Full wwPDB X-ray Structure Validation Report (i)

Jan 31, 2016 – 11:43 PM GMT

PDB ID	:	1YDN
Title	:	Crystal Structure of the HMG-CoA Lyase from Brucella melitensis, Northeast Structural Genomics Target LR35.
Authors	:	Forouhar, F.; Abashidze, M.; Hussain, M.; Vorobiev, S.M.; Xiao, R.; Ciano, M.; Acton, T.B.; Montelione, G.T.; Tong, L.; Hunt, J.F.; Northeast Structural Genomics Consortium (NESG)
Deposited on	:	2004-12-24
Resolution	:	2.30 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 (i) symbol.

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

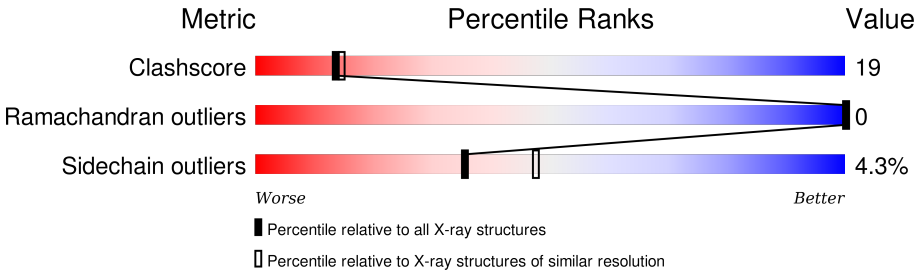
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	trunk26865

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.30 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	102246	4452 (2.30-2.30)
Ramachandran outliers	100387	4410 (2.30-2.30)
Sidechain outliers	100360	4409 (2.30-2.30)

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 <=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.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	295	62% 32%
1	B	295	65% 30%
1	C	295	66% 27%
1	D	295	62% 32%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 8972 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 HYDROXYMETHYLGLUTARYL-COA LYASE.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	283	Total	C	N	O	S	Se	0	0	0
			2093	1306	370	405	6	6			
1	B	283	Total	C	N	O	S	Se	0	0	0
			2093	1306	370	405	6	6			
1	C	283	Total	C	N	O	S	Se	0	0	0
			2093	1306	370	405	6	6			
1	D	283	Total	C	N	O	S	Se	0	0	0
			2093	1306	370	405	6	6			

There are 56 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	10	MSE	MET	MODIFIED RESIDUE	UNP Q8YEF2
A	64	MSE	MET	MODIFIED RESIDUE	UNP Q8YEF2
A	82	MSE	MET	MODIFIED RESIDUE	UNP Q8YEF2
A	189	MSE	MET	MODIFIED RESIDUE	UNP Q8YEF2
A	256	MSE	MET	MODIFIED RESIDUE	UNP Q8YEF2
A	260	MSE	MET	MODIFIED RESIDUE	UNP Q8YEF2
A	288	LEU	-	CLONING ARTIFACT	UNP Q8YEF2
A	289	GLU	-	CLONING ARTIFACT	UNP Q8YEF2
A	290	HIS	-	EXPRESSION TAG	UNP Q8YEF2
A	291	HIS	-	EXPRESSION TAG	UNP Q8YEF2
A	292	HIS	-	EXPRESSION TAG	UNP Q8YEF2
A	293	HIS	-	EXPRESSION TAG	UNP Q8YEF2
A	294	HIS	-	EXPRESSION TAG	UNP Q8YEF2
A	295	HIS	-	EXPRESSION TAG	UNP Q8YEF2
B	10	MSE	MET	MODIFIED RESIDUE	UNP Q8YEF2
B	64	MSE	MET	MODIFIED RESIDUE	UNP Q8YEF2
B	82	MSE	MET	MODIFIED RESIDUE	UNP Q8YEF2
B	189	MSE	MET	MODIFIED RESIDUE	UNP Q8YEF2
B	256	MSE	MET	MODIFIED RESIDUE	UNP Q8YEF2
B	260	MSE	MET	MODIFIED RESIDUE	UNP Q8YEF2
B	288	LEU	-	CLONING ARTIFACT	UNP Q8YEF2

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Chain	Residue	Modelled	Actual	Comment	Reference
B	289	GLU	-	CLONING ARTIFACT	UNP Q8YEF2
B	290	HIS	-	EXPRESSION TAG	UNP Q8YEF2
B	291	HIS	-	EXPRESSION TAG	UNP Q8YEF2
B	292	HIS	-	EXPRESSION TAG	UNP Q8YEF2
B	293	HIS	-	EXPRESSION TAG	UNP Q8YEF2
B	294	HIS	-	EXPRESSION TAG	UNP Q8YEF2
B	295	HIS	-	EXPRESSION TAG	UNP Q8YEF2
C	10	MSE	MET	MODIFIED RESIDUE	UNP Q8YEF2
C	64	MSE	MET	MODIFIED RESIDUE	UNP Q8YEF2
C	82	MSE	MET	MODIFIED RESIDUE	UNP Q8YEF2
C	189	MSE	MET	MODIFIED RESIDUE	UNP Q8YEF2
C	256	MSE	MET	MODIFIED RESIDUE	UNP Q8YEF2
C	260	MSE	MET	MODIFIED RESIDUE	UNP Q8YEF2
C	288	LEU	-	CLONING ARTIFACT	UNP Q8YEF2
C	289	GLU	-	CLONING ARTIFACT	UNP Q8YEF2
C	290	HIS	-	EXPRESSION TAG	UNP Q8YEF2
C	291	HIS	-	EXPRESSION TAG	UNP Q8YEF2
C	292	HIS	-	EXPRESSION TAG	UNP Q8YEF2
C	293	HIS	-	EXPRESSION TAG	UNP Q8YEF2
C	294	HIS	-	EXPRESSION TAG	UNP Q8YEF2
C	295	HIS	-	EXPRESSION TAG	UNP Q8YEF2
D	10	MSE	MET	MODIFIED RESIDUE	UNP Q8YEF2
D	64	MSE	MET	MODIFIED RESIDUE	UNP Q8YEF2
D	82	MSE	MET	MODIFIED RESIDUE	UNP Q8YEF2
D	189	MSE	MET	MODIFIED RESIDUE	UNP Q8YEF2
D	256	MSE	MET	MODIFIED RESIDUE	UNP Q8YEF2
D	260	MSE	MET	MODIFIED RESIDUE	UNP Q8YEF2
D	288	LEU	-	CLONING ARTIFACT	UNP Q8YEF2
D	289	GLU	-	CLONING ARTIFACT	UNP Q8YEF2
D	290	HIS	-	EXPRESSION TAG	UNP Q8YEF2
D	291	HIS	-	EXPRESSION TAG	UNP Q8YEF2
D	292	HIS	-	EXPRESSION TAG	UNP Q8YEF2
D	293	HIS	-	EXPRESSION TAG	UNP Q8YEF2
D	294	HIS	-	EXPRESSION TAG	UNP Q8YEF2
D	295	HIS	-	EXPRESSION TAG	UNP Q8YEF2

