



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 10, 2026 – 01:27 AM UTC

PDB ID : 2O18 / pdb_00002o18
Title : Crystal structure of a Thiamine biosynthesis lipoprotein apbE, NorthEast Structural Genomics target ER559
Authors : Seetharaman, J.; Su, M.; Wang, D.; Fang, Y.; Cunningham, K.; Ma, L.; Xiao, R.; Liu, J.; Baran, M.C.; Acton, T.B.; Rost, B.; Montelione, G.T.; Hunt, J.F.; Tong, L.; Northeast Structural Genomics Consortium (NESG)
Deposited on : 2006-11-28
Resolution : 2.20 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 types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

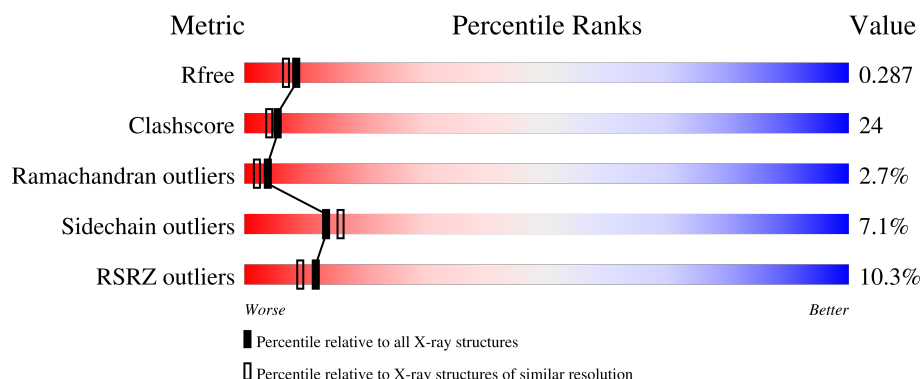
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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}	180053	6164 (2.20-2.20)
Clashscore	190562	6851 (2.20-2.20)
Ramachandran outliers	187476	6768 (2.20-2.20)
Sidechain outliers	187428	6769 (2.20-2.20)
RSRZ outliers	180081	6166 (2.20-2.20)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. 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	340	
1	B	340	
1	C	340	
1	D	340	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 9555 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 Thiamine biosynthesis lipoprotein apbE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	307	Total	C	N	O	Se	0	0	0
			2351	1476	406	459	10			
1	B	300	Total	C	N	O	Se	0	0	0
			2307	1449	396	452	10			
1	C	313	Total	C	N	O	Se	0	0	0
			2374	1491	410	463	10			
1	D	306	Total	C	N	O	Se	0	0	0
			2316	1457	398	451	10			

There are 76 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MSE	-	initiating methionine	UNP P0AB85
A	23	MSE	MET	modified residue	UNP P0AB85
A	67	MSE	MET	modified residue	UNP P0AB85
A	84	MSE	MET	modified residue	UNP P0AB85
A	102	MSE	MET	modified residue	UNP P0AB85
A	133	MSE	MET	modified residue	UNP P0AB85
A	180	MSE	MET	modified residue	UNP P0AB85
A	201	MSE	MET	modified residue	UNP P0AB85
A	287	MSE	MET	modified residue	UNP P0AB85
A	307	MSE	MET	modified residue	UNP P0AB85
A	319	MSE	MET	modified residue	UNP P0AB85
A	333	LEU	-	cloning artifact	UNP P0AB85
A	334	GLU	-	cloning artifact	UNP P0AB85
A	335	HIS	-	expression tag	UNP P0AB85
A	336	HIS	-	expression tag	UNP P0AB85
A	337	HIS	-	expression tag	UNP P0AB85
A	338	HIS	-	expression tag	UNP P0AB85
A	339	HIS	-	expression tag	UNP P0AB85
A	340	HIS	-	expression tag	UNP P0AB85
B	1	MSE	-	initiating methionine	UNP P0AB85
B	23	MSE	MET	modified residue	UNP P0AB85

