



Full wwPDB X-ray Structure Validation Report ⓘ

May 21, 2020 – 06:01 pm BST

PDB ID : 1PWE
Title : Rat Liver L-Serine Dehydratase Apo Enzyme
Authors : Yamada, T.; Komoto, J.; Takata, Y.; Ogawa, H.; Takusagawa, F.
Deposited on : 2003-07-01
Resolution : 2.80 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 ⓘ symbol.

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

MolProbity : 4.02b-467
Xtrriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.11

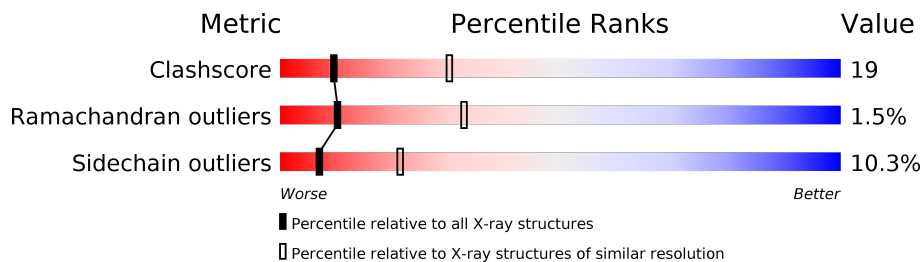
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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	141614	3569 (2.80-2.80)
Ramachandran outliers	138981	3498 (2.80-2.80)
Sidechain outliers	138945	3500 (2.80-2.80)

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 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 $\leq 5\%$

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	327	
1	B	327	
1	C	327	
1	D	327	
1	E	327	
1	F	327	

2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 14065 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 L-serine dehydratase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	315	2326	1484	395	434	13	0	0	0
1	B	315	2326	1484	395	434	13	0	0	0
1	C	315	2326	1484	395	434	13	0	0	0
1	D	315	2326	1484	395	434	13	0	0	0
1	E	315	2326	1484	395	434	13	0	0	0
1	F	315	2326	1484	395	434	13	0	0	0

- Molecule 2 is water.

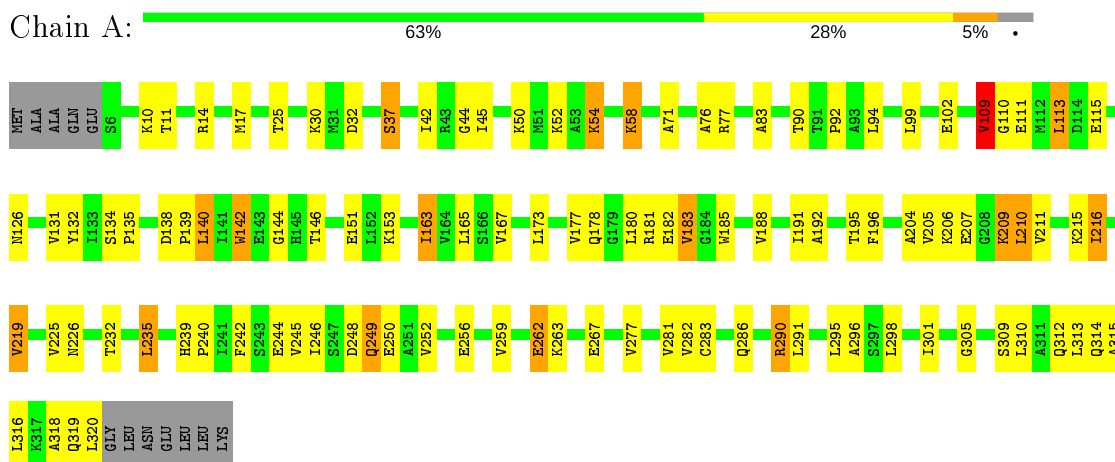
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	19	Total	O	0	0
			19	19		
2	B	22	Total	O	0	0
			22	22		
2	C	14	Total	O	0	0
			14	14		
2	D	16	Total	O	0	0
			16	16		
2	E	16	Total	O	0	0
			16	16		
2	F	22	Total	O	0	0
			22	22		

3 Residue-property plots [i](#)

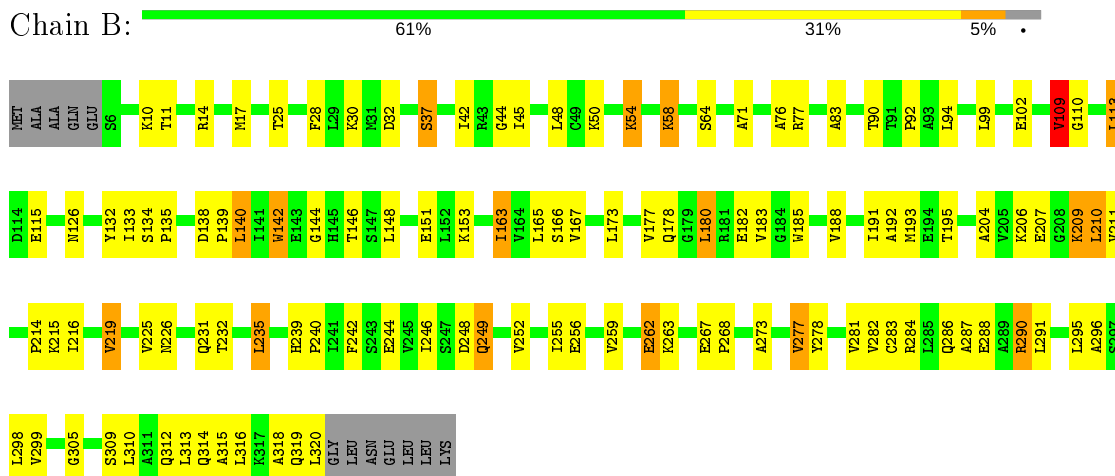
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded according 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. 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: L-serine dehydratase