- Molecule 2 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	B	1	Total Ca 1 1	0	0
2	A	1	Total Ca 1 1	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	D	1	Total Ca 1 1	0	0
2	C	1	Total Ca 1 1	0	0

- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	197	Total O 197 197	0	0
3	B	131	Total O 131 131	0	0
3	C	143	Total O 143 143	0	0
3	D	125	Total O 125 125	0	0

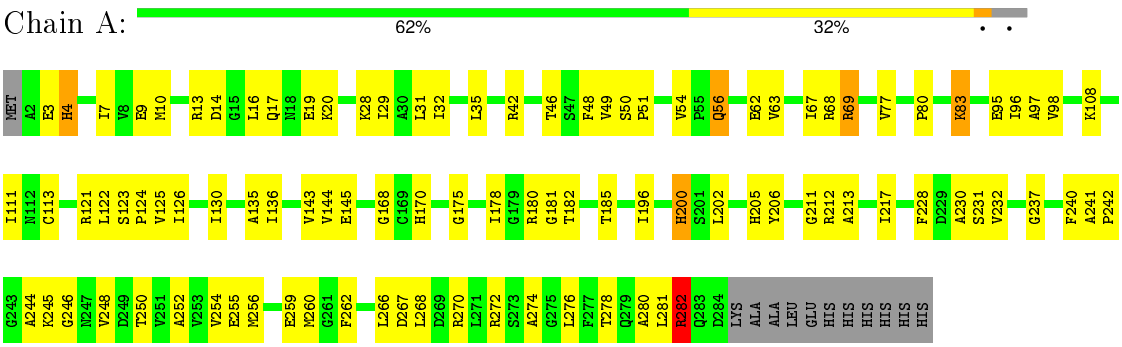
3 Residue-property plots (i)

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

Note EDS was not executed.

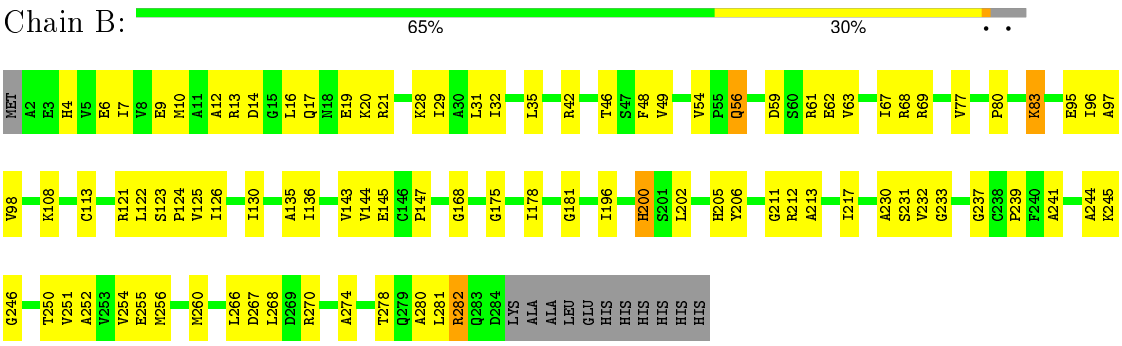
• Molecule 1: HYDROXYMETHYLGLUTARYL-COA LYASE

Chain A:



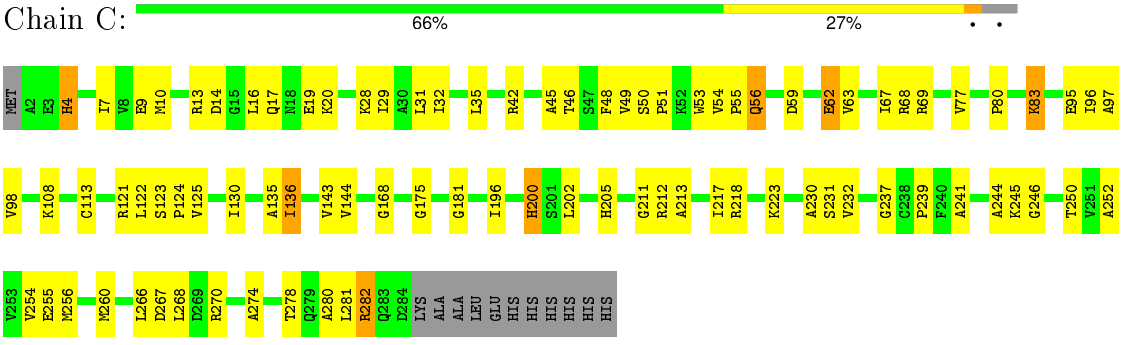
• Molecule 1: HYDROXYMETHYLGLUTARYL-COA LYASE