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Chain	Residue	Modelled	Actual	Comment	Reference
B	67	MSE	MET	modified residue	UNP P0AB85
B	84	MSE	MET	modified residue	UNP P0AB85
B	102	MSE	MET	modified residue	UNP P0AB85
B	133	MSE	MET	modified residue	UNP P0AB85
B	180	MSE	MET	modified residue	UNP P0AB85
B	201	MSE	MET	modified residue	UNP P0AB85
B	287	MSE	MET	modified residue	UNP P0AB85
B	307	MSE	MET	modified residue	UNP P0AB85
B	319	MSE	MET	modified residue	UNP P0AB85
B	333	LEU	-	cloning artifact	UNP P0AB85
B	334	GLU	-	cloning artifact	UNP P0AB85
B	335	HIS	-	expression tag	UNP P0AB85
B	336	HIS	-	expression tag	UNP P0AB85
B	337	HIS	-	expression tag	UNP P0AB85
B	338	HIS	-	expression tag	UNP P0AB85
B	339	HIS	-	expression tag	UNP P0AB85
B	340	HIS	-	expression tag	UNP P0AB85
C	1	MSE	-	initiating methionine	UNP P0AB85
C	23	MSE	MET	modified residue	UNP P0AB85
C	67	MSE	MET	modified residue	UNP P0AB85
C	84	MSE	MET	modified residue	UNP P0AB85
C	102	MSE	MET	modified residue	UNP P0AB85
C	133	MSE	MET	modified residue	UNP P0AB85
C	180	MSE	MET	modified residue	UNP P0AB85
C	201	MSE	MET	modified residue	UNP P0AB85
C	287	MSE	MET	modified residue	UNP P0AB85
C	307	MSE	MET	modified residue	UNP P0AB85
C	319	MSE	MET	modified residue	UNP P0AB85
C	333	LEU	-	cloning artifact	UNP P0AB85
C	334	GLU	-	cloning artifact	UNP P0AB85
C	335	HIS	-	expression tag	UNP P0AB85
C	336	HIS	-	expression tag	UNP P0AB85
C	337	HIS	-	expression tag	UNP P0AB85
C	338	HIS	-	expression tag	UNP P0AB85
C	339	HIS	-	expression tag	UNP P0AB85
C	340	HIS	-	expression tag	UNP P0AB85
D	1	MSE	-	initiating methionine	UNP P0AB85
D	23	MSE	MET	modified residue	UNP P0AB85
D	67	MSE	MET	modified residue	UNP P0AB85
D	84	MSE	MET	modified residue	UNP P0AB85
D	102	MSE	MET	modified residue	UNP P0AB85
D	133	MSE	MET	modified residue	UNP P0AB85

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Chain	Residue	Modelled	Actual	Comment	Reference
D	180	MSE	MET	modified residue	UNP P0AB85
D	201	MSE	MET	modified residue	UNP P0AB85
D	287	MSE	MET	modified residue	UNP P0AB85
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D	333	LEU	-	cloning artifact	UNP P0AB85
D	334	GLU	-	cloning artifact	UNP P0AB85
D	335	HIS	-	expression tag	UNP P0AB85
D	336	HIS	-	expression tag	UNP P0AB85
D	337	HIS	-	expression tag	UNP P0AB85
D	338	HIS	-	expression tag	UNP P0AB85
D	339	HIS	-	expression tag	UNP P0AB85
D	340	HIS	-	expression tag	UNP P0AB85

- Molecule 2 is CALCIUM ION (CCD ID: CA) (formula: Ca).

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

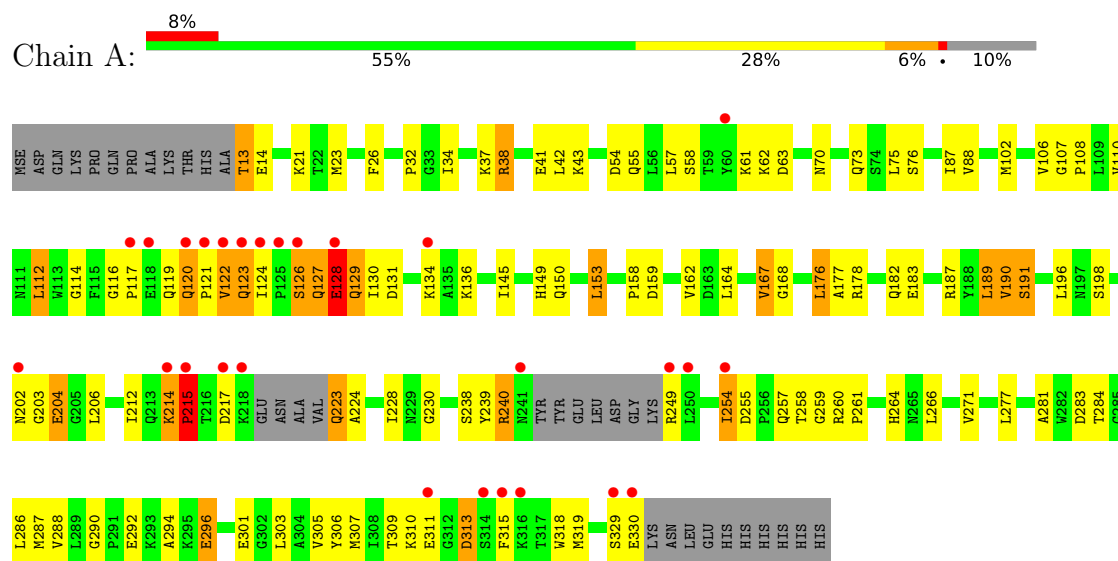
- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	52	Total 52 O 52	0	0
3	B	47	Total 47 O 47	0	0
3	C	48	Total 48 O 48	0	0
3	D	56	Total 56 O 56	0	0

