1.72	0.54
1:D:135:SER:OG	1:D:236:ILE:HG21	2.08	0.54
1:E:40:MET:HG3	1:E:47:LEU:HD22	1.88	0.54
1:C:276:ASN:ND2	1:C:276:ASN:N	2.57	0.53
1:D:269:MET:HE3	1:D:271:GLU:HB2	1.91	0.53
1:F:105:ASN:OD1	1:F:107:GLU:HB3	2.07	0.53
1:B:131:MET:CB	1:B:132:ASP:CA	2.87	0.53
1:D:51:LEU:HD23	1:D:279:TYR:CE1	2.43	0.53
1:E:2:LEU:HD23	1:E:3:GLU:C	2.29	0.53
1:E:40:MET:HG3	1:E:47:LEU:CD2	2.37	0.53
1:B:130:GLU:N	1:B:130:GLU:OE1	2.42	0.53
1:B:31:ASN:HD22	1:B:65:ASN:HB3	1.74	0.52
1:D:31:ASN:HD22	1:D:65:ASN:HB3	1.73	0.52
1:A:135:SER:OG	1:A:236:ILE:HG21	2.10	0.52
1:C:108:LYS:HB3	1:C:108:LYS:HZ2	1.70	0.52
1:E:70:LEU:HD23	1:E:99:VAL:HG11	1.92	0.52
1:D:164:LYS:HG3	1:D:165:GLU:HG3	1.92	0.52
1:A:123:ALA:HB1	1:A:125:SER:OG	2.10	0.52
1:C:135:SER:OG	1:C:236:ILE:HG21	2.10	0.52
1:D:50:MET:HE2	1:D:52:LEU:HG	1.89	0.52
1:B:40:MET:HG3	1:B:47:LEU:CD2	2.40	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:263:ALA:HB3	1:E:266:SER:HB2	1.90	0.52
1:A:50:MET:HE2	1:A:52:LEU:HG	1.92	0.52
1:B:131:MET:HG2	1:B:132:ASP:CB	2.40	0.52
1:B:43:SER:OG	1:B:45:VAL:HG23	2.09	0.52
1:B:134:ARG:HH11	1:B:234:GLU:HG3	1.76	0.51
1:B:135:SER:OG	1:B:236:ILE:HG21	2.09	0.51
1:E:51:LEU:HD23	1:E:279:TYR:CE1	2.46	0.51
1:E:134:ARG:NH1	1:E:233:GLU:HB3	2.25	0.51
1:F:51:LEU:HD23	1:F:279:TYR:CE1	2.47	0.50
1:E:50:MET:HE2	1:E:52:LEU:HG	1.92	0.50
1:E:53:ARG:HB3	1:E:55:ASP:OD1	2.11	0.50
1:E:134:ARG:HG3	1:E:134:ARG:HH21	1.76	0.50
1:D:19:ILE:HG22	1:D:48:VAL:HG11	1.94	0.50
1:F:135:SER:OG	1:F:236:ILE:HG21	2.12	0.50
1:E:135:SER:OG	1:E:236:ILE:HG21	2.12	0.49
1:A:43:SER:OG	1:A:45:VAL:HG23	2.10	0.49
1:D:51:LEU:HD23	1:D:279:TYR:HE1	1.76	0.49
1:B:184:ALA:HB2	1:B:228:VAL:CB	2.42	0.49
1:F:19:ILE:HD11	1:F:72:LEU:HD11	1.94	0.49
1:C:2:LEU:HD12	1:C:3:GLU:H	1.78	0.48
1:E:130:GLU:OE2	1:E:130:GLU:N	2.46	0.48
1:D:134:ARG:HD3	1:D:232:MET:HA	1.96	0.48
1:D:53:ARG:HB3	1:D:55:ASP:OD1	2.14	0.48
1:F:90:LEU:HD23	1:F:91:ARG:N	2.29	0.48
1:D:134:ARG:HG3	1:D:233:GLU:CB	2.43	0.48
1:A:71:ASN:HB2	1:A:119:LEU:HD11	1.96	0.48
1:D:134:ARG:HG3	1:D:233:GLU:CG	2.44	0.48
1:F:119:LEU:HD23	1:F:119:LEU:N	2.29	0.47
1:B:289:ASP:OD1	1:B:289:ASP:N	2.47	0.47
1:E:87:SER:O	1:E:103:SER:HA	2.14	0.47
1:B:87:SER:O	1:B:103:SER:HA	2.15	0.47
1:D:87:SER:O	1:D:103:SER:HA	2.15	0.47
1:F:264:LYS:HE2	1:F:265:ASP:N	2.29	0.47
1:E:279:TYR:CD2	1:E:281:ARG:HD3	2.49	0.47