Chain B:



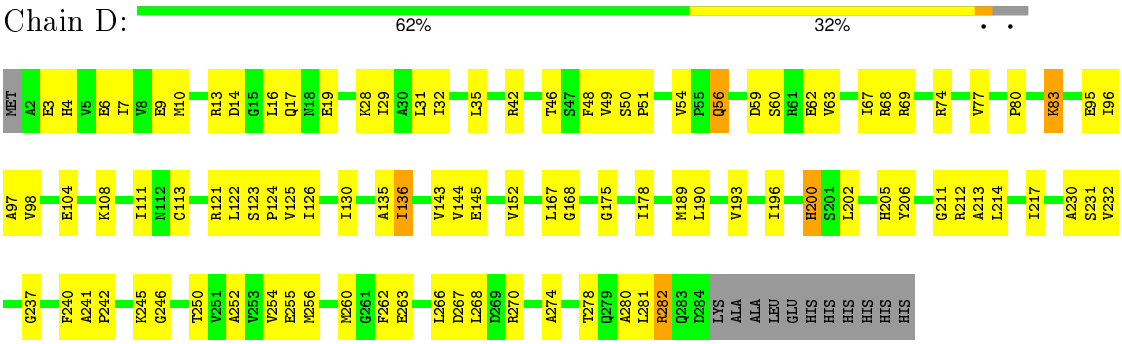
• Molecule 1: HYDROXYMETHYLGLUTARYL-COA LYASE

Chain C:



• Molecule 1: HYDROXYMETHYLGLUTARYL-COA LYASE

Chain D:



4 Data and refinement statistics (i)

Xtriage (Phenix) and EDS were not executed - this section will therefore be incomplete.

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	82.27Å 86.40Å 87.68Å 90.00° 118.70° 90.00°	Depositor
Resolution (Å)	28.94 – 2.30	Depositor
% Data completeness (in resolution range)	94.5 (28.94-2.30)	Depositor
R_{merge}	0.10	Depositor
R_{sym}	0.10	Depositor
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.271 , 0.304	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	8972	wwPDB-VP
Average B, all atoms (Å^2)	30.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

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

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	0.40	0/2122	1.00	6/2871 (0.2%)
1	B	0.38	0/2122	0.61	4/2871 (0.1%)
1	C	0.37	0/2122	0.62	4/2871 (0.1%)
1	D	0.37	0/2122	0.62	3/2871 (0.1%)
All	All	0.38	0/8488	0.73	17/11484 (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	69	ARG	NE-CZ-NH1	-23.89	108.36	120.30
1	A	69	ARG	NE-CZ-NH2	21.20	130.90	120.30
1	A	282	ARG	NE-CZ-NH2	-19.27	110.66	120.30
1	A	282	ARG	NE-CZ-NH1	19.09	129.84	120.30
1	A	69	ARG	CD-NE-CZ	9.99	137.59	123.60
1	A	282	ARG	CD-NE-CZ	9.28	136.59	123.60
1	D	69	ARG	NE-CZ-NH2	-6.90	116.85	120.30
1	C	69	ARG	NE-CZ-NH2	-6.66	116.97	120.30
1	B	69	ARG	NE-CZ-NH2	-6.42	117.09	120.30
1	B	282	ARG	NE-CZ-NH1	-6.32	117.14	120.30
1	D	282	ARG	NE-CZ-NH1	-6.24	117.18	120.30
1	D	282	ARG	NE-CZ-NH2	6.20	123.40	120.30
1	C	282	ARG	NE-CZ-NH1	-5.97	117.32	120.30
1	B	282	ARG	NE-CZ-NH2	5.82	123.21	120.30
1	C	282	ARG	NE-CZ-NH2	5.67	123.14	120.30
1	B	69	ARG	NE-CZ-NH1	5.25	122.93	120.30
1	C	69	ARG	NE-CZ-NH1	5.25	122.92	120.30

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	2093	0	2071	81	0
1	B	2093	0	2071	78	0
1	C	2093	0	2071	78	0
1	D	2093	0	2071	84	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
3	A	197	0	0	12	0
3	B	131	0	0	10	0
3	C	143	0	0	10	0
3	D	125	0	0	15	0
All	All	8972	0	8284	309	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 19.