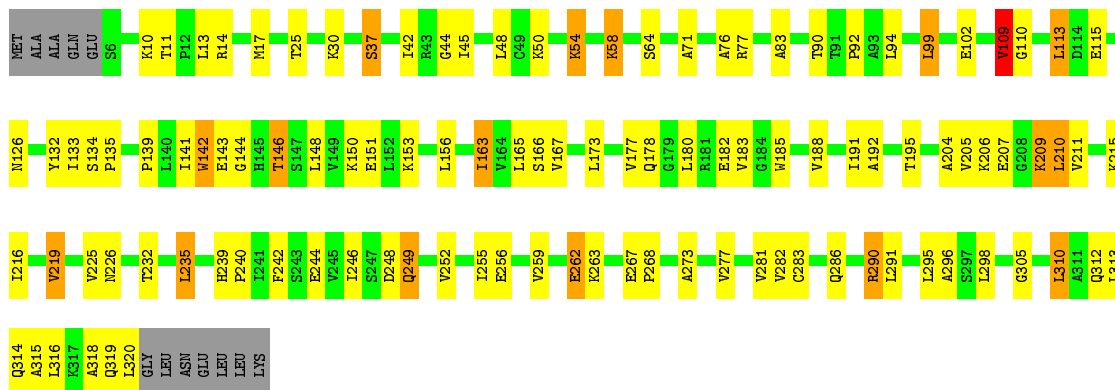


- Molecule 1: L-serine dehydratase

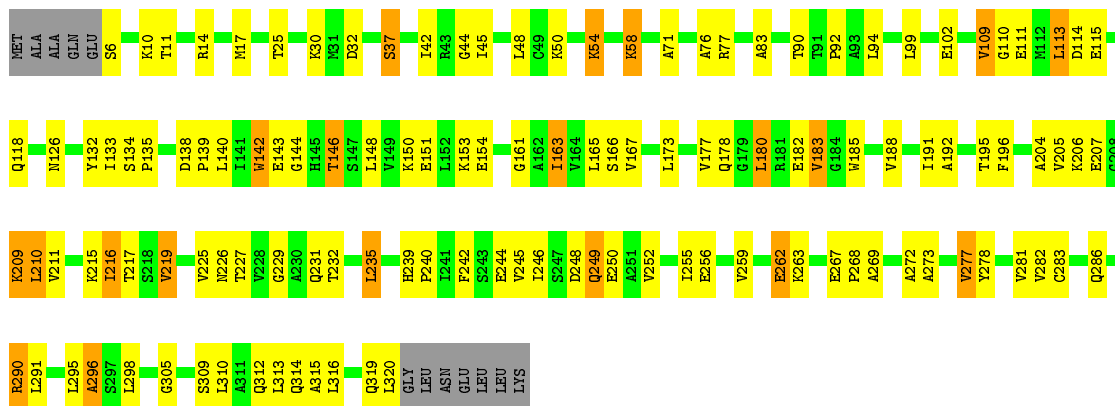


- Molecule 1: L-serine dehydratase

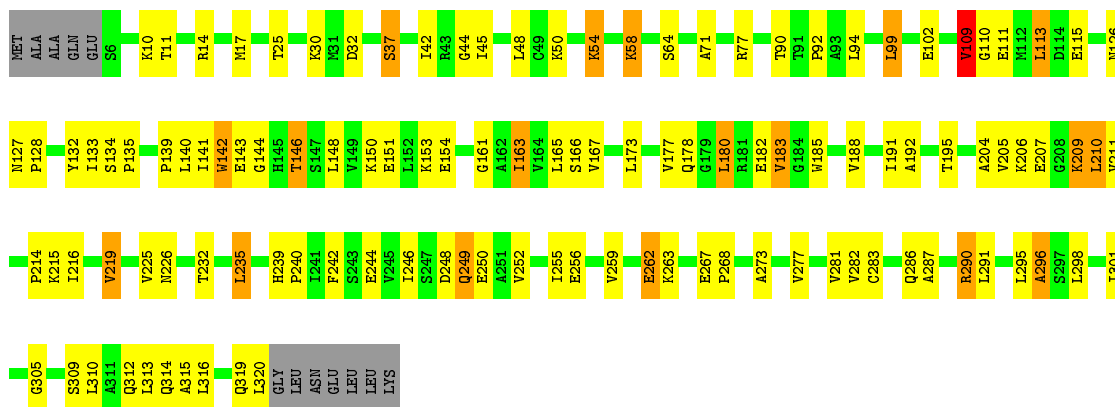




- Molecule 1: L-serine dehydratase

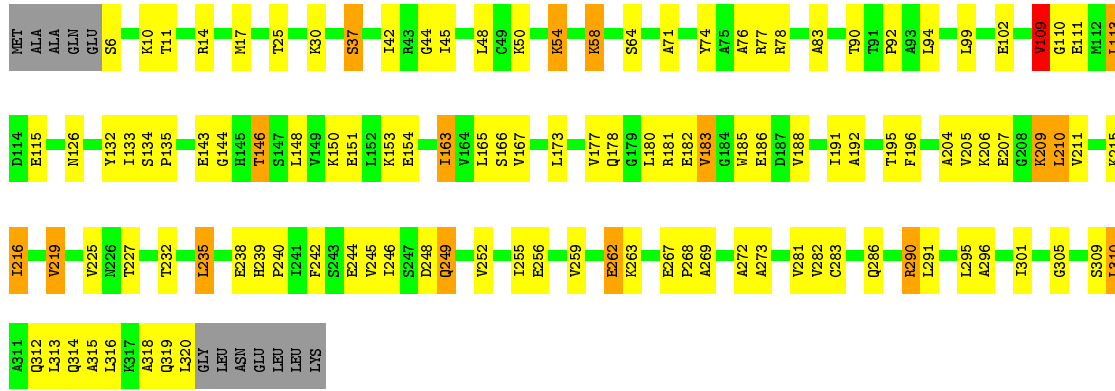


- Molecule 1: L-serine dehydratase



- Molecule 1: L-serine dehydratase





4 Data and refinement statistics

Xtrriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	70.63Å 169.84Å 96.00Å 90.00° 92.75° 90.00°	Depositor
Resolution (Å)	23.52 – 2.80	Depositor
% Data completeness (in resolution range)	86.3 (23.52-2.80)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	0.07	Depositor
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.218 , 0.247	Depositor
Estimated twinning fraction	No twinning to report.	Xtrriage
Total number of atoms	14065	wwPDB-VP
Average B, all atoms (Å ²)	25.0	wwPDB-VP

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	0.45	0/2365	0.64	0/3207
1	B	0.45	0/2365	0.64	0/3207
1	C	0.45	0/2365	0.64	0/3207
1	D	0.46	0/2365	0.65	0/3207
1	E	0.46	0/2365	0.64	0/3207
1	F	0.46	0/2365	0.64	0/3207
All	All	0.45	0/14190	0.64	0/19242

There are no bond length outliers.

There are no bond angle outliers.