1:E:119:LEU:N	1:E:119:LEU:HD23	2.29	0.47
1:B:53:ARG:HB3	1:B:55:ASP:OD1	2.15	0.47
1:C:87:SER:O	1:C:103:SER:HA	2.14	0.47
1:D:274:ILE:O	1:D:276:ASN:N	2.49	0.46
1:F:124:GLU:CD	1:F:124:GLU:H	2.17	0.46
1:A:1:MET:HE2	1:A:94:ASP:CA	2.40	0.46
1:A:87:SER:O	1:A:103:SER:HA	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:144:PHE:CZ	1:A:245:MET:HE3	2.48	0.46
1:D:74:SER:HB3	1:E:175:VAL:HG13	1.98	0.46
1:F:87:SER:O	1:F:103:SER:HA	2.14	0.46
1:E:243:ARG:O	1:E:247:ILE:HG12	2.15	0.46
1:F:274:ILE:HD12	1:F:274:ILE:N	2.30	0.46
1:D:31:ASN:HD22	1:D:65:ASN:CB	2.28	0.46
1:E:274:ILE:HG22	1:E:277:VAL:HG22	1.97	0.46
1:A:243:ARG:O	1:A:247:ILE:HG12	2.16	0.46
1:A:130:GLU:HB2	1:A:131:MET:HB2	1.98	0.46
1:F:2:LEU:HD23	1:F:2:LEU:C	2.37	0.46
1:D:274:ILE:HG22	1:D:277:VAL:HG22	1.97	0.45
1:B:125:SER:OG	1:B:126:MET:N	2.50	0.45
1:C:243:ARG:O	1:C:247:ILE:HG12	2.16	0.45
1:F:264:LYS:HE2	1:F:265:ASP:H	1.82	0.45
1:D:249:ALA:HA	1:D:272:TYR:OH	2.17	0.45
1:E:132:ASP:OD1	1:E:133:TYR:N	2.49	0.45
1:D:243:ARG:O	1:D:247:ILE:HG12	2.16	0.45
1:A:183:GLN:HE21	1:E:109:THR:HA	1.79	0.45
1:E:2:LEU:CD2	1:E:3:GLU:N	2.70	0.45
1:C:163:SER:C	1:C:232:MET:HE3	2.36	0.45
1:C:70:LEU:HD23	1:C:99:VAL:HG11	1.99	0.45
1:B:119:LEU:HD23	1:B:119:LEU:N	2.32	0.45
1:B:249:ALA:HA	1:B:272:TYR:OH	2.17	0.45
1:C:128:ILE:CD1	1:C:128:ILE:N	2.79	0.45
1:D:70:LEU:HD23	1:D:99:VAL:HG11	1.99	0.45
1:E:232:MET:HG3	1:E:234:GLU:O	2.17	0.45
1:F:128:ILE:N	1:F:128:ILE:CD1	2.73	0.45
1:A:249:ALA:HA	1:A:272:TYR:OH	2.17	0.44
1:E:21:GLY:O	1:E:247:ILE:HD12	2.17	0.44
1:F:243:ARG:O	1:F:247:ILE:HG12	2.16	0.44
1:C:249:ALA:HA	1:C:272:TYR:OH	2.17	0.44
1:C:15:LEU:HD13	1:C:50:MET:HE2	1.99	0.44
1:E:22:LEU:HD12	1:E:48:VAL:CG2	2.47	0.44
1:C:128:ILE:HD12	1:C:128:ILE:N	2.31	0.44
1:D:69:GLY:O	1:D:118:LEU:HB2	2.17	0.44
1:F:22:LEU:HD12	1:F:48:VAL:CG2	2.47	0.44
1:F:249:ALA:HA	1:F:272:TYR:OH	2.17	0.44
1:E:69:GLY:O	1:E:118:LEU:HB2	2.17	0.44
1:E:249:ALA:HA	1:E:272:TYR:OH	2.17	0.44
1:C:128:ILE:H	1:C:128:ILE:CD1	2.31	0.44
1:D:22:LEU:HD12	1:D:48:VAL:CG2	2.48	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:53:ARG:HB3	1:A:55:ASP:OD1	2.18	0.43
1:F:55:ASP:HB2	1:F:277:VAL:HG12	2.00	0.43
1:A:70:LEU:HD21	1:A:99:VAL:HG11	2.00	0.43
1:A:21:GLY:O	1:A:247:ILE:HD12	2.17	0.43
1:B:263:ALA:HB3	1:B:266:SER:HB3	1.99	0.43