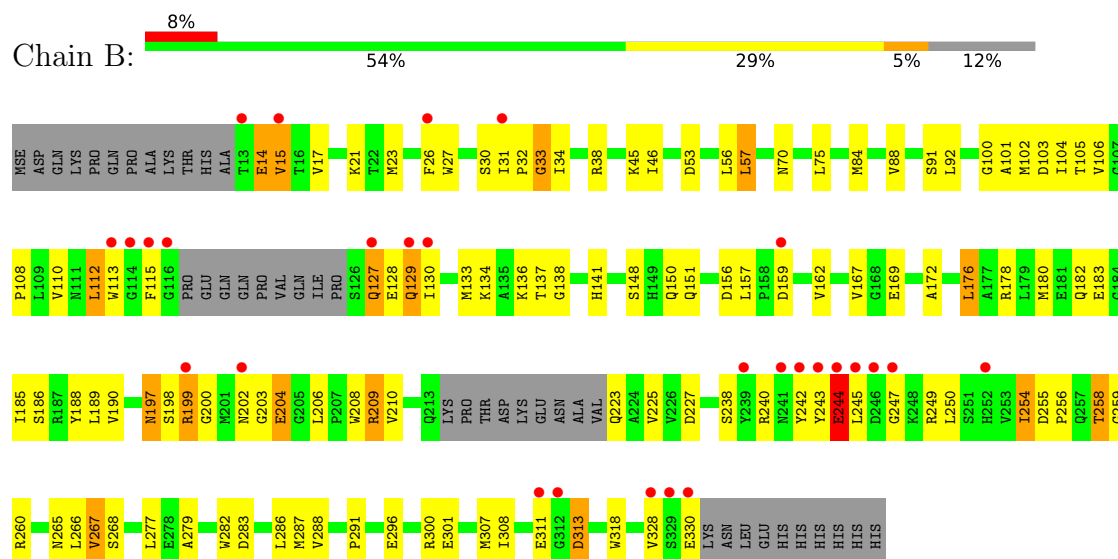
3 Residue-property plots

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

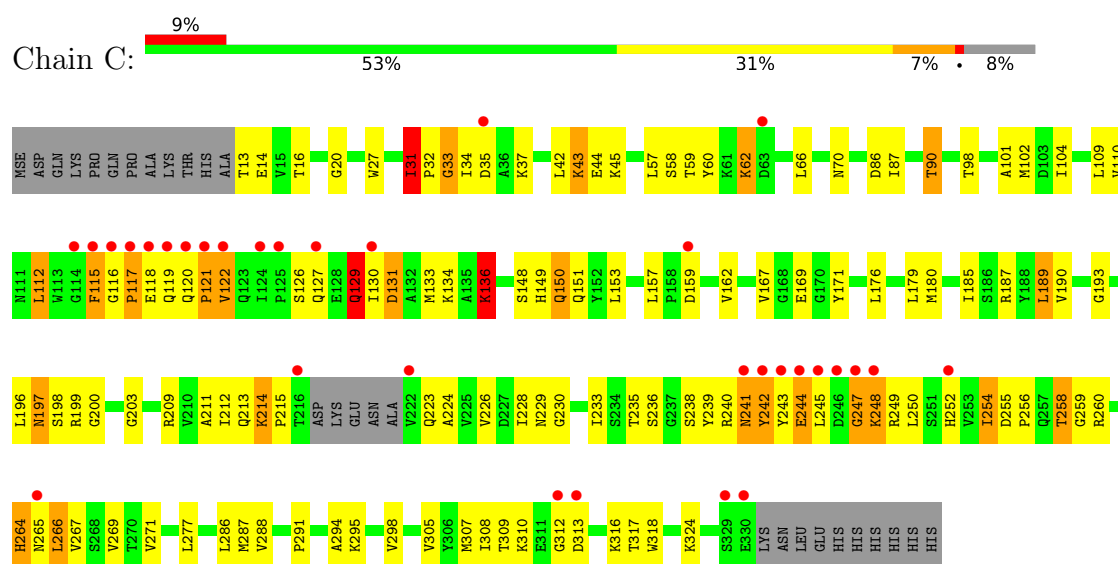
- Molecule 1: Thiamine biosynthesis lipoprotein apbE