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	2326	0	2415	92	0
1	B	2326	0	2415	95	0
1	C	2326	0	2415	89	0
1	D	2326	0	2415	103	0
1	E	2326	0	2415	97	0
1	F	2326	0	2415	99	0
2	A	19	0	0	0	0
2	B	22	0	0	0	0
2	C	14	0	0	0	0
2	D	16	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	E	16	0	0	0	0
2	F	22	0	0	2	0
All	All	14065	0	14490	554	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 (554) 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:209:LYS:HG3	1:C:210:LEU:H	1.20	1.07
1:D:209:LYS:HG3	1:D:210:LEU:H	1.25	1.00
1:F:209:LYS:HG3	1:F:210:LEU:H	1.32	0.95
1:C:249:GLN:H	1:C:249:GLN:HE21	1.14	0.94
1:D:249:GLN:HE21	1:D:249:GLN:H	1.15	0.91
1:B:249:GLN:HE21	1:B:249:GLN:H	1.12	0.90
1:D:209:LYS:HG3	1:D:210:LEU:N	1.87	0.90
1:E:249:GLN:HE21	1:E:249:GLN:H	1.14	0.90
1:F:249:GLN:H	1:F:249:GLN:HE21	1.16	0.89
1:A:249:GLN:HE21	1:A:249:GLN:H	1.19	0.89
1:C:249:GLN:H	1:C:249:GLN:NE2	1.73	0.86
1:D:173:LEU:HD23	1:D:232:THR:HG23	1.58	0.85
1:D:249:GLN:NE2	1:D:249:GLN:H	1.75	0.85
1:A:249:GLN:NE2	1:A:249:GLN:H	1.75	0.84
1:B:249:GLN:NE2	1:B:249:GLN:H	1.74	0.84
1:A:173:LEU:HD23	1:A:232:THR:HG23	1.57	0.84
1:C:14:ARG:HH11	1:C:262:GLU:HG3	1.42	0.84
1:A:267:GLU:HG3	1:A:305:GLY:HA3	1.59	0.84
1:E:249:GLN:NE2	1:E:249:GLN:H	1.75	0.84
1:F:173:LEU:HD23	1:F:232:THR:HG23	1.59	0.84
1:A:10:LYS:HG3	1:A:151:GLU:HG2	1.59	0.84
1:C:209:LYS:HG3	1:C:210:LEU:N	1.93	0.84
1:C:14:ARG:NH1	1:C:262:GLU:HG3	1.93	0.83
1:C:173:LEU:HD23	1:C:232:THR:HG23	1.61	0.82
1:F:249:GLN:H	1:F:249:GLN:NE2	1.78	0.82
1:B:267:GLU:HG3	1:B:305:GLY:HA3	1.60	0.82
1:C:109:VAL:HG13	1:C:110:GLY:N	1.94	0.81
1:C:10:LYS:HG3	1:C:151:GLU:HG2	1.64	0.80
1:A:109:VAL:HG13	1:A:110:GLY:N	1.97	0.80
1:E:173:LEU:HD23	1:E:232:THR:HG23	1.62	0.80
1:F:109:VAL:HG13	1:F:110:GLY:N	1.96	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:109:VAL:HG13	1:D:110:GLY:N	1.98	0.78
1:B:206:LYS:HE3	1:B:207:GLU:HG2	1.64	0.78
1:E:109:VAL:HG13	1:E:110:GLY:N	1.99	0.78
1:E:267:GLU:HG3	1:E:305:GLY:HA3	1.65	0.78
1:B:173:LEU:HD23	1:B:232:THR:HG23	1.63	0.78
1:B:109:VAL:HG13	1:B:110:GLY:N	1.99	0.78
1:A:182:GLU:HB2	1:F:186:GLU:HG3	1.66	0.77
1:D:10:LYS:HG3	1:D:151:GLU:HG2	1.65	0.77
1:D:14:ARG:NH1	1:D:262:GLU:HG3	1.99	0.77
1:F:205:VAL:HA	1:F:209:LYS:O	1.86	0.75
1:B:10:LYS:HG3	1:B:151:GLU:HG2	1.69	0.74
1:A:14:ARG:HH11	1:A:262:GLU:HG3	1.51	0.74
1:F:209:LYS:HG3	1:F:210:LEU:N	2.02	0.74
1:B:14:ARG:NH1	1:B:262:GLU:HG3	2.01	0.74
1:D:14:ARG:HH11	1:D:262:GLU:HG3	1.50	0.74
1:A:14:ARG:NH1	1:A:262:GLU:HG3	2.03	0.74
1:D:267:GLU:HG3	1:D:305:GLY:HA3	1.68	0.74
1:F:14:ARG:HH11	1:F:262:GLU:HG3	1.52	0.74
1:A:206:LYS:HE3	1:A:207:GLU:HG2	1.68	0.74
1:D:206:LYS:HE3	1:D:207:GLU:HG2	1.69	0.73
1:F:14:ARG:NH1	1:F:262:GLU:HG3	2.02	0.73
1:F:10:LYS:HG3	1:F:151:GLU:HG2	1.70	0.73
1:E:14:ARG:HH11	1:E:262:GLU:HG3	1.52	0.73
1:E:10:LYS:HG3	1:E:151:GLU:HG2	1.71	0.73
1:B:14:ARG:HH11	1:B:262:GLU:HG3	1.54	0.73
1:C:191:ILE:HD11	1:C:291:LEU:HD11	1.70	0.72
1:C:206:LYS:HE3	1:C:207:GLU:HG2	1.70	0.72
1:B:290:ARG:HD2	1:B:290:ARG:H	1.54	0.72
1:A:209:LYS:HG3	1:A:210:LEU:H	1.55	0.71
1:D:209:LYS:CG	1:D:210:LEU:H	1.92	0.71
1:E:209:LYS:HG3	1:E:210:LEU:H	1.55	0.71
1:A:290:ARG:H	1:A:290:ARG:HD2	1.55	0.70
1:E:92:PRO:HG3	1:F:92:PRO:HG3	1.72	0.70
1:D:191:ILE:HD11	1:D:291:LEU:HD11	1.74	0.70
1:E:14:ARG:NH1	1:E:262:GLU:HG3	2.07	0.70
1:C:290:ARG:HD2	1:C:290:ARG:H	1.58	0.69
1:E:290:ARG:H	1:E:290:ARG:HD2	1.57	0.69
1:F:177:VAL:HG21	1:F:235:LEU:HG	1.73	0.69
1:E:191:ILE:HD11	1:E:291:LEU:HD11	1.74	0.69
1:C:113:LEU:HG	1:D:113:LEU:HG	1.74	0.69
1:D:242:PHE:CE2	1:D:290:ARG:HB3	2.28	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:206:LYS:HE3	1:F:207:GLU:HG2	1.75	0.68
1:F:290:ARG:HD2	1:F:290:ARG:H	1.59	0.68
1:D:37:SER:HB3	1:D:42:ILE:HB	1.76	0.68
1:A:191:ILE:HD11	1:A:291:LEU:HD11	1.75	0.68
1:E:206:LYS:HE3	1:E:207:GLU:HG2	1.76	0.68
1:F:312:GLN:O	1:F:316:LEU:HD13	1.94	0.68
1:B:191:ILE:HD11	1:B:291:LEU:HD11	1.77	0.67
1:F:191:ILE:HD11	1:F:291:LEU:HD11	1.76	0.67
1:C:209:LYS:CG	1:C:210:LEU:H	1.90	0.67
1:C:312:GLN:O	1:C:316:LEU:HD13	1.94	0.67
1:A:92:PRO:HG3	1:B:92:PRO:HG3	1.77	0.67
1:A:113:LEU:HG	1:B:113:LEU:HG	1.77	0.67
1:D:290:ARG:HD2	1:D:290:ARG:H	1.59	0.66
1:E:209:LYS:HG3	1:E:210:LEU:N	2.10	0.66
1:C:267:GLU:HG3	1:C:305:GLY:HA3	1.75	0.66
1:F:267:GLU:HG3	1:F:305:GLY:HA3	1.78	0.66
1:C:177:VAL:HG21	1:C:235:LEU:HG	1.78	0.66
1:B:316:LEU:O	1:B:320:LEU:HB3	1.96	0.66
1:E:242:PHE:CE2	1:E:290:ARG:HB3	2.32	0.65
1:A:316:LEU:O	1:A:320:LEU:HB3	1.97	0.65
1:C:92:PRO:HG3	1:D:92:PRO:HG3	1.78	0.65
1:D:146:THR:HG23	1:D:150:LYS:HE3	1.78	0.65
1:D:286:GLN:NE2	1:D:295:LEU:HB2	2.12	0.64
1:B:209:LYS:HG3	1:B:210:LEU:N	2.12	0.64
1:D:177:VAL:HG21	1:D:235:LEU:HG	1.80	0.64
1:A:77:ARG:NH1	1:A:102:GLU:OE2	2.31	0.64
1:E:239:HIS:CG	1:E:240:PRO:HD2	2.32	0.64
1:E:37:SER:HB3	1:E:42:ILE:HB	1.79	0.64
1:E:58:LYS:NZ	1:E:58:LYS:HB3	2.13	0.63
1:A:209:LYS:HG3	1:A:210:LEU:N	2.14	0.63
1:F:50:LYS:HG3	1:F:54:LYS:NZ	2.14	0.63
1:A:242:PHE:CE2	1:A:290:ARG:HB3	2.34	0.62
1:B:209:LYS:CG	1:B:210:LEU:H	2.12	0.62
1:C:37:SER:HB3	1:C:42:ILE:HB	1.81	0.62
1:F:45:ILE:HD11	1:F:135:PRO:HG3	1.80	0.62
1:B:209:LYS:HG3	1:B:210:LEU:H	1.64	0.62
1:F:37:SER:HB3	1:F:42:ILE:HB	1.81	0.62
1:D:316:LEU:O	1:D:320:LEU:HB3	1.99	0.62
1:E:209:LYS:CG	1:E:210:LEU:H	2.11	0.62
1:E:113:LEU:HG	1:F:113:LEU:HG	1.81	0.61
1:B:177:VAL:HG21	1:B:235:LEU:HG	1.81	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:249:GLN:HE21	1:B:249:GLN:N	1.93	0.61
1:C:316:LEU:O	1:C:320:LEU:HB3	2.01	0.61
1:B:37:SER:HB3	1:B:42:ILE:HB	1.82	0.61
1:B:209:LYS:HD2	1:B:210:LEU:HG	1.83	0.61
1:B:312:GLN:O	1:B:316:LEU:HD13	2.01	0.61
1:F:316:LEU:O	1:F:320:LEU:HB3	2.01	0.61
1:A:58:LYS:NZ	1:A:58:LYS:HB3	2.16	0.60
1:B:167:VAL:CG2	1:B:192:ALA:HB1	2.31	0.60
1:E:286:GLN:NE2	1:E:295:LEU:HB2	2.15	0.60
1:B:185:TRP:HB3	1:B:188:VAL:HG23	1.84	0.60
1:F:248:ASP:O	1:F:252:VAL:HG23	2.01	0.60
1:D:45:ILE:HD11	1:D:135:PRO:HG3	1.83	0.60
1:D:167:VAL:CG2	1:D:192:ALA:HB1	2.31	0.60
1:D:77:ARG:NH1	1:D:102:GLU:OE2	2.35	0.60
1:D:242:PHE:HE2	1:D:290:ARG:HB3	1.67	0.60
1:F:286:GLN:NE2	1:F:295:LEU:HB2	2.16	0.60
1:A:10:LYS:HG3	1:A:151:GLU:CG	2.31	0.59
1:B:242:PHE:CE2	1:B:290:ARG:HB3	2.37	0.59
1:A:177:VAL:HG21	1:A:235:LEU:HG	1.84	0.59