1:B:70:LEU:HD23	1:B:99:VAL:HG11	1.98	0.43
1:D:40:MET:HG2	1:D:47:LEU:HD23	1.99	0.43
1:D:119:LEU:N	1:D:119:LEU:HD23	2.33	0.43
1:D:21:GLY:O	1:D:247:ILE:HD12	2.18	0.43
1:C:234:GLU:HG2	1:C:235:PRO:HD2	2.00	0.43
1:F:274:ILE:HG22	1:F:277:VAL:HG23	2.00	0.43
1:B:232:MET:HG3	1:B:234:GLU:O	2.19	0.43
1:B:69:GLY:O	1:B:118:LEU:HB2	2.19	0.43
1:C:128:ILE:CG2	1:C:131:MET:HE2	2.48	0.43
1:A:69:GLY:O	1:A:118:LEU:HB2	2.19	0.43
1:C:21:GLY:O	1:C:247:ILE:HD12	2.19	0.43
1:F:21:GLY:O	1:F:247:ILE:HD12	2.19	0.42
1:B:21:GLY:O	1:B:247:ILE:HD13	2.20	0.42
1:A:124:GLU:H	1:A:124:GLU:CD	2.22	0.42
1:F:69:GLY:O	1:F:118:LEU:HB2	2.20	0.42
1:A:22:LEU:HD12	1:A:48:VAL:CG2	2.50	0.42
1:B:90:LEU:HD11	1:B:99:VAL:HG21	2.02	0.42
1:F:51:LEU:HD23	1:F:279:TYR:HE1	1.82	0.42
1:F:70:LEU:HD23	1:F:99:VAL:HG11	2.00	0.42
1:F:97:ASP:O	1:F:97:ASP:OD1	2.37	0.42
1:D:263:ALA:HB3	1:D:266:SER:HB2	2.02	0.42
1:F:264:LYS:HA	1:F:264:LYS:HD2	1.95	0.42
1:A:233:GLU:HG2	1:A:234:GLU:HG3	2.02	0.41
1:C:127:GLY:O	1:C:128:ILE:C	2.58	0.41
1:E:51:LEU:HD23	1:E:279:TYR:HE1	1.81	0.41
1:E:90:LEU:HD11	1:E:99:VAL:HG21	2.02	0.41
1:A:130:GLU:HB2	1:A:131:MET:HA	2.03	0.41
1:B:131:MET:HB3	1:B:132:ASP:CA	2.50	0.41
1:D:165:GLU:HG3	1:D:165:GLU:H	1.64	0.41
1:F:127:GLY:C	1:F:128:ILE:HD12	2.41	0.41
1:A:31:ASN:HB2	1:A:32:PRO:CD	2.51	0.41
1:B:134:ARG:HA	1:B:233:GLU:CB	2.50	0.41
1:C:22:LEU:HD12	1:C:48:VAL:CG2	2.51	0.41
1:C:90:LEU:HD11	1:C:99:VAL:HG21	2.03	0.41
1:B:31:ASN:ND2	1:B:65:ASN:HB3	2.35	0.41
1:C:183:GLN:O	1:C:228:VAL:HB	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:134:ARG:HA	1:D:134:ARG:NE	2.36	0.41
1:D:97:ASP:O	1:D:97:ASP:OD1	2.38	0.41
1:B:132:ASP:O	1:B:133:TYR:C	2.59	0.40
1:D:232:MET:HG3	1:D:234:GLU:O	2.20	0.40
1:A:9:ALA:O	1:A:13:LYS:HG3	2.21	0.40
1:C:133:TYR:CG	1:C:261:LYS:HB3	2.56	0.40
1:D:182:LEU:N	1:D:182:LEU:HD23	2.36	0.40
1:E:165:GLU:HA	1:E:184:ALA:HB2	2.03	0.40
1:F:22:LEU:HD12	1:F:48:VAL:HG22	2.03	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	244/292 (84%)	228 (93%)	16 (7%)	0	100	100
1	B	244/292 (84%)	232 (95%)	12 (5%)	0	100	100
1	C	244/292 (84%)	228 (93%)	14 (6%)	2 (1%)	24	64
1	D	244/292 (84%)	232 (95%)	11 (4%)	1 (0%)	39	78
1	E	244/292 (84%)	231 (95%)	12 (5%)	1 (0%)	39	78
1	F	244/292 (84%)	233 (96%)	11 (4%)	0	100	100
All	All	1464/1752 (84%)	1384 (94%)	76 (5%)	4 (0%)	46	81