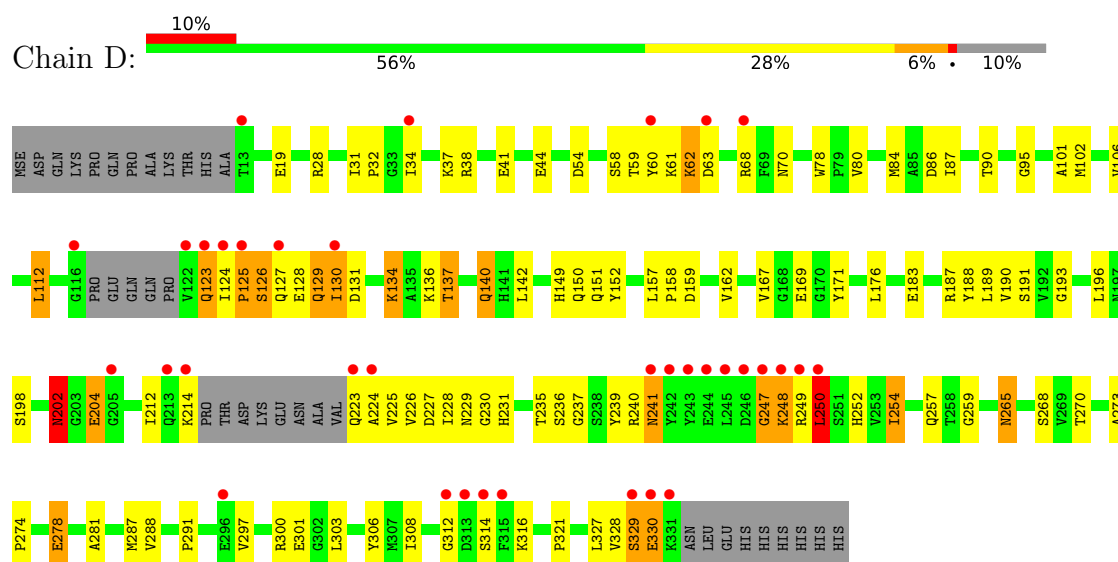
- Molecule 1: Thiamine biosynthesis lipoprotein apbE



- Molecule 1: Thiamine biosynthesis lipoprotein apbE



• Molecule 1: Thiamine biosynthesis lipoprotein apbE



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	57.32Å 70.65Å 86.64Å 75.76° 71.67° 69.46°	Depositor
Resolution (Å)	49.74 – 2.20 49.74 – 2.20	Depositor EDS
% Data completeness (in resolution range)	78.0 (49.74-2.20) 91.1 (49.74-2.20)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	0.04	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.86 (at 2.20Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.233 , 0.284 0.237 , 0.287	Depositor DCC
R_{free} test set	4629 reflections (4.05%)	wwPDB-VP
Wilson B-factor (Å ²)	20.9	Xtriage
Anisotropy	0.358	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 40.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	9555	wwPDB-VP
Average B, all atoms (Å ²)	25.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.59% 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

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	0.45	0/2383	0.97	10/3215 (0.3%)
1	B	0.41	0/2338	0.95	9/3149 (0.3%)
1	C	0.45	0/2407	0.98	10/3250 (0.3%)
1	D	0.45	0/2346	0.93	8/3165 (0.3%)
All	All	0.44	0/9474	0.96	37/12779 (0.3%)

There are no bond length outliers.