1:E:177:VAL:HG21	1:E:235:LEU:HG	1.83	0.59
1:B:244:GLU:HG2	1:B:281:VAL:CG1	2.33	0.59
1:B:286:GLN:NE2	1:B:295:LEU:HB2	2.17	0.59
1:C:45:ILE:HD11	1:C:135:PRO:HG3	1.84	0.59
1:E:185:TRP:HB3	1:E:188:VAL:HG23	1.84	0.59
1:E:316:LEU:O	1:E:320:LEU:HB3	2.01	0.59
1:C:77:ARG:NH1	1:C:102:GLU:OE2	2.36	0.59
1:C:256:GLU:O	1:C:259:VAL:HG12	2.03	0.59
1:D:249:GLN:NE2	1:D:249:GLN:N	2.50	0.59
1:C:58:LYS:HB3	1:C:58:LYS:NZ	2.18	0.59
1:D:312:GLN:O	1:D:316:LEU:HD13	2.02	0.58
1:E:312:GLN:O	1:E:316:LEU:HD13	2.03	0.58
1:B:239:HIS:CG	1:B:240:PRO:HD2	2.39	0.58
1:C:185:TRP:HB3	1:C:188:VAL:HG23	1.85	0.58
1:E:249:GLN:HE21	1:E:249:GLN:N	1.93	0.58
1:C:286:GLN:NE2	1:C:295:LEU:HB2	2.17	0.58
1:C:249:GLN:HE21	1:C:249:GLN:N	1.93	0.58
1:F:239:HIS:CG	1:F:240:PRO:HD2	2.38	0.58
1:E:167:VAL:CG2	1:E:192:ALA:HB1	2.33	0.58
1:A:109:VAL:HG13	1:A:110:GLY:H	1.68	0.57
1:A:167:VAL:CG2	1:A:192:ALA:HB1	2.34	0.57
1:C:163:ILE:C	1:C:163:ILE:HD13	2.24	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:185:TRP:HB3	1:C:188:VAL:CG2	2.34	0.57
1:F:209:LYS:CG	1:F:210:LEU:H	1.99	0.57
1:A:256:GLU:O	1:A:259:VAL:HG12	2.03	0.57
1:D:165:LEU:HD12	1:D:165:LEU:C	2.24	0.57
1:D:58:LYS:HB3	1:D:58:LYS:NZ	2.19	0.57
1:B:58:LYS:HB3	1:B:58:LYS:NZ	2.18	0.57
1:D:248:ASP:O	1:D:252:VAL:HG23	2.03	0.57
1:D:165:LEU:HD12	1:D:165:LEU:O	2.04	0.57
1:A:312:GLN:O	1:A:316:LEU:HD13	2.04	0.57
1:F:185:TRP:HB3	1:F:188:VAL:CG2	2.34	0.57
1:A:165:LEU:C	1:A:165:LEU:HD12	2.25	0.57
1:A:248:ASP:O	1:A:252:VAL:HG23	2.05	0.57
1:C:167:VAL:CG2	1:C:192:ALA:HB1	2.34	0.57
1:A:182:GLU:HB2	1:F:186:GLU:CG	2.35	0.57
1:E:165:LEU:C	1:E:165:LEU:HD12	2.24	0.57
1:A:182:GLU:CB	1:F:186:GLU:HG3	2.33	0.57
1:F:185:TRP:HB3	1:F:188:VAL:HG23	1.86	0.57
1:D:239:HIS:CG	1:D:240:PRO:HD2	2.39	0.57
1:F:195:THR:HA	1:F:246:ILE:O	2.05	0.57
1:F:244:GLU:HG2	1:F:281:VAL:CG1	2.35	0.57
1:F:58:LYS:HB3	1:F:58:LYS:NZ	2.20	0.57
1:A:153:LYS:HD3	1:A:183:VAL:HG13	1.87	0.56
1:A:205:VAL:HA	1:A:209:LYS:O	2.05	0.56
1:A:37:SER:HB3	1:A:42:ILE:HB	1.87	0.56
1:C:165:LEU:HD12	1:C:165:LEU:C	2.25	0.56
1:F:242:PHE:CE2	1:F:290:ARG:HB3	2.40	0.56
1:C:165:LEU:O	1:C:165:LEU:HD12	2.04	0.56
1:A:165:LEU:O	1:A:165:LEU:HD12	2.04	0.56
1:C:242:PHE:CE2	1:C:290:ARG:HB3	2.41	0.56
1:E:185:TRP:HB3	1:E:188:VAL:CG2	2.34	0.56
1:E:244:GLU:HG2	1:E:281:VAL:CG1	2.35	0.56
1:B:248:ASP:O	1:B:252:VAL:HG23	2.05	0.56
1:E:44:GLY:HA2	1:E:144:GLY:HA3	1.88	0.56
1:A:45:ILE:HD11	1:A:135:PRO:HG3	1.88	0.56
1:A:178:GLN:O	1:A:182:GLU:HG2	2.06	0.56
1:D:185:TRP:HB3	1:D:188:VAL:HG23	1.88	0.56
1:A:286:GLN:NE2	1:A:295:LEU:HB2	2.20	0.56
1:C:146:THR:HG23	1:C:150:LYS:HE3	1.86	0.56
1:C:10:LYS:HG3	1:C:151:GLU:CG	2.34	0.55
1:C:239:HIS:CG	1:C:240:PRO:HD2	2.42	0.55
1:E:50:LYS:HG3	1:E:54:LYS:NZ	2.21	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:209:LYS:CG	1:A:210:LEU:H	2.15	0.55
1:C:109:VAL:HG13	1:C:110:GLY:H	1.69	0.55
1:D:209:LYS:CG	1:D:210:LEU:N	2.57	0.55
1:C:50:LYS:HG3	1:C:54:LYS:NZ	2.21	0.55
1:D:195:THR:HA	1:D:246:ILE:O	2.07	0.55
1:D:173:LEU:CD2	1:D:232:THR:HG23	2.35	0.55
1:D:249:GLN:HE21	1:D:249:GLN:N	1.94	0.55
1:E:45:ILE:HD11	1:E:135:PRO:HG3	1.88	0.55
1:F:109:VAL:HG13	1:F:110:GLY:H	1.68	0.55
1:A:239:HIS:CG	1:A:240:PRO:HD2	2.42	0.55
1:A:195:THR:HA	1:A:246:ILE:O	2.07	0.55
1:C:210:LEU:O	1:C:210:LEU:HD12	2.06	0.54
1:B:45:ILE:HD11	1:B:135:PRO:HG3	1.90	0.54
1:E:165:LEU:O	1:E:165:LEU:HD12	2.08	0.54
1:F:146:THR:HG23	1:F:150:LYS:HE3	1.89	0.54
1:F:165:LEU:C	1:F:165:LEU:HD12	2.28	0.54
1:B:185:TRP:HB3	1:B:188:VAL:CG2	2.37	0.54
1:C:195:THR:HA	1:C:246:ILE:O	2.07	0.54
1:F:165:LEU:HD12	1:F:165:LEU:O	2.08	0.54
1:A:282:VAL:HG23	1:A:283:CYS:N	2.22	0.54
1:B:165:LEU:HD12	1:B:165:LEU:C	2.28	0.54
1:C:109:VAL:HG22	1:C:115:GLU:OE2	2.06	0.54
1:E:109:VAL:CG1	1:E:110:GLY:N	2.71	0.54
1:F:309:SER:OG	1:F:312:GLN:HG3	2.08	0.54
1:C:244:GLU:HG2	1:C:281:VAL:CG1	2.38	0.54
1:A:210:LEU:O	1:A:210:LEU:HD12	2.06	0.54
1:B:50:LYS:HG3	1:B:54:LYS:NZ	2.23	0.54
1:C:249:GLN:NE2	1:C:249:GLN:N	2.49	0.54
1:F:109:VAL:CG1	1:F:110:GLY:N	2.69	0.54
1:B:206:LYS:HE3	1:B:207:GLU:CG	2.34	0.54
1:D:10:LYS:HG3	1:D:151:GLU:CG	2.34	0.54
1:E:195:THR:HA	1:E:246:ILE:O	2.07	0.54
1:F:132:TYR:CE1	1:F:134:SER:HB2	2.42	0.54
1:A:249:GLN:NE2	1:A:249:GLN:N	2.52	0.54
1:C:205:VAL:HA	1:C:209:LYS:O	2.07	0.53
1:C:282:VAL:HG23	1:C:283:CYS:N	2.23	0.53
1:A:244:GLU:HG2	1:A:281:VAL:CG1	2.38	0.53
1:B:195:THR:HA	1:B:246:ILE:O	2.08	0.53
1:E:10:LYS:HZ2	1:E:154:GLU:CD	2.12	0.53
1:E:163:ILE:HD13	1:E:163:ILE:C	2.29	0.53
1:A:173:LEU:CD2	1:A:232:THR:HG23	2.34	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:242:PHE:HE2	1:E:290:ARG:HB3	1.72	0.53
1:E:249:GLN:NE2	1:E:249:GLN:N	2.51	0.53
1:B:249:GLN:NE2	1:B:249:GLN:N	2.51	0.53
1:F:163:ILE:HD13	1:F:163:ILE:C	2.29	0.53
1:F:167:VAL:CG2	1:F:192:ALA:HB1	2.38	0.53
1:A:185:TRP:HB3	1:A:188:VAL:HG23	1.90	0.53
1:A:50:LYS:HG3	1:A:54:LYS:NZ	2.23	0.53
1:C:206:LYS:HE3	1:C:207:GLU:CG	2.38	0.53
1:D:50:LYS:HG3	1:D:54:LYS:NZ	2.24	0.53
1:E:10:LYS:HG3	1:E:151:GLU:CG	2.38	0.53
1:F:11:THR:OG1	1:F:30:LYS:HE3	2.09	0.53
1:E:210:LEU:O	1:E:210:LEU:HD12	2.09	0.52
1:B:165:LEU:HD12	1:B:165:LEU:O	2.09	0.52
1:E:256:GLU:O	1:E:259:VAL:HG12	2.10	0.52
1:B:209:LYS:CG	1:B:210:LEU:N	2.72	0.52
1:E:64:SER:HB3	1:F:111:GLU:OE1	2.09	0.52
1:A:259:VAL:O	1:A:263:LYS:HA	2.09	0.52
1:A:92:PRO:HD3	1:B:90:THR:O	2.09	0.52
1:C:248:ASP:O	1:C:252:VAL:HG23	2.10	0.52
1:F:215:LYS:O	1:F:219:VAL:HG12	2.10	0.52
1:F:50:LYS:HG3	1:F:54:LYS:HZ2	1.72	0.52
1:C:109:VAL:CG1	1:C:110:GLY:N	2.67	0.52
1:F:77:ARG:NH1	1:F:102:GLU:OE2	2.41	0.52
1:A:206:LYS:HE3	1:A:207:GLU:CG	2.38	0.52
1:B:10:LYS:HG3	1:B:151:GLU:CG	2.37	0.52
1:D:185:TRP:HB3	1:D:188:VAL:CG2	2.39	0.52
1:B:256:GLU:O	1:B:259:VAL:HG12	2.10	0.52
1:D:244:GLU:HG2	1:D:281:VAL:CG1	2.39	0.52
1:F:48:LEU:HD12	1:F:133:ILE:HD12	1.92	0.52
1:A:109:VAL:CG1	1:A:110:GLY:N	2.70	0.51
1:E:173:LEU:CD2	1:E:232:THR:HG23	2.38	0.51
1:F:249:GLN:HE21	1:F:249:GLN:N	1.97	0.51
1:B:148:LEU:C	1:B:148:LEU:HD23	2.30	0.51
1:A:163:ILE:C	1:A:163:ILE:HD13	2.30	0.51
1:B:109:VAL:HG13	1:B:110:GLY:H	1.73	0.51
1:D:132:TYR:CE1	1:D:134:SER:HB2	2.45	0.51
1:D:210:LEU:O	1:D:210:LEU:HD12	2.10	0.51
1:F:10:LYS:HG3	1:F:151:GLU:CG	2.40	0.51
1:F:37:SER:HB2	1:F:71:ALA:HA	1.93	0.51
1:D:44:GLY:HA2	1:D:144:GLY:HA3	1.91	0.51