All (309) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:7:ILE:HD11	1:A:230:ALA:HB3	1.59	0.85
1:B:7:ILE:HD11	1:B:230:ALA:HB3	1.59	0.85
1:C:7:ILE:HD11	1:C:230:ALA:HB3	1.60	0.84
1:A:259:GLU:HA	3:A:674:HOH:O	1.78	0.82
1:D:7:ILE:HD11	1:D:230:ALA:HB3	1.60	0.81
1:D:6:GLU:HG2	3:D:634:HOH:O	1.80	0.80
1:A:7:ILE:HD13	1:A:250:THR:HG23	1.64	0.78
1:C:7:ILE:HD13	1:C:250:THR:HG23	1.65	0.78
1:D:7:ILE:HD13	1:D:250:THR:HG23	1.65	0.77
1:B:7:ILE:HD13	1:B:250:THR:HG23	1.66	0.77
1:B:6:GLU:HG2	3:B:604:HOH:O	1.85	0.76
1:D:190:LEU:HA	3:D:661:HOH:O	1.83	0.76
1:D:232:VAL:HA	1:D:250:THR:HB	1.69	0.74
1:B:232:VAL:HA	1:B:250:THR:HB	1.68	0.73
1:C:232:VAL:HA	1:C:250:THR:HB	1.71	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:16:LEU:HD23	1:A:28:LYS:HE3	1.71	0.72
1:A:232:VAL:HA	1:A:250:THR:HB	1.71	0.71
1:B:56:GLN:HE21	1:B:56:GLN:H	1.38	0.71
1:D:16:LEU:HD23	1:D:28:LYS:HE3	1.74	0.70
1:C:16:LEU:HD23	1:C:28:LYS:HE3	1.73	0.70
1:D:167:LEU:HD23	3:D:630:HOH:O	1.91	0.69
1:C:63:VAL:O	1:C:67:ILE:HG12	1.94	0.68
1:B:63:VAL:O	1:B:67:ILE:HG12	1.94	0.68
1:B:147:PRO:HA	3:B:656:HOH:O	1.92	0.68
1:B:239:PRO:HB2	1:D:242:PRO:O	1.94	0.67
1:B:83:LYS:H	1:B:83:LYS:HD3	1.61	0.66
1:C:83:LYS:HD3	1:C:83:LYS:H	1.61	0.66
1:B:16:LEU:HD23	1:B:28:LYS:HE3	1.76	0.66
1:B:56:GLN:NE2	1:B:56:GLN:H	1.94	0.66
1:B:46:THR:O	1:B:77:VAL:HG23	1.95	0.66
1:B:206:TYR:HB3	3:B:651:HOH:O	1.95	0.66
1:D:56:GLN:H	1:D:56:GLN:HE21	1.44	0.66
1:D:63:VAL:O	1:D:67:ILE:HG12	1.95	0.65
1:C:56:GLN:H	1:C:56:GLN:HE21	1.43	0.65
1:C:49:VAL:HG23	3:C:618:HOH:O	1.94	0.65
1:A:83:LYS:H	1:A:83:LYS:HD3	1.61	0.65
1:A:63:VAL:O	1:A:67:ILE:HG12	1.97	0.64
1:C:175:GLY:HA2	1:C:205:HIS:HB3	1.80	0.64
1:A:56:GLN:H	1:A:56:GLN:HE21	1.45	0.64
1:D:83:LYS:H	1:D:83:LYS:HD3	1.61	0.64
1:D:46:THR:O	1:D:77:VAL:HG23	1.98	0.64
1:A:98:VAL:HG22	1:A:136:ILE:HD11	1.79	0.64
1:D:175:GLY:HA2	1:D:205:HIS:HB3	1.80	0.64
1:C:46:THR:O	1:C:77:VAL:HG23	1.97	0.64
1:D:193:VAL:HB	3:D:661:HOH:O	1.97	0.63
1:A:49:VAL:HG11	3:A:604:HOH:O	1.98	0.63
1:B:98:VAL:HG22	1:B:136:ILE:HD11	1.79	0.63
1:C:98:VAL:HG22	1:C:136:ILE:HD11	1.79	0.63
1:B:7:ILE:CG2	1:B:266:LEU:HD11	2.28	0.63
1:D:56:GLN:NE2	1:D:56:GLN:H	1.97	0.63
1:D:7:ILE:CG2	1:D:266:LEU:HD11	2.29	0.63
1:B:175:GLY:HA2	1:B:205:HIS:HB3	1.81	0.63
1:D:98:VAL:HG22	1:D:136:ILE:HD11	1.79	0.63
1:B:200:HIS:H	1:B:200:HIS:CD2	2.16	0.63
1:C:252:ALA:O	1:C:255:GLU:HG3	2.00	0.62
1:A:200:HIS:CD2	1:A:200:HIS:H	2.16	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:200:HIS:CD2	1:D:200:HIS:H	2.17	0.62
1:A:256:MSE:HE3	1:A:260:MSE:SE	2.50	0.62
1:C:121:ARG:O	1:C:124:PRO:HD2	2.01	0.61
1:B:256:MSE:HE3	1:B:260:MSE:SE	2.51	0.61
1:A:7:ILE:CG2	1:A:266:LEU:HD11	2.31	0.61
1:A:242:PRO:O	1:C:239:PRO:CB	2.49	0.61
1:C:56:GLN:H	1:C:56:GLN:NE2	1.98	0.61
1:A:175:GLY:HA2	1:A:205:HIS:HB3	1.82	0.61
1:C:49:VAL:HG11	3:C:620:HOH:O	2.01	0.60
1:A:56:GLN:NE2	1:A:56:GLN:H	1.99	0.60
1:A:180:ARG:NH2	1:C:20:LYS:HE2	2.17	0.60
1:C:7:ILE:CG2	1:C:266:LEU:HD11	2.32	0.60
1:C:49:VAL:HG13	1:C:54:VAL:HG11	1.83	0.60
1:C:200:HIS:H	1:C:200:HIS:CD2	2.17	0.59
1:A:32:ILE:HB	1:A:67:ILE:HD12	1.85	0.59
1:B:20:LYS:HD3	1:D:241:ALA:HB2	1.83	0.59
1:D:49:VAL:HG13	1:D:54:VAL:HG11	1.84	0.59
1:A:252:ALA:O	1:A:255:GLU:HG3	2.02	0.59
1:B:108:LYS:HA	1:B:113:CYS:H	1.68	0.59
1:A:46:THR:O	1:A:77:VAL:HG23	2.02	0.59
1:B:252:ALA:O	1:B:255:GLU:HG3	2.03	0.59
1:A:49:VAL:HG13	1:A:54:VAL:HG11	1.84	0.58