All (37) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	243	TYR	N-CA-C	10.84	125.89	109.41
1	C	129	GLN	N-CA-C	-8.29	103.17	113.28
1	A	204	GLU	N-CA-C	-8.03	98.63	110.52
1	C	203	GLY	N-CA-C	-7.76	105.03	114.66
1	D	123	GLN	N-CA-C	7.16	117.32	107.73
1	B	203	GLY	N-CA-C	-6.83	104.29	113.24
1	B	57	LEU	N-CA-C	6.73	122.31	113.30
1	B	204	GLU	N-CA-C	-6.62	100.15	110.42
1	D	129	GLN	N-CA-C	-6.60	104.71	112.89
1	C	59	THR	N-CA-C	-6.49	105.36	113.28
1	C	121	PRO	N-CA-CB	6.45	110.03	103.25
1	B	313	ASP	N-CA-C	-6.43	104.69	113.30
1	A	129	GLN	N-CA-C	-6.33	104.82	112.54
1	C	136	LYS	N-CA-C	-6.14	105.43	113.17
1	A	215	PRO	N-CA-CB	6.02	109.57	103.25
1	C	266	LEU	N-CA-C	6.01	117.80	109.15
1	A	57	LEU	N-CA-C	5.93	121.56	113.97
1	B	188	TYR	N-CA-C	5.86	116.14	107.88
1	D	95	GLY	N-CA-C	-5.75	105.53	112.49
1	A	189	LEU	N-CA-C	-5.69	97.89	108.02

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	204	GLU	N-CA-C	-5.59	103.32	110.53
1	A	75	LEU	N-CA-C	-5.52	106.45	114.12
1	C	58	SER	N-CA-C	5.48	118.42	110.42
1	A	313	ASP	N-CA-C	-5.43	105.31	113.89
1	D	259	GLY	N-CA-C	-5.39	108.18	115.36
1	C	264	HIS	N-CA-C	5.37	117.77	110.35
1	D	188	TYR	N-CA-C	5.32	117.16	108.76
1	A	153	LEU	N-CA-C	-5.22	100.89	109.40
1	B	247	GLY	N-CA-C	-5.22	108.49	115.32
1	A	296	GLU	N-CA-C	-5.21	105.68	111.36
1	C	130	ILE	N-CA-C	-5.15	104.66	111.09
1	D	250	LEU	N-CA-C	5.15	121.76	110.80
1	B	244	GLU	N-CA-C	5.13	121.74	110.80
1	D	247	GLY	N-CA-C	-5.13	106.99	114.90
1	A	58	SER	N-CA-C	5.13	117.47	110.24
1	C	31	ILE	N-CA-CB	-5.10	108.31	111.83
1	B	148	SER	N-CA-C	5.03	117.15	111.11

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of 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	2351	0	2321	112	0
1	B	2307	0	2275	115	0
1	C	2374	0	2333	132	0
1	D	2316	0	2277	93	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	52	0	0	7	0
3	B	47	0	0	9	0
3	C	48	0	0	5	0
3	D	56	0	0	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	9555	0	9206	442	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 24.