1:F:143:GLU:O	1:F:146:THR:HB	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:215:LYS:O	1:A:219:VAL:HG12	2.10	0.51
1:B:44:GLY:HA2	1:B:144:GLY:HA3	1.92	0.51
1:B:290:ARG:HD2	1:B:290:ARG:N	2.24	0.51
1:D:259:VAL:O	1:D:263:LYS:HA	2.10	0.51
1:F:249:GLN:NE2	1:F:249:GLN:N	2.54	0.51
1:D:206:LYS:HE3	1:D:207:GLU:CG	2.39	0.51
1:A:185:TRP:HB3	1:A:188:VAL:CG2	2.41	0.51
1:C:215:LYS:O	1:C:219:VAL:HG12	2.10	0.51
1:F:282:VAL:HG23	1:F:283:CYS:N	2.26	0.51
1:D:290:ARG:HD2	1:D:290:ARG:N	2.26	0.51
1:F:204:ALA:O	1:F:210:LEU:HA	2.11	0.51
1:A:249:GLN:HE21	1:A:249:GLN:N	1.98	0.50
1:B:259:VAL:O	1:B:263:LYS:HA	2.11	0.50
1:B:267:GLU:CG	1:B:305:GLY:HA3	2.36	0.50
1:B:173:LEU:CD2	1:B:232:THR:HG23	2.38	0.50
1:E:248:ASP:O	1:E:252:VAL:HG23	2.10	0.50
1:E:92:PRO:HD3	1:F:90:THR:O	2.11	0.50
1:D:178:GLN:O	1:D:182:GLU:HG2	2.11	0.50
1:D:256:GLU:O	1:D:259:VAL:HG12	2.12	0.50
1:C:209:LYS:HG3	1:C:210:LEU:HG	1.93	0.50
1:D:163:ILE:HD13	1:D:163:ILE:C	2.32	0.50
1:D:309:SER:OG	1:D:312:GLN:HG3	2.12	0.50
1:A:37:SER:HB2	1:A:71:ALA:HA	1.93	0.50
1:C:132:TYR:CE1	1:C:134:SER:HB2	2.47	0.50
1:D:109:VAL:CG1	1:D:110:GLY:N	2.71	0.50
1:D:37:SER:HB2	1:D:71:ALA:HA	1.93	0.50
1:B:163:ILE:HD13	1:B:163:ILE:C	2.33	0.49
1:E:246:ILE:HG13	1:E:250:GLU:OE1	2.12	0.49
1:E:37:SER:HB2	1:E:71:ALA:HA	1.92	0.49
1:E:209:LYS:CG	1:E:210:LEU:N	2.73	0.49
1:F:259:VAL:O	1:F:263:LYS:HA	2.13	0.49
1:B:215:LYS:O	1:B:219:VAL:HG12	2.12	0.49
1:D:282:VAL:HG23	1:D:283:CYS:N	2.27	0.49
1:E:205:VAL:HA	1:E:209:LYS:O	2.11	0.49
1:A:44:GLY:HA2	1:A:144:GLY:HA3	1.94	0.49
1:D:109:VAL:HG13	1:D:110:GLY:H	1.75	0.49
1:E:77:ARG:NH1	1:E:102:GLU:OE2	2.45	0.49
1:D:215:LYS:O	1:D:219:VAL:HG12	2.13	0.49
1:E:146:THR:HG23	1:E:150:LYS:HE3	1.95	0.49
1:C:44:GLY:HA2	1:C:144:GLY:HA3	1.95	0.49
1:C:204:ALA:O	1:C:210:LEU:HA	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:132:TYR:CE1	1:E:134:SER:HB2	2.47	0.49
1:B:282:VAL:HG23	1:B:283:CYS:N	2.27	0.49
1:F:173:LEU:CD2	1:F:232:THR:HG23	2.36	0.49
1:A:309:SER:OG	1:A:312:GLN:HG3	2.13	0.48
1:B:14:ARG:HH11	1:B:262:GLU:CG	2.24	0.48
1:C:173:LEU:CD2	1:C:232:THR:HG23	2.38	0.48
1:E:248:ASP:C	1:E:320:LEU:HD21	2.34	0.48
1:C:37:SER:HB2	1:C:71:ALA:HA	1.96	0.48
1:D:248:ASP:C	1:D:320:LEU:HD21	2.33	0.48
1:F:178:GLN:O	1:F:182:GLU:HG2	2.13	0.48
1:F:256:GLU:O	1:F:259:VAL:HG12	2.13	0.48
1:E:111:GLU:OE1	1:F:64:SER:HB3	2.13	0.48
1:C:259:VAL:O	1:C:263:LYS:HA	2.14	0.48
1:B:109:VAL:CG1	1:B:110:GLY:N	2.72	0.48
1:E:290:ARG:N	1:E:290:ARG:HD2	2.26	0.48
1:F:210:LEU:O	1:F:210:LEU:HD12	2.14	0.48
1:C:92:PRO:HD3	1:D:90:THR:O	2.14	0.48
1:D:315:ALA:O	1:D:319:GLN:HB3	2.14	0.48
1:B:77:ARG:NH1	1:B:102:GLU:OE2	2.47	0.48
1:F:153:LYS:HD3	1:F:183:VAL:HG13	1.96	0.47
1:F:290:ARG:HA	2:F:346:HOH:O	2.14	0.47
1:A:58:LYS:HB3	1:A:58:LYS:HZ3	1.79	0.47
1:E:109:VAL:HG13	1:E:110:GLY:H	1.74	0.47
1:C:90:THR:O	1:D:92:PRO:HD3	2.14	0.47
1:D:109:VAL:HG22	1:D:115:GLU:OE2	2.14	0.47
1:B:244:GLU:HG2	1:B:281:VAL:HG11	1.95	0.47
1:C:50:LYS:HG3	1:C:54:LYS:HZ2	1.77	0.47
1:F:315:ALA:O	1:F:319:GLN:HB3	2.14	0.47
1:B:37:SER:HB2	1:B:71:ALA:HA	1.95	0.47
1:C:209:LYS:CG	1:C:210:LEU:N	2.59	0.47
1:E:259:VAL:O	1:E:263:LYS:HA	2.15	0.47
1:A:52:LYS:HG3	1:A:131:VAL:HG11	1.97	0.47
1:C:153:LYS:HA	1:C:185:TRP:CH2	2.49	0.47
1:F:255:ILE:HD11	1:F:268:PRO:HA	1.96	0.47
1:A:248:ASP:C	1:A:320:LEU:HD21	2.35	0.47
1:C:14:ARG:HH11	1:C:262:GLU:CG	2.20	0.47
1:D:148:LEU:C	1:D:148:LEU:HD23	2.35	0.47
1:A:267:GLU:CG	1:A:305:GLY:HA3	2.37	0.47
1:A:181:ARG:NH1	1:F:238:GLU:HG2	2.30	0.46
1:B:178:GLN:O	1:B:182:GLU:HG2	2.14	0.46
1:C:225:VAL:HG22	1:C:226:ASN:N	2.30	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:206:LYS:HE3	1:E:207:GLU:CG	2.43	0.46
1:D:246:ILE:HG13	1:D:250:GLU:OE1	2.15	0.46
1:F:44:GLY:HA2	1:F:144:GLY:HA3	1.96	0.46
1:B:132:TYR:CE1	1:B:134:SER:HB2	2.51	0.46
1:D:6:SER:N	2:D:331:HOH:O	2.47	0.46
1:F:290:ARG:HD2	1:F:290:ARG:N	2.27	0.46
1:D:298:LEU:C	1:D:298:LEU:HD12	2.36	0.46
1:E:215:LYS:O	1:E:219:VAL:HG12	2.16	0.46
1:A:76:ALA:CB	1:A:83:ALA:HB2	2.46	0.46
1:B:284:ARG:O	1:B:288:GLU:HG3	2.15	0.46
1:B:248:ASP:C	1:B:320:LEU:HD21	2.36	0.46
1:E:282:VAL:HG23	1:E:283:CYS:N	2.30	0.46
1:B:14:ARG:NH1	1:B:262:GLU:CG	2.75	0.46
1:B:166:SER:HB2	1:B:273:ALA:HB2	1.97	0.46
1:C:318:ALA:O	1:C:320:LEU:O	2.33	0.46
1:A:216:ILE:O	1:A:219:VAL:HG13	2.16	0.46
1:D:48:LEU:HD12	1:D:133:ILE:HD12	1.98	0.46
1:C:248:ASP:C	1:C:320:LEU:HD21	2.36	0.46
1:D:166:SER:HB2	1:D:273:ALA:HB2	1.98	0.46
1:A:139:PRO:HA	1:A:142:TRP:CD2	2.51	0.45
1:A:242:PHE:HE2	1:A:290:ARG:HB3	1.80	0.45
1:B:282:VAL:HG23	1:B:283:CYS:H	1.82	0.45
1:C:143:GLU:O	1:C:146:THR:HB	2.16	0.45
1:E:309:SER:OG	1:E:312:GLN:HG3	2.16	0.45
1:F:216:ILE:O	1:F:219:VAL:HG13	2.16	0.45
1:F:76:ALA:CB	1:F:83:ALA:HB2	2.46	0.45
1:A:315:ALA:O	1:A:319:GLN:HB3	2.15	0.45
1:B:242:PHE:HE2	1:B:290:ARG:HB3	1.82	0.45
1:C:11:THR:OG1	1:C:30:LYS:HE3	2.16	0.45
1:D:205:VAL:HA	1:D:209:LYS:O	2.17	0.45
1:E:11:THR:OG1	1:E:30:LYS:HE3	2.15	0.45
1:C:315:ALA:O	1:C:319:GLN:HB3	2.16	0.45
1:D:143:GLU:O	1:D:146:THR:HB	2.17	0.45
1:F:109:VAL:HG22	1:F:115:GLU:OE2	2.16	0.45
1:A:181:ARG:O	1:F:181:ARG:HD3	2.17	0.45
1:A:163:ILE:O	1:A:163:ILE:HG23	2.16	0.45
1:E:139:PRO:HA	1:E:142:TRP:CD2	2.52	0.45
1:E:244:GLU:HG2	1:E:281:VAL:HG11	1.98	0.45
1:B:139:PRO:HA	1:B:142:TRP:CD2	2.52	0.45
1:A:290:ARG:N	1:A:290:ARG:HD2	2.25	0.45
1:C:178:GLN:O	1:C:182:GLU:HG2	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:315:ALA:O	1:B:319:GLN:HB3	2.16	0.45
1:F:14:ARG:NH1	1:F:262:GLU:CG	2.77	0.45
1:A:282:VAL:HG23	1:A:283:CYS:H	1.81	0.45
1:B:138:ASP:OD2	1:B:140:LEU:HB2	2.17	0.45
1:F:206:LYS:HE3	1:F:207:GLU:CG	2.46	0.45
1:F:255:ILE:HD11	1:F:268:PRO:CA	2.47	0.45
1:A:196:PHE:CE1	1:A:245:VAL:HG13	2.52	0.44
1:B:180:LEU:HD12	1:B:180:LEU:HA	1.87	0.44
1:D:180:LEU:HA	1:D:180:LEU:HD12	1.84	0.44
1:F:14:ARG:HH11	1:F:262:GLU:CG	2.24	0.44
1:F:318:ALA:O	1:F:320:LEU:O	2.35	0.44
1:B:225:VAL:HG22	1:B:226:ASN:N	2.33	0.44
1:F:10:LYS:HZ2	1:F:154:GLU:CD	2.20	0.44
1:A:209:LYS:CG	1:A:210:LEU:N	2.78	0.44
1:D:153:LYS:HD3	1:D:183:VAL:HG13	1.98	0.44
1:F:244:GLU:HG2	1:F:281:VAL:HG13	1.98	0.44
1:A:109:VAL:HG22	1:A:115:GLU:OE2	2.17	0.44
1:B:298:LEU:HD12	1:B:298:LEU:C	2.38	0.44
1:D:138:ASP:OD2	1:D:140:LEU:HB2	2.17	0.44
1:D:146:THR:CG2	1:D:150:LYS:HE3	2.47	0.44