1:C:256:MSE:HE3	1:C:260:MSE:SE	2.53	0.58
1:B:49:VAL:HG13	1:B:54:VAL:HG11	1.85	0.58
1:D:167:LEU:HA	3:D:630:HOH:O	2.04	0.58
1:B:49:VAL:HG23	3:B:610:HOH:O	2.02	0.58
1:D:108:LYS:HA	1:D:113:CYS:H	1.68	0.58
1:D:121:ARG:O	1:D:124:PRO:HD2	2.03	0.58
1:B:20:LYS:HA	1:D:240:PHE:O	2.03	0.57
1:D:256:MSE:HE3	1:D:260:MSE:SE	2.54	0.57
1:D:130:ILE:HD11	1:D:168:GLY:HA3	1.86	0.57
1:D:98:VAL:HB	1:D:122:LEU:HD21	1.87	0.56
1:A:212:ARG:HA	3:A:627:HOH:O	2.05	0.56
1:A:108:LYS:HA	1:A:113:CYS:H	1.70	0.56
1:D:232:VAL:HG21	1:D:274:ALA:HB3	1.88	0.56
1:A:98:VAL:HB	1:A:122:LEU:HD21	1.88	0.56
1:C:200:HIS:N	1:C:200:HIS:CD2	2.73	0.56
1:C:32:ILE:HB	1:C:67:ILE:HD12	1.88	0.56
1:B:200:HIS:CD2	1:B:200:HIS:N	2.73	0.56
1:A:20:LYS:HB3	1:C:53:TRP:CZ2	2.41	0.56
1:B:121:ARG:O	1:B:124:PRO:HD2	2.06	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:62:GLU:HG3	3:C:632:HOH:O	2.05	0.56
1:D:190:LEU:HD23	3:D:661:HOH:O	2.05	0.55
1:C:130:ILE:HD11	1:C:168:GLY:HA3	1.88	0.55
1:D:252:ALA:O	1:D:255:GLU:HG3	2.06	0.55
1:D:29:ILE:HG22	3:D:641:HOH:O	2.06	0.55
1:C:49:VAL:HG13	1:C:54:VAL:CG1	2.37	0.55
1:A:130:ILE:HD11	1:A:168:GLY:HA3	1.88	0.55
1:A:182:THR:HG21	1:D:83:LYS:HE2	1.89	0.55
1:A:232:VAL:HG21	1:A:274:ALA:HB3	1.88	0.54
1:B:42:ARG:HB3	3:B:684:HOH:O	2.07	0.54
1:B:32:ILE:HB	1:B:67:ILE:HD12	1.88	0.54
1:D:200:HIS:CD2	1:D:200:HIS:N	2.74	0.54
1:A:31:LEU:O	1:A:35:LEU:HG	2.07	0.54
1:B:98:VAL:HB	1:B:122:LEU:HD21	1.89	0.54
1:A:242:PRO:O	1:C:239:PRO:HB2	2.08	0.54
1:A:121:ARG:O	1:A:124:PRO:HD2	2.08	0.54
1:B:10:MSE:HB3	1:B:14:ASP:HB3	1.89	0.54
1:C:49:VAL:CG1	1:C:54:VAL:HG11	2.38	0.54
1:D:49:VAL:HG13	1:D:54:VAL:CG1	2.37	0.54
1:B:130:ILE:HD11	1:B:168:GLY:HA3	1.88	0.54
1:D:32:ILE:HB	1:D:67:ILE:HD12	1.88	0.54
1:A:49:VAL:HG13	1:A:54:VAL:CG1	2.37	0.54
1:C:232:VAL:HG21	1:C:274:ALA:HB3	1.87	0.54
1:A:49:VAL:CG1	1:A:54:VAL:HG11	2.38	0.54
1:A:272:ARG:NE	3:A:660:HOH:O	2.41	0.54
1:B:49:VAL:HG13	1:B:54:VAL:CG1	2.38	0.54
1:D:10:MSE:HB3	1:D:14:ASP:HB3	1.89	0.54
1:D:49:VAL:CG1	1:D:54:VAL:HG11	2.38	0.53
1:C:10:MSE:HB3	1:C:14:ASP:HB3	1.88	0.53
1:A:200:HIS:CD2	1:A:200:HIS:N	2.74	0.53
1:A:10:MSE:HB3	1:A:14:ASP:HB3	1.91	0.53
1:C:108:LYS:HA	1:C:113:CYS:H	1.73	0.53
1:B:232:VAL:HG21	1:B:274:ALA:HB3	1.90	0.53
1:B:49:VAL:CG1	1:B:54:VAL:HG11	2.40	0.52
1:C:282:ARG:HD3	3:C:673:HOH:O	2.09	0.52
1:B:239:PRO:CB	1:D:242:PRO:O	2.57	0.52
1:C:98:VAL:HB	1:C:122:LEU:HD21	1.91	0.52
1:A:95:GLU:HG2	1:A:135:ALA:HB3	1.91	0.52
1:D:189:MSE:SE	3:D:661:HOH:O	2.78	0.52
1:D:74:ARG:HD2	3:D:633:HOH:O	2.08	0.52
1:D:7:ILE:CD1	1:D:250:THR:HG23	2.38	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:123:SER:N	1:A:124:PRO:HD2	2.25	0.52
1:D:206:TYR:HB3	3:D:638:HOH:O	2.10	0.52
1:D:31:LEU:O	1:D:35:LEU:HG	2.11	0.51
1:B:19:GLU:CD	1:B:282:ARG:HH21	2.12	0.51
1:D:19:GLU:CD	1:D:282:ARG:HH21	2.14	0.51
1:B:213:ALA:O	1:B:217:ILE:HG13	2.10	0.51
1:B:14:ASP:HB2	3:B:628:HOH:O	2.11	0.51
1:C:123:SER:N	1:C:124:PRO:HD2	2.25	0.51
1:C:19:GLU:CD	1:C:282:ARG:HH21	2.14	0.51
1:B:7:ILE:CD1	1:B:250:THR:HG23	2.39	0.51
1:D:123:SER:N	1:D:124:PRO:HD2	2.25	0.51
1:D:152:VAL:HG13	3:D:660:HOH:O	2.10	0.51
1:D:83:LYS:CD	1:D:83:LYS:H	2.24	0.51
1:C:31:LEU:O	1:C:35:LEU:HG	2.11	0.51
1:D:237:GLY:HA2	1:D:246:GLY:HA3	1.94	0.50
1:A:7:ILE:CD1	1:A:250:THR:HG23	2.38	0.50
1:A:206:TYR:HB3	3:A:605:HOH:O	2.10	0.50
1:B:267:ASP:HB3	1:B:270:ARG:HG3	1.93	0.50
1:A:280:ALA:C	1:A:281:LEU:HD22	2.32	0.50