All (442) 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:120:GLN:HB2	1:A:121:PRO:C	1.95	0.90
1:A:202:ASN:HB3	3:A:343:HOH:O	1.71	0.89
1:B:189:LEU:HD12	1:B:208:TRP:HB3	1.53	0.89
1:B:46:ILE:HG23	1:B:176:LEU:HD21	1.56	0.86
1:A:112:LEU:HD22	1:A:126:SER:HB3	1.56	0.86
1:D:19:GLU:HG2	1:D:28:ARG:HG3	1.57	0.85
1:D:140:GLN:H	1:D:140:GLN:NE2	1.74	0.85
1:D:62:LYS:HZ3	1:D:62:LYS:HB2	1.43	0.83
1:A:239:TYR:O	1:A:240:ARG:HB3	1.74	0.83
1:C:133:MSE:HE3	1:C:133:MSE:HA	1.59	0.83
1:C:199:ARG:HA	1:C:229:ASN:HD22	1.41	0.83
1:C:13:THR:HG23	1:C:14:GLU:H	1.45	0.82
1:C:70:ASN:HD21	1:C:162:VAL:H	1.25	0.82
1:A:136:LYS:HD3	1:A:159:ASP:HB3	1.61	0.80
1:A:177:ALA:HA	3:A:372:HOH:O	1.82	0.79
1:D:140:GLN:H	1:D:140:GLN:HE21	1.27	0.79
1:A:212:ILE:HD11	1:A:224:ALA:HB3	1.63	0.79
1:A:176:LEU:HD23	1:A:190:VAL:HG22	1.63	0.78
1:A:114:GLY:O	1:A:121:PRO:HB3	1.84	0.78
1:A:191:SER:HB2	1:A:196:LEU:HG	1.65	0.77
1:B:169:GLU:HG3	3:B:346:HOH:O	1.85	0.77
1:C:45:LYS:HA	1:C:45:LYS:HE2	1.67	0.76
1:B:245:LEU:HD11	1:B:250:LEU:HD21	1.68	0.76
1:D:212:ILE:HD11	1:D:224:ALA:HB3	1.68	0.75
1:A:120:GLN:HB2	1:A:121:PRO:CA	2.16	0.75
1:A:123:GLN:O	1:A:124:ILE:HG13	1.86	0.75
1:B:254:ILE:C	1:B:254:ILE:HD13	2.10	0.75
1:B:127:GLN:C	1:B:129:GLN:H	1.96	0.73
1:C:136:LYS:HZ2	1:C:159:ASP:HB2	1.52	0.73
1:B:199:ARG:HD2	1:B:200:GLY:N	2.04	0.72
1:A:130:ILE:HD13	1:A:259:GLY:HA3	1.70	0.72
1:D:198:SER:HB3	1:D:228:ILE:HG13	1.72	0.72
1:B:34:ILE:HD11	1:B:38:ARG:HG2	1.71	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:258:THR:HG22	1:B:260:ARG:H	1.55	0.71
1:B:225:VAL:HG13	1:B:328:VAL:HG23	1.71	0.70
1:C:102:MSE:HE2	1:C:104:ILE:HG23	1.72	0.70
1:C:241:ASN:ND2	1:C:242:TYR:H	1.88	0.70
1:D:212:ILE:HG12	1:D:224:ALA:O	1.90	0.70
1:B:197:ASN:HD22	1:B:198:SER:N	1.90	0.70
1:C:62:LYS:H	1:C:62:LYS:HD2	1.55	0.69
1:B:136:LYS:HA	1:B:157:LEU:HD21	1.75	0.69
1:B:176:LEU:HB3	1:B:190:VAL:HG21	1.75	0.69
1:C:238:SER:C	1:C:240:ARG:H	2.01	0.69
1:D:265:ASN:ND2	1:D:265:ASN:H	1.91	0.68
1:C:112:LEU:HD12	1:C:126:SER:HB3	1.75	0.68
1:C:243:TYR:CB	1:C:250:LEU:H	2.06	0.68
1:D:86:ASP:O	1:D:90:THR:HG23	1.92	0.68
1:A:271:VAL:HG22	1:A:305:VAL:HG22	1.76	0.68
1:B:14:GLU:HB2	1:B:33:GLY:HA3	1.75	0.68
1:B:136:LYS:HD3	1:B:159:ASP:HB3	1.74	0.68
1:D:134:LYS:O	1:D:137:THR:HG22	1.93	0.68
1:B:209:ARG:O	1:B:209:ARG:HG3	1.93	0.68
1:A:306:TYR:HE2	1:A:319:MSE:HE2	1.60	0.67
1:A:230:GLY:HA3	1:C:229:ASN:HD21	1.59	0.67
1:B:199:ARG:NH1	1:B:200:GLY:HA2	2.09	0.67