1:E:267:GLU:CG	1:E:305:GLY:HA3	2.43	0.44
1:D:153:LYS:HA	1:D:185:TRP:CH2	2.52	0.44
1:D:11:THR:OG1	1:D:30:LYS:HE3	2.17	0.44
1:C:64:SER:HB3	1:D:111:GLU:OE1	2.17	0.44
1:A:244:GLU:HG2	1:A:281:VAL:HG13	1.98	0.44
1:C:14:ARG:NH1	1:C:262:GLU:CG	2.74	0.44
1:D:167:VAL:HG22	1:D:192:ALA:HB1	2.00	0.44
1:D:204:ALA:O	1:D:210:LEU:HA	2.18	0.44
1:E:163:ILE:HD11	1:E:301:ILE:HG13	1.99	0.44
1:F:166:SER:HB2	1:F:273:ALA:HB2	1.99	0.44
1:A:11:THR:OG1	1:A:30:LYS:HE3	2.18	0.44
1:C:298:LEU:C	1:C:298:LEU:HD12	2.38	0.44
1:E:163:ILE:O	1:E:163:ILE:HG23	2.18	0.44
1:E:298:LEU:HD12	1:E:298:LEU:C	2.38	0.44
1:F:225:VAL:HG13	1:F:227:THR:HG23	2.00	0.44
1:A:138:ASP:OD2	1:A:140:LEU:HB2	2.18	0.43
1:D:14:ARG:HH11	1:D:262:GLU:CG	2.24	0.43
1:D:161:GLY:CA	1:D:296:ALA:HB3	2.47	0.43
1:D:225:VAL:HG22	1:D:226:ASN:N	2.33	0.43
1:D:286:GLN:HE21	1:D:295:LEU:HB2	1.82	0.43
1:E:143:GLU:O	1:E:146:THR:HB	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:315:ALA:O	1:E:319:GLN:HB3	2.18	0.43
1:E:50:LYS:HG3	1:E:54:LYS:HZ1	1.83	0.43
1:F:209:LYS:CG	1:F:210:LEU:N	2.68	0.43
1:B:309:SER:OG	1:B:312:GLN:HG3	2.18	0.43
1:C:148:LEU:C	1:C:148:LEU:HD23	2.39	0.43
1:E:127:ASN:HA	1:E:128:PRO:HD3	1.91	0.43
1:E:166:SER:HB2	1:E:273:ALA:HB2	1.99	0.43
1:E:178:GLN:O	1:E:182:GLU:HG2	2.18	0.43
1:C:139:PRO:HA	1:C:142:TRP:CD2	2.53	0.43
1:A:225:VAL:HG22	1:A:226:ASN:N	2.34	0.43
1:C:13:LEU:HD21	1:C:156:LEU:HD21	2.00	0.43
1:D:216:ILE:O	1:D:219:VAL:HG13	2.17	0.43
1:E:148:LEU:C	1:E:148:LEU:HD23	2.38	0.43
1:E:161:GLY:CA	1:E:296:ALA:HB3	2.48	0.43
1:F:248:ASP:C	1:F:320:LEU:HD21	2.38	0.43
1:C:48:LEU:HD12	1:C:133:ILE:HD12	2.00	0.43
1:D:209:LYS:HG3	1:D:210:LEU:HG	2.00	0.43
1:F:148:LEU:HD23	1:F:148:LEU:C	2.39	0.43
1:B:283:CYS:O	1:B:287:ALA:N	2.45	0.43
1:E:99:LEU:HD12	1:E:99:LEU:HA	1.89	0.43
1:B:210:LEU:O	1:B:210:LEU:HD12	2.19	0.43
1:B:267:GLU:HG3	1:B:305:GLY:CA	2.41	0.43
1:D:231:GLN:HE21	1:D:231:GLN:HA	1.83	0.43
1:D:269:ALA:O	1:D:272:ALA:HB3	2.18	0.43
1:C:282:VAL:HG23	1:C:283:CYS:H	1.83	0.43
1:A:204:ALA:O	1:A:210:LEU:HA	2.19	0.43
1:B:76:ALA:CB	1:B:83:ALA:HB2	2.48	0.43
1:E:109:VAL:HG22	1:E:115:GLU:OE2	2.19	0.43
1:A:132:TYR:CE1	1:A:134:SER:HB2	2.54	0.43
1:F:153:LYS:HA	1:F:185:TRP:CH2	2.54	0.43
1:A:210:LEU:C	1:A:210:LEU:CD1	2.87	0.42
1:D:114:ASP:O	1:D:118:GLN:HG3	2.19	0.42
1:D:267:GLU:CG	1:D:305:GLY:HA3	2.43	0.42
1:E:153:LYS:HD3	1:E:183:VAL:HG13	2.01	0.42
1:E:214:PRO:O	1:E:215:LYS:C	2.56	0.42
1:E:90:THR:O	1:F:92:PRO:HD3	2.19	0.42
1:B:255:ILE:HD11	1:B:268:PRO:N	2.34	0.42
1:C:58:LYS:HZ2	1:C:58:LYS:HB3	1.83	0.42
1:F:244:GLU:HG2	1:F:281:VAL:HG11	2.01	0.42
1:A:318:ALA:O	1:A:319:GLN:C	2.57	0.42
1:A:318:ALA:O	1:A:320:LEU:O	2.37	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:166:SER:HB2	1:C:273:ALA:HB2	2.01	0.42
1:E:167:VAL:HG22	1:E:192:ALA:HB1	2.01	0.42
1:F:196:PHE:CE1	1:F:245:VAL:HG13	2.54	0.42
1:F:255:ILE:HD11	1:F:268:PRO:N	2.33	0.42
1:C:318:ALA:O	1:C:319:GLN:C	2.57	0.42
1:E:135:PRO:HA	1:E:141:ILE:HD12	2.01	0.42
1:E:58:LYS:HZ2	1:E:58:LYS:HB3	1.83	0.42
1:A:246:ILE:HG13	1:A:250:GLU:OE1	2.20	0.42
1:B:252:VAL:HG21	1:B:320:LEU:HD23	2.01	0.42
1:C:244:GLU:HG2	1:C:281:VAL:HG13	2.02	0.42
1:D:298:LEU:O	1:D:298:LEU:HD12	2.20	0.42
1:E:244:GLU:HG2	1:E:281:VAL:HG13	2.01	0.42
1:C:163:ILE:HG23	1:C:163:ILE:O	2.19	0.42
1:F:163:ILE:HD11	1:F:301:ILE:HG13	2.01	0.42
1:A:153:LYS:HA	1:A:185:TRP:CH2	2.55	0.42
1:B:277:VAL:HG22	1:B:278:TYR:N	2.34	0.42
1:D:10:LYS:HZ2	1:D:154:GLU:CD	2.23	0.42
1:D:244:GLU:HG2	1:D:281:VAL:HG13	2.01	0.42
1:E:255:ILE:HD11	1:E:268:PRO:HA	2.01	0.42
1:F:310:LEU:HD12	1:F:310:LEU:HA	1.79	0.42
1:B:204:ALA:O	1:B:210:LEU:HA	2.20	0.42
1:B:318:ALA:O	1:B:320:LEU:O	2.37	0.42
1:F:74:TYR:O	1:F:78:ARG:HG2	2.20	0.41
1:B:244:GLU:HG2	1:B:281:VAL:HG13	2.00	0.41
1:B:318:ALA:O	1:B:319:GLN:C	2.58	0.41
1:B:28:PHE:HB2	1:B:299:VAL:HG22	2.02	0.41
1:C:76:ALA:CB	1:C:83:ALA:HB2	2.50	0.41
1:D:76:ALA:CB	1:D:83:ALA:HB2	2.50	0.41
1:E:204:ALA:O	1:E:210:LEU:HA	2.19	0.41
1:B:50:LYS:HG3	1:B:54:LYS:HZ1	1.85	0.41
1:C:210:LEU:C	1:C:210:LEU:CD1	2.89	0.41
1:A:163:ILE:HD11	1:A:301:ILE:HG13	2.03	0.41
1:B:231:GLN:HA	1:B:231:GLN:HE21	1.85	0.41
1:D:50:LYS:HG3	1:D:54:LYS:HZ1	1.85	0.41
1:E:48:LEU:HD12	1:E:133:ILE:HD12	2.03	0.41
1:D:14:ARG:NH1	1:D:262:GLU:CG	2.77	0.41
1:B:109:VAL:HG22	1:B:115:GLU:OE2	2.20	0.41
1:E:210:LEU:C	1:E:210:LEU:CD1	2.89	0.41
1:E:283:CYS:O	1:E:287:ALA:N	2.42	0.41
1:B:11:THR:OG1	1:B:30:LYS:HE3	2.21	0.41
1:D:225:VAL:HG13	1:D:227:THR:HG23	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:282:VAL:HG23	1:D:283:CYS:H	1.86	0.41
1:F:210:LEU:CD1	1:F:210:LEU:C	2.89	0.41
1:B:286:GLN:HE21	1:B:295:LEU:HB2	1.86	0.41
1:C:135:PRO:HA	1:C:141:ILE:HD12	2.03	0.41
1:E:48:LEU:HD13	1:E:48:LEU:C	2.42	0.41
1:F:6:SER:N	2:F:330:HOH:O	2.53	0.41
1:A:50:LYS:HG3	1:A:54:LYS:HZ1	1.86	0.41
1:B:48:LEU:HD12	1:B:133:ILE:HD12	2.02	0.41
1:A:111:GLU:OE1	1:B:64:SER:HB3	2.21	0.41
1:E:246:ILE:HA	1:E:246:ILE:HD12	1.97	0.41
1:A:90:THR:O	1:B:92:PRO:HD3	2.21	0.40
1:C:235:LEU:HD12	1:C:235:LEU:HA	1.87	0.40
1:C:255:ILE:HD11	1:C:268:PRO:N	2.36	0.40
1:C:310:LEU:HA	1:C:310:LEU:HD12	1.89	0.40
1:D:277:VAL:HG22	1:D:278:TYR:N	2.36	0.40
1:A:298:LEU:HD12	1:A:298:LEU:C	2.41	0.40
1:B:214:PRO:O	1:B:215:LYS:C	2.59	0.40
1:C:99:LEU:HA	1:C:99:LEU:HD12	1.82	0.40
1:D:217:THR:HG22	1:D:229:GLY:O	2.22	0.40
1:D:42:ILE:HG13	1:D:42:ILE:O	2.20	0.40
1:E:180:LEU:HA	1:E:180:LEU:HD12	1.83	0.40
1:E:225:VAL:HG22	1:E:226:ASN:N	2.36	0.40
1:B:153:LYS:HA	1:B:185:TRP:CH2	2.56	0.40
1:A:235:LEU:HD12	1:A:235:LEU:HA	1.89	0.40
1:B:193:MET:SD	1:B:244:GLU:HB3	2.62	0.40
1:D:139:PRO:HA	1:D:142:TRP:CD2	2.56	0.40
1:D:196:PHE:CE1	1:D:245:VAL:HG13	2.57	0.40
1:D:255:ILE:HD11	1:D:268:PRO:N	2.37	0.40
1:E:239:HIS:ND1	1:E:240:PRO:HD2	2.36	0.40
1:F:269:ALA:O	1:F:272:ALA:HB3	2.21	0.40
1:F:282:VAL:HG23	1:F:283:CYS:H	1.86	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	313/327 (96%)	289 (92%)	19 (6%)	5 (2%)	9	31
1	B	313/327 (96%)	287 (92%)	21 (7%)	5 (2%)	9	31
1	C	313/327 (96%)	288 (92%)	20 (6%)	5 (2%)	9	31
1	D	313/327 (96%)	288 (92%)	21 (7%)	4 (1%)	12	36
1	E	313/327 (96%)	290 (93%)	18 (6%)	5 (2%)	9	31
1	F	313/327 (96%)	289 (92%)	19 (6%)	5 (2%)	9	31
All	All	1878/1962 (96%)	1731 (92%)	118 (6%)	29 (2%)	10	33