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	275	ASP
1	E	184	ALA
1	C	132	ASP
1	C	184	ALA

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	216/251 (86%)	179 (83%)	37 (17%)	2	10
1	B	216/251 (86%)	183 (85%)	33 (15%)	3	14
1	C	216/251 (86%)	180 (83%)	36 (17%)	3	11
1	D	216/251 (86%)	175 (81%)	41 (19%)	2	8
1	E	216/251 (86%)	179 (83%)	37 (17%)	2	10
1	F	216/251 (86%)	178 (82%)	38 (18%)	2	10
All	All	1296/1506 (86%)	1074 (83%)	222 (17%)	2	10

All (222) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	13	LYS
1	A	19	ILE
1	A	22	LEU
1	A	29	ASP
1	A	40	MET
1	A	50	MET
1	A	53	ARG
1	A	59	LYS
1	A	64	ARG
1	A	80	LYS
1	A	84	SER
1	A	89	SER
1	A	94	ASP
1	A	97	ASP
1	A	99	VAL
1	A	102	THR
1	A	103	SER
1	A	109	THR
1	A	116	LEU
1	A	120	GLU
1	A	122	GLU
1	A	124	GLU

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Mol	Chain	Res	Type
1	A	126	MET
1	A	128	ILE
1	A	130	GLU
1	A	134	ARG
1	A	137	VAL
1	A	168	LYS
1	A	170	SER
1	A	232	MET
1	A	239	SER
1	A	250	LYS
1	A	264	LYS
1	A	265	ASP
1	A	266	SER
1	A	270	VAL
1	A	276	ASN
1	B	10	SER
1	B	19	ILE
1	B	22	LEU
1	B	29	ASP
1	B	40	MET
1	B	47	LEU
1	B	50	MET
1	B	53	ARG
1	B	62	CYS
1	B	64	ARG
1	B	70	LEU
1	B	89	SER
1	B	97	ASP
1	B	99	VAL
1	B	102	THR
1	B	103	SER
1	B	104	GLU
1	B	109	THR
1	B	116	LEU
1	B	117	LYS
1	B	119	LEU
1	B	128	ILE
1	B	137	VAL
1	B	164	LYS
1	B	170	SER
1	B	183	GLN
1	B	231	THR