1:B:199:ARG:NE	1:D:231:HIS:CE1	2.63	0.67
1:C:241:ASN:HD22	1:C:242:TYR:H	1.43	0.66
1:C:176:LEU:HD23	1:C:190:VAL:HG13	1.77	0.66
1:C:255:ASP:HB3	1:C:258:THR:HG22	1.78	0.66
1:D:191:SER:HB3	1:D:196:LEU:HG	1.78	0.66
1:C:266:LEU:HB2	1:C:291:PRO:HD3	1.78	0.66
1:C:209:ARG:HH12	1:C:211:ALA:HB2	1.61	0.65
1:A:127:GLN:C	1:A:129:GLN:H	2.03	0.65
1:B:197:ASN:HD22	1:B:197:ASN:C	2.04	0.65
1:B:199:ARG:NH1	1:D:229:ASN:O	2.30	0.64
1:A:202:ASN:OD1	1:A:203:GLY:N	2.21	0.64
1:C:324:LYS:HD2	3:C:372:HOH:O	1.96	0.64
1:B:15:VAL:HG13	3:B:368:HOH:O	1.96	0.64
1:C:258:THR:CG2	1:C:260:ARG:H	2.10	0.64
1:C:136:LYS:NZ	1:C:159:ASP:HB2	2.11	0.64
1:C:214:LYS:HG2	1:C:223:GLN:HB3	1.80	0.64
1:D:202:ASN:C	1:D:202:ASN:HD22	2.06	0.64
1:C:265:ASN:OD1	1:C:309:THR:HB	1.98	0.63
1:A:37:LYS:O	1:A:41:GLU:HG3	1.98	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:266:LEU:HD23	1:C:287:MSE:HA	1.81	0.63
1:A:254:ILE:HD11	1:A:259:GLY:HA2	1.81	0.63
1:D:191:SER:CB	1:D:196:LEU:HG	2.28	0.63
1:B:127:GLN:O	1:B:130:ILE:HG23	1.98	0.62
1:A:134:LYS:HE3	3:A:362:HOH:O	1.98	0.62
1:C:254:ILE:HD13	1:C:254:ILE:C	2.24	0.62
1:D:202:ASN:ND2	1:D:204:GLU:O	2.33	0.62
1:B:178:ARG:NH2	1:D:278:GLU:OE1	2.32	0.62
1:B:127:GLN:C	1:B:129:GLN:N	2.57	0.62
1:C:266:LEU:HD21	1:C:269:VAL:HG21	1.83	0.61
1:A:258:THR:HG22	1:A:260:ARG:HG2	1.82	0.61
1:B:110:VAL:HG22	1:B:254:ILE:CG2	2.31	0.61
1:A:266:LEU:O	1:A:287:MSE:HE1	2.00	0.61
1:B:199:ARG:NE	1:D:231:HIS:HE1	1.99	0.61
1:B:227:ASP:HB2	1:B:328:VAL:HG11	1.83	0.60
1:C:70:ASN:ND2	1:C:162:VAL:H	1.96	0.60
1:D:254:ILE:HD13	1:D:254:ILE:C	2.25	0.60
1:A:128:GLU:HA	1:A:128:GLU:OE1	2.00	0.60
1:A:202:ASN:CG	1:A:203:GLY:H	2.08	0.60
1:A:120:GLN:HB2	1:A:121:PRO:O	2.02	0.60
1:B:186:SER:C	1:B:199:ARG:HH21	2.10	0.60
1:A:306:TYR:CE2	1:A:319:MSE:HE2	2.36	0.60
1:B:70:ASN:HD21	1:B:162:VAL:H	1.49	0.60
3:B:351:HOH:O	1:D:151:GLN:HG3	2.02	0.60
1:A:121:PRO:C	1:A:123:GLN:N	2.59	0.60
1:B:113:TRP:NE1	1:B:259:GLY:O	2.35	0.60
1:C:266:LEU:HD21	1:C:269:VAL:CG2	2.32	0.60
1:D:31:ILE:HG21	1:D:34:ILE:HD11	1.83	0.60
1:C:214:LYS:H	1:C:214:LYS:CE	2.15	0.59
1:D:128:GLU:OE2	1:D:130:ILE:HG23	2.01	0.59
1:D:158:PRO:HD2	3:D:384:HOH:O	2.02	0.59
1:B:23:MSE:HE1	1:B:172:ALA:HB2	1.84	0.59
1:D:150:GLN:HG3	1:D:152:TYR:OH	2.02	0.59
1:D:214:LYS:HE3	1:D:223:GLN:HG3	1.83	0.59
1:A:127:GLN:HG3	1:A:129:GLN:H	1.67	0.59
1:B:238:SER:OG	1:B:240:ARG:HG2	2.02	0.59
1:C:258:THR:HG22	1:C:260:ARG:H	1.67	0.59
1:A:120:GLN:H	1:A:120:GLN:NE2	2.00	0.59