All (29) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	290	ARG
1	A	296	ALA
1	B	290	ARG
1	B	296	ALA
1	C	290	ARG
1	C	296	ALA
1	D	290	ARG
1	D	296	ALA
1	E	290	ARG
1	E	296	ALA
1	F	290	ARG
1	F	296	ALA
1	A	211	VAL
1	B	211	VAL
1	C	211	VAL
1	D	211	VAL
1	E	211	VAL
1	F	211	VAL
1	A	209	LYS
1	C	209	LYS
1	E	209	LYS
1	B	209	LYS
1	D	209	LYS
1	F	209	LYS
1	A	109	VAL
1	C	109	VAL
1	F	109	VAL

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Mol	Chain	Res	Type
1	E	109	VAL
1	B	109	VAL

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	250/259 (96%)	223 (89%)	27 (11%)	6 19
1	B	250/259 (96%)	223 (89%)	27 (11%)	6 19
1	C	250/259 (96%)	225 (90%)	25 (10%)	7 22
1	D	250/259 (96%)	224 (90%)	26 (10%)	7 21
1	E	250/259 (96%)	223 (89%)	27 (11%)	6 19
1	F	250/259 (96%)	227 (91%)	23 (9%)	9 27
All	All	1500/1554 (96%)	1345 (90%)	155 (10%)	7 21