1:A:4:HIS:HB3	3:A:701:HOH:O	2.10	0.50
1:C:267:ASP:HB3	1:C:270:ARG:HG3	1.93	0.50
1:A:83:LYS:H	1:A:83:LYS:CD	2.25	0.50
1:B:48:PHE:CD2	1:B:77:VAL:HG21	2.47	0.49
1:B:211:GLY:C	1:B:212:ARG:HD2	2.33	0.49
1:B:123:SER:N	1:B:124:PRO:HD2	2.26	0.49
1:A:213:ALA:O	1:A:217:ILE:HG13	2.12	0.49
1:C:83:LYS:CD	1:C:83:LYS:H	2.25	0.49
1:B:31:LEU:O	1:B:35:LEU:HG	2.13	0.49
1:A:267:ASP:HB3	1:A:270:ARG:HG3	1.94	0.49
1:D:48:PHE:CD2	1:D:77:VAL:HG21	2.48	0.49
1:C:48:PHE:CD2	1:C:77:VAL:HG21	2.48	0.49
1:A:48:PHE:CD2	1:A:77:VAL:HG21	2.48	0.49
1:D:267:ASP:HB3	1:D:270:ARG:HG3	1.95	0.49
1:A:212:ARG:HH11	1:D:121:ARG:HG3	1.78	0.49
1:C:31:LEU:HD11	1:C:278:THR:HG22	1.95	0.49
1:D:280:ALA:C	1:D:281:LEU:HD22	2.34	0.49
1:A:237:GLY:HA2	1:A:246:GLY:HA3	1.95	0.49
1:D:211:GLY:C	1:D:212:ARG:HD2	2.33	0.49
1:A:211:GLY:C	1:A:212:ARG:HD2	2.33	0.48
1:B:280:ALA:C	1:B:281:LEU:HD22	2.33	0.48
1:B:237:GLY:HA2	1:B:246:GLY:HA3	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:223:LYS:HE3	3:C:662:HOH:O	2.13	0.48
1:A:31:LEU:HD23	1:A:31:LEU:O	2.13	0.48
1:C:29:ILE:HG23	1:C:67:ILE:HD13	1.96	0.48
1:D:143:VAL:HG23	1:D:144:VAL:HG23	1.96	0.48
1:C:213:ALA:O	1:C:217:ILE:HG13	2.14	0.48
1:D:31:LEU:HD11	1:D:278:THR:HG22	1.95	0.47
3:A:716:HOH:O	1:B:61:ARG:HD3	2.12	0.47
1:D:242:PRO:HB3	3:D:654:HOH:O	2.12	0.47
1:D:95:GLU:HG2	1:D:135:ALA:HB3	1.95	0.47
1:B:143:VAL:HG23	1:B:144:VAL:HG23	1.95	0.47
1:C:31:LEU:O	1:C:31:LEU:HD23	2.15	0.47
1:B:95:GLU:HG2	1:B:135:ALA:HB3	1.96	0.47
1:B:42:ARG:NH1	3:B:604:HOH:O	2.47	0.47
1:B:121:ARG:HB2	3:B:620:HOH:O	2.13	0.47
1:D:31:LEU:O	1:D:31:LEU:HD23	2.13	0.47
1:C:211:GLY:C	1:C:212:ARG:HD2	2.35	0.47
1:A:13:ARG:HD2	1:A:13:ARG:C	2.34	0.47
1:A:143:VAL:HG23	1:A:144:VAL:HG23	1.95	0.47
1:C:95:GLU:HG2	1:C:135:ALA:HB3	1.97	0.47
1:C:237:GLY:HA2	1:C:246:GLY:HA3	1.96	0.47
1:C:7:ILE:CD1	1:C:250:THR:HG23	2.40	0.47
1:C:280:ALA:C	1:C:281:LEU:HD22	2.35	0.47
1:A:185:THR:HG21	3:A:692:HOH:O	2.15	0.46
1:C:254:VAL:HG23	1:C:268:LEU:HD11	1.97	0.46
1:A:170:HIS:HB3	3:A:630:HOH:O	2.14	0.46
1:B:83:LYS:CD	1:B:83:LYS:H	2.26	0.46
1:B:31:LEU:HD11	1:B:278:THR:HG22	1.97	0.46
1:B:59:ASP:O	1:B:63:VAL:HG23	2.17	0.45
1:B:21:ARG:HD3	3:B:648:HOH:O	2.15	0.45
1:A:96:ILE:HG22	1:A:97:ALA:N	2.31	0.45
1:C:7:ILE:CD1	1:C:230:ALA:HB3	2.40	0.45
1:B:17:GLN:HG3	1:B:54:VAL:HG21	1.98	0.45
1:B:31:LEU:O	1:B:31:LEU:HD23	2.17	0.45
1:D:3:GLU:HG2	1:D:262:PHE:HE1	1.82	0.45
1:C:241:ALA:O	1:C:244:ALA:HB3	2.17	0.45
1:A:9:GLU:OE2	1:A:231:SER:HA	2.17	0.45
1:A:19:GLU:CD	1:A:282:ARG:HH21	2.20	0.45
1:B:254:VAL:HG23	1:B:268:LEU:HD11	1.98	0.45
1:B:196:ILE:C	1:B:196:ILE:HD12	2.38	0.44
1:A:248:VAL:HG12	3:A:741:HOH:O	2.17	0.44
1:D:108:LYS:HA	1:D:113:CYS:N	2.33	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:49:VAL:HA	1:C:80:PRO:HG3	2.00	0.44
1:C:46:THR:HG22	3:C:738:HOH:O	2.17	0.44
1:D:17:GLN:HG3	1:D:54:VAL:HG21	1.99	0.44
1:D:49:VAL:HA	1:D:80:PRO:HG3	2.00	0.44
1:C:196:ILE:HD12	1:C:196:ILE:C	2.38	0.44
1:B:29:ILE:HG23	1:B:67:ILE:HD13	1.98	0.44
1:B:7:ILE:CD1	1:B:230:ALA:HB3	2.40	0.44
1:A:49:VAL:HA	1:A:80:PRO:HG3	2.00	0.44
1:C:143:VAL:HG23	1:C:144:VAL:HG23	1.98	0.44
1:A:3:GLU:HG2	1:A:262:PHE:HE1	1.83	0.43
1:D:9:GLU:OE2	1:D:231:SER:HA	2.17	0.43
1:B:108:LYS:HA	1:B:113:CYS:N	2.33	0.43
1:B:144:VAL:HG11	1:B:181:GLY:HA2	2.00	0.43
1:C:42:ARG:HD2	1:C:95:GLU:OE2	2.18	0.43
1:C:59:ASP:O	1:C:63:VAL:HG23	2.19	0.43
1:C:13:ARG:HD2	1:C:13:ARG:C	2.38	0.43