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Mol	Chain	Res	Type
1	B	232	MET
1	B	239	SER
1	B	250	LYS
1	B	264	LYS
1	B	265	ASP
1	B	289	ASP
1	C	10	SER
1	C	19	ILE
1	C	22	LEU
1	C	24	ASN
1	C	29	ASP
1	C	47	LEU
1	C	53	ARG
1	C	64	ARG
1	C	65	ASN
1	C	70	LEU
1	C	80	LYS
1	C	89	SER
1	C	94	ASP
1	C	97	ASP
1	C	99	VAL
1	C	102	THR
1	C	103	SER
1	C	108	LYS
1	C	116	LEU
1	C	125	SER
1	C	126	MET
1	C	131	MET
1	C	137	VAL
1	C	163	SER
1	C	164	LYS
1	C	168	LYS
1	C	170	SER
1	C	231	THR
1	C	232	MET
1	C	239	SER
1	C	250	LYS
1	C	264	LYS
1	C	265	ASP
1	C	266	SER
1	C	270	VAL
1	C	276	ASN

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Mol	Chain	Res	Type
1	D	1	MET
1	D	2	LEU
1	D	3	GLU
1	D	10	SER
1	D	19	ILE
1	D	22	LEU
1	D	31	ASN
1	D	40	MET
1	D	47	LEU
1	D	50	MET
1	D	53	ARG
1	D	61	GLN
1	D	62	CYS
1	D	65	ASN
1	D	70	LEU
1	D	89	SER
1	D	94	ASP
1	D	97	ASP
1	D	99	VAL
1	D	102	THR
1	D	103	SER
1	D	104	GLU
1	D	109	THR
1	D	117	LYS
1	D	119	LEU
1	D	124	GLU
1	D	126	MET
1	D	133	TYR
1	D	134	ARG
1	D	137	VAL
1	D	164	LYS
1	D	170	SER
1	D	174	ASP
1	D	231	THR
1	D	232	MET
1	D	234	GLU
1	D	239	SER
1	D	250	LYS
1	D	264	LYS
1	D	270	VAL
1	D	276	ASN
1	E	1	MET

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Mol	Chain	Res	Type
1	E	19	ILE
1	E	22	LEU
1	E	24	ASN
1	E	40	MET
1	E	47	LEU
1	E	50	MET
1	E	62	CYS
1	E	64	ARG
1	E	65	ASN
1	E	70	LEU
1	E	89	SER
1	E	94	ASP
1	E	97	ASP
1	E	99	VAL
1	E	102	THR
1	E	103	SER
1	E	105	ASN
1	E	108	LYS
1	E	109	THR
1	E	117	LYS
1	E	119	LEU
1	E	124	GLU
1	E	130	GLU
1	E	137	VAL
1	E	139	LEU
1	E	163	SER
1	E	164	LYS
1	E	170	SER
1	E	231	THR
1	E	232	MET
1	E	239	SER
1	E	250	LYS
1	E	265	ASP
1	E	270	VAL
1	E	281	ARG
1	E	287	LYS
1	F	1	MET
1	F	10	SER
1	F	19	ILE
1	F	22	LEU
1	F	24	ASN
1	F	47	LEU