All (155) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	17	MET
1	A	25	THR
1	A	32	ASP
1	A	37	SER
1	A	54	LYS
1	A	58	LYS
1	A	94	LEU
1	A	99	LEU
1	A	109	VAL
1	A	113	LEU
1	A	126	ASN
1	A	140	LEU
1	A	142	TRP
1	A	146	THR
1	A	163	ILE
1	A	180	LEU

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Mol	Chain	Res	Type
1	A	183	VAL
1	A	210	LEU
1	A	216	ILE
1	A	219	VAL
1	A	235	LEU
1	A	249	GLN
1	A	262	GLU
1	A	277	VAL
1	A	310	LEU
1	A	313	LEU
1	A	314	GLN
1	B	17	MET
1	B	25	THR
1	B	32	ASP
1	B	37	SER
1	B	54	LYS
1	B	58	LYS
1	B	94	LEU
1	B	99	LEU
1	B	109	VAL
1	B	113	LEU
1	B	126	ASN
1	B	140	LEU
1	B	142	TRP
1	B	146	THR
1	B	163	ILE
1	B	180	LEU
1	B	183	VAL
1	B	210	LEU
1	B	216	ILE
1	B	219	VAL
1	B	235	LEU
1	B	249	GLN
1	B	262	GLU
1	B	277	VAL
1	B	310	LEU
1	B	313	LEU
1	B	314	GLN
1	C	17	MET
1	C	25	THR
1	C	37	SER
1	C	54	LYS

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Mol	Chain	Res	Type
1	C	58	LYS
1	C	94	LEU
1	C	99	LEU
1	C	109	VAL
1	C	113	LEU
1	C	126	ASN
1	C	142	TRP
1	C	146	THR
1	C	163	ILE
1	C	180	LEU
1	C	183	VAL
1	C	210	LEU
1	C	216	ILE
1	C	219	VAL
1	C	235	LEU
1	C	249	GLN
1	C	262	GLU
1	C	277	VAL
1	C	310	LEU
1	C	313	LEU
1	C	314	GLN
1	D	17	MET
1	D	25	THR
1	D	32	ASP
1	D	37	SER
1	D	54	LYS
1	D	58	LYS
1	D	94	LEU
1	D	99	LEU
1	D	109	VAL
1	D	113	LEU
1	D	126	ASN
1	D	142	TRP
1	D	146	THR
1	D	163	ILE
1	D	180	LEU
1	D	183	VAL
1	D	210	LEU
1	D	216	ILE
1	D	219	VAL
1	D	235	LEU
1	D	249	GLN

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Mol	Chain	Res	Type
1	D	262	GLU
1	D	277	VAL
1	D	310	LEU
1	D	313	LEU
1	D	314	GLN
1	E	17	MET
1	E	25	THR
1	E	32	ASP
1	E	37	SER
1	E	54	LYS
1	E	58	LYS
1	E	94	LEU
1	E	99	LEU
1	E	109	VAL
1	E	113	LEU
1	E	126	ASN
1	E	140	LEU
1	E	142	TRP
1	E	146	THR
1	E	163	ILE
1	E	180	LEU
1	E	183	VAL
1	E	210	LEU
1	E	216	ILE
1	E	219	VAL
1	E	235	LEU
1	E	249	GLN
1	E	262	GLU
1	E	277	VAL
1	E	310	LEU
1	E	313	LEU
1	E	314	GLN
1	F	17	MET
1	F	25	THR
1	F	37	SER
1	F	54	LYS
1	F	58	LYS
1	F	94	LEU
1	F	99	LEU
1	F	109	VAL
1	F	113	LEU
1	F	126	ASN

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Mol	Chain	Res	Type
1	F	146	THR
1	F	163	ILE
1	F	180	LEU
1	F	183	VAL
1	F	210	LEU
1	F	216	ILE
1	F	219	VAL
1	F	235	LEU
1	F	249	GLN
1	F	262	GLU
1	F	310	LEU
1	F	313	LEU
1	F	314	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (31) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	55	GLN
1	A	199	HIS
1	A	231	GLN
1	A	249	GLN
1	A	286	GLN
1	B	55	GLN
1	B	199	HIS
1	B	231	GLN
1	B	249	GLN
1	B	286	GLN
1	C	55	GLN
1	C	199	HIS
1	C	231	GLN
1	C	249	GLN
1	C	286	GLN
1	D	55	GLN
1	D	199	HIS
1	D	231	GLN
1	D	249	GLN
1	D	286	GLN
1	E	55	GLN
1	E	199	HIS
1	E	231	GLN
1	E	249	GLN
1	E	286	GLN

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Mol	Chain	Res	Type
1	F	8	HIS
1	F	55	GLN
1	F	199	HIS
1	F	231	GLN
1	F	249	GLN
1	F	286	GLN

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 [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

6.1 Protein, DNA and RNA chains

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.