1:C:96:ILE:HG22	1:C:97:ALA:N	2.33	0.43
1:B:96:ILE:HG22	1:B:97:ALA:N	2.34	0.43
1:B:241:ALA:O	1:B:244:ALA:HB3	2.19	0.43
1:A:254:VAL:HG23	1:A:268:LEU:HD11	1.99	0.43
1:C:46:THR:C	1:C:77:VAL:HG23	2.39	0.43
1:D:254:VAL:HG23	1:D:268:LEU:HD11	2.00	0.43
1:B:13:ARG:C	1:B:13:ARG:HD2	2.39	0.43
1:A:145:GLU:HG2	1:A:178:ILE:HD11	2.00	0.43
1:D:59:ASP:O	1:D:63:VAL:HG23	2.18	0.42
1:C:77:VAL:HB	3:C:738:HOH:O	2.19	0.42
1:A:108:LYS:HA	1:A:113:CYS:N	2.33	0.42
1:D:196:ILE:C	1:D:196:ILE:HD12	2.39	0.42
1:B:46:THR:C	1:B:77:VAL:HG23	2.39	0.42
1:D:145:GLU:HG2	1:D:178:ILE:HD11	2.01	0.42
1:A:196:ILE:HD12	1:A:196:ILE:C	2.39	0.42
1:C:218:ARG:HD2	3:C:722:HOH:O	2.18	0.42
1:C:17:GLN:HG3	1:C:54:VAL:HG21	2.01	0.42
1:D:122:LEU:O	1:D:125:VAL:HG22	2.20	0.42
1:A:111:ILE:HG23	3:A:686:HOH:O	2.18	0.42
1:C:4:HIS:HB2	3:C:711:HOH:O	2.20	0.42
1:D:104:GLU:HG2	3:D:646:HOH:O	2.20	0.42
1:D:42:ARG:HD2	1:D:95:GLU:OE2	2.20	0.42
1:D:13:ARG:C	1:D:13:ARG:HD2	2.40	0.42
1:D:96:ILE:HG22	1:D:97:ALA:N	2.35	0.42
1:B:19:GLU:OE2	1:B:282:ARG:NH2	2.50	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:122:LEU:O	1:A:125:VAL:HG22	2.20	0.42
1:A:242:PRO:O	1:C:239:PRO:CG	2.68	0.42
1:C:267:ASP:CB	1:C:270:ARG:HG3	2.50	0.41
1:D:50:SER:HA	1:D:51:PRO:HD3	1.93	0.41
1:A:31:LEU:HD11	1:A:278:THR:HG22	2.02	0.41
1:D:111:ILE:O	1:D:111:ILE:HG22	2.20	0.41
1:D:214:LEU:HB2	3:D:679:HOH:O	2.20	0.41
1:B:122:LEU:O	1:B:125:VAL:HG22	2.20	0.41
1:A:144:VAL:HG11	1:A:181:GLY:HA2	2.02	0.41
1:B:49:VAL:HA	1:B:80:PRO:HG3	2.02	0.41
1:B:9:GLU:OE2	1:B:231:SER:HA	2.20	0.41
1:A:42:ARG:HD2	1:A:95:GLU:OE2	2.21	0.41
1:C:50:SER:HA	1:C:51:PRO:HD3	1.94	0.41
1:B:42:ARG:HD2	1:B:95:GLU:OE2	2.20	0.41
1:B:56:GLN:N	1:B:56:GLN:HE21	2.12	0.41
1:D:46:THR:C	1:D:77:VAL:HG23	2.40	0.41
1:C:108:LYS:HA	1:C:113:CYS:N	2.36	0.41
1:D:263:GLU:HB3	3:D:725:HOH:O	2.20	0.41
1:A:240:PHE:CE1	1:C:55:PRO:HG3	2.55	0.41
1:B:145:GLU:HG2	1:B:178:ILE:HD11	2.02	0.41
1:D:46:THR:HG21	1:D:60:SER:HB2	2.02	0.41
1:A:130:ILE:HG22	3:A:753:HOH:O	2.20	0.41
1:B:251:VAL:O	1:B:254:VAL:HG22	2.20	0.41
1:B:12:ALA:HB3	3:B:603:HOH:O	2.20	0.41
1:D:29:ILE:HG23	1:D:67:ILE:HD13	2.02	0.41
1:A:29:ILE:HG23	1:A:67:ILE:HD13	2.01	0.41
1:D:54:VAL:HG22	1:D:54:VAL:O	2.21	0.41
1:A:7:ILE:CD1	1:A:230:ALA:HB3	2.39	0.41
1:D:7:ILE:CD1	1:D:230:ALA:HB3	2.42	0.41
1:C:54:VAL:O	1:C:54:VAL:HG22	2.21	0.41
1:A:125:VAL:HG23	1:A:126:ILE:N	2.36	0.41
1:B:125:VAL:HG23	1:B:126:ILE:N	2.35	0.41
1:D:213:ALA:O	1:D:217:ILE:HG13	2.21	0.41
1:B:232:VAL:HG13	1:B:233:GLY:N	2.36	0.41
1:C:45:ALA:HB3	3:C:738:HOH:O	2.21	0.41
1:A:241:ALA:O	1:A:244:ALA:HB3	2.20	0.41
1:A:46:THR:C	1:A:77:VAL:HG23	2.42	0.40
1:A:267:ASP:CB	1:A:270:ARG:HG3	2.51	0.40
1:C:4:HIS:HD1	1:C:4:HIS:H	1.65	0.40
1:C:122:LEU:O	1:C:125:VAL:HG22	2.20	0.40
1:C:144:VAL:HG11	1:C:181:GLY:HA2	2.02	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:50:SER:HA	1:A:51:PRO:HD3	1.92	0.40
1:A:7:ILE:HA	1:A:228:PHE:O	2.21	0.40
1:D:125:VAL:HG23	1:D:126:ILE:N	2.37	0.40
1:D:31:LEU:C	1:D:31:LEU:HD23	2.41	0.40
1:C:9:GLU:OE2	1:C:231:SER:HA	2.22	0.40
1:C:54:VAL:O	1:C:54:VAL:HG13	2.21	0.40
1:A:17:GLN:HG3	1:A:54:VAL:HG21	2.02	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	281/295 (95%)	264 (94%)	17 (6%)	0	100	100
1	B	281/295 (95%)	265 (94%)	16 (6%)	0	100	100
1	C	281/295 (95%)	264 (94%)	17 (6%)	0	100	100
1	D	281/295 (95%)	264 (94%)	17 (6%)	0	100	100
All	All	1124/1180 (95%)	1057 (94%)	67 (6%)	0	100	100