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Mol	Chain	Res	Type
1	F	50	MET
1	F	53	ARG
1	F	62	CYS
1	F	64	ARG
1	F	70	LEU
1	F	80	LYS
1	F	97	ASP
1	F	99	VAL
1	F	102	THR
1	F	103	SER
1	F	108	LYS
1	F	118	LEU
1	F	119	LEU
1	F	120	GLU
1	F	126	MET
1	F	130	GLU
1	F	131	MET
1	F	132	ASP
1	F	137	VAL
1	F	148	VAL
1	F	164	LYS
1	F	165	GLU
1	F	170	SER
1	F	172	SER
1	F	231	THR
1	F	232	MET
1	F	239	SER
1	F	250	LYS
1	F	264	LYS
1	F	266	SER
1	F	270	VAL
1	F	277	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (28) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	44	HIS
1	A	115	GLN
1	A	183	GLN
1	A	276	ASN
1	B	31	ASN
1	B	38	GLN

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Mol	Chain	Res	Type
1	B	44	HIS
1	B	115	GLN
1	C	44	HIS
1	C	49	HIS
1	C	115	GLN
1	C	276	ASN
1	D	31	ASN
1	D	44	HIS
1	D	61	GLN
1	D	92	HIS
1	D	115	GLN
1	D	276	ASN
1	E	44	HIS
1	E	49	HIS
1	E	105	ASN
1	E	115	GLN
1	E	276	ASN
1	F	44	HIS
1	F	49	HIS
1	F	61	GLN
1	F	115	GLN
1	F	276	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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

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, 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	248/292 (84%)	0.11	3 (1%) 81 63	51, 83, 143, 186	0
1	B	248/292 (84%)	0.13	6 (2%) 62 41	53, 89, 147, 206	0
1	C	248/292 (84%)	0.23	14 (5%) 28 15	56, 88, 144, 192	0
1	D	248/292 (84%)	0.13	7 (2%) 56 36	65, 98, 148, 178	0
1	E	248/292 (84%)	0.20	14 (5%) 28 15	66, 97, 162, 253	0
1	F	248/292 (84%)	0.15	8 (3%) 51 32	65, 103, 159, 196	0
All	All	1488/1752 (84%)	0.16	52 (3%) 48 29	51, 94, 153, 253	0

All (52) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	289	ASP	8.5
1	B	133	TYR	4.7
1	E	289	ASP	4.2
1	B	134	ARG	3.9
1	D	131	MET	3.9
1	C	167	VAL	3.8
1	A	185	ALA	3.8
1	B	165	GLU	3.8
1	E	169	PHE	3.5
1	E	165	GLU	3.5
1	C	289	ASP	3.4
1	A	288	VAL	3.3
1	B	185	ALA	3.3
1	D	133	TYR	3.3
1	D	185	ALA	3.3
1	F	129	PRO	3.3
1	C	162	ILE	3.2
1	C	95	ASP	3.1
1	D	262	PHE	3.1

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Mol	Chain	Res	Type	RSRZ
1	C	185	ALA	2.9
1	F	262	PHE	2.8
1	F	160	ILE	2.8
1	D	238	LEU	2.7
1	C	169	PHE	2.6
1	C	166	GLY	2.6
1	E	276	ASN	2.6
1	E	166	GLY	2.6
1	F	131	MET	2.5
1	C	182	LEU	2.5
1	B	184	ALA	2.5
1	E	160	ILE	2.5
1	C	262	PHE	2.4
1	C	165	GLU	2.4
1	E	161	ALA	2.4
1	F	185	ALA	2.4
1	C	230	VAL	2.4
1	E	132	ASP	2.3
1	D	161	ALA	2.3
1	E	288	VAL	2.3
1	C	160	ILE	2.3
1	E	167	VAL	2.3
1	F	95	ASP	2.3
1	C	161	ALA	2.2
1	C	184	ALA	2.2
1	E	162	ILE	2.2
1	B	110	ARG	2.2
1	E	231	THR	2.2
1	F	289	ASP	2.2
1	F	165	GLU	2.1
1	E	84	SER	2.1
1	D	130	GLU	2.1
1	E	181	PHE	2.0

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

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

6.3 Carbohydrates ⓘ

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.