There are no Ramachandran outliers to report.

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	217/221 (98%)	206 (95%)	11 (5%)	29	39
1	B	217/221 (98%)	209 (96%)	8 (4%)	41	55
1	C	217/221 (98%)	208 (96%)	9 (4%)	37	50
1	D	217/221 (98%)	208 (96%)	9 (4%)	37	50
All	All	868/884 (98%)	831 (96%)	37 (4%)	35	47

All (37) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	4	HIS
1	A	56	GLN
1	A	62	GLU
1	A	68	ARG
1	A	69	ARG
1	A	83	LYS
1	A	200	HIS
1	A	202	LEU
1	A	245	LYS
1	A	276	LEU
1	A	282	ARG
1	B	4	HIS
1	B	56	GLN
1	B	62	GLU
1	B	68	ARG
1	B	83	LYS
1	B	200	HIS
1	B	202	LEU
1	B	245	LYS
1	C	4	HIS
1	C	56	GLN
1	C	62	GLU
1	C	68	ARG
1	C	83	LYS
1	C	136	ILE
1	C	200	HIS
1	C	202	LEU
1	C	245	LYS
1	D	4	HIS
1	D	56	GLN
1	D	62	GLU
1	D	68	ARG
1	D	83	LYS

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Mol	Chain	Res	Type
1	D	136	ILE
1	D	200	HIS
1	D	202	LEU
1	D	245	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (19) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	33	ASN
1	A	56	GLN
1	A	110	ASN
1	A	200	HIS
1	B	33	ASN
1	B	56	GLN
1	B	110	ASN
1	B	200	HIS
1	B	283	GLN
1	C	33	ASN
1	C	56	GLN
1	C	110	ASN
1	C	200	HIS
1	D	33	ASN
1	D	56	GLN
1	D	110	ASN
1	D	112	ASN
1	D	163	GLN
1	D	200	HIS

5.3.3 RNA

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates

There are no carbohydrates in this entry.

5.6 Ligand geometry

Of 4 ligands modelled in this entry, 4 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

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

EDS was not executed - this section will therefore be empty.

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

EDS was not executed - this section will therefore be empty.

6.3 Carbohydrates

EDS was not executed - this section will therefore be empty.

6.4 Ligands

EDS was not executed - this section will therefore be empty.

6.5 Other polymers

EDS was not executed - this section will therefore be empty.