1:D:101:ALA:HB1	1:D:288:VAL:HB	1.84	0.59
1:C:43:LYS:C	1:C:43:LYS:HE2	2.27	0.59
1:C:213:GLN:O	1:C:215:PRO:HD3	2.03	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:241:ASN:HD22	1:C:243:TYR:H	1.51	0.58
1:B:92:LEU:HD23	3:B:369:HOH:O	2.02	0.58
1:B:204:GLU:N	1:B:204:GLU:OE1	2.37	0.58
1:B:279:ALA:O	1:B:283:ASP:HB2	2.03	0.58
1:C:187:ARG:HH11	1:C:187:ARG:HG3	1.69	0.58
1:A:127:GLN:O	1:A:130:ILE:HG23	2.03	0.58
1:C:31:ILE:HG13	1:C:185:ILE:HG21	1.86	0.58
1:B:31:ILE:HD13	1:B:185:ILE:HD13	1.85	0.57
1:C:197:ASN:C	1:C:197:ASN:HD22	2.12	0.57
1:C:269:VAL:HG22	1:C:307:MSE:HG2	1.86	0.57
1:A:258:THR:CG2	1:A:260:ARG:HG2	2.34	0.57
1:B:21:LYS:HE2	1:B:26:PHE:HE1	1.69	0.57
1:B:110:VAL:HG22	1:B:254:ILE:HG21	1.87	0.57
1:B:210:VAL:O	1:B:225:VAL:HG23	2.05	0.57
1:A:120:GLN:H	1:A:120:GLN:CD	2.13	0.57
1:B:199:ARG:HE	1:D:231:HIS:HE1	1.51	0.57
1:B:31:ILE:HD11	1:B:180:MSE:SE	2.54	0.57
1:C:13:THR:HG23	1:C:14:GLU:N	2.16	0.57
1:C:45:LYS:HE3	3:C:359:HOH:O	2.04	0.57
1:C:254:ILE:HG12	1:C:260:ARG:C	2.29	0.57
1:D:270:THR:HB	1:D:306:TYR:HB3	1.86	0.57
1:C:215:PRO:HG3	1:C:308:ILE:HD13	1.87	0.56
1:A:70:ASN:ND2	1:A:162:VAL:H	2.02	0.56
1:D:102:MSE:HG3	1:D:281:ALA:O	2.05	0.56
1:A:254:ILE:HD13	1:A:255:ASP:C	2.30	0.56
1:C:31:ILE:HG13	1:C:32:PRO:HD2	1.87	0.56
1:C:271:VAL:HG22	1:C:305:VAL:HG22	1.87	0.56
1:C:62:LYS:HD2	1:C:62:LYS:N	2.20	0.56
1:C:176:LEU:HD23	1:C:190:VAL:CG1	2.35	0.56
1:C:197:ASN:HD22	1:C:198:SER:N	2.04	0.56
1:C:316:LYS:HB3	3:C:375:HOH:O	2.05	0.56
1:A:54:ASP:OD2	1:A:61:LYS:HE3	2.06	0.56
1:A:23:MSE:HE1	1:A:168:GLY:C	2.30	0.56
1:B:249:ARG:NH2	1:B:287:MSE:HE1	2.21	0.55
1:A:206:LEU:HB2	3:A:343:HOH:O	2.05	0.55
1:A:329:SER:O	1:A:330:GLU:HG3	2.07	0.55
1:C:87:ILE:HD11	1:C:171:TYR:CG	2.41	0.55
1:A:70:ASN:HD21	1:A:162:VAL:H	1.55	0.55
1:C:60:TYR:OH	1:C:117:PRO:HB3	2.06	0.55
1:C:112:LEU:HD12	1:C:126:SER:CB	2.35	0.55
1:D:32:PRO:HD2	1:D:187:ARG:O	2.06	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:217:ASP:CB	1:A:315:PHE:HZ	2.18	0.55
1:C:131:ASP:HA	1:C:134:LYS:HE2	1.88	0.55
1:A:239:TYR:O	1:A:240:ARG:CB	2.50	0.55
1:C:215:PRO:HG2	1:C:317:THR:HG22	1.89	0.55
1:B:91:SER:HB3	1:B:104:ILE:HG21	1.89	0.54
1:B:300:ARG:HB2	1:B:300:ARG:HH11	1.72	0.54
1:A:212:ILE:O	1:A:223:GLN:HA	2.07	0.54
1:D:130:ILE:HD13	1:D:131:ASP:N	2.22	0.54
1:B:178:ARG:O	1:B:182:GLN:HG3	2.08	0.54
1:D:62:LYS:H	1:D:62:LYS:NZ	2.06	0.54
1:A:114:GLY:HA2	1:A:119:GLN:CD	2.33	0.54
1:B:189:LEU:C	1:B:189:LEU:HD23	2.33	0.54
1:A:136:LYS:HG2	1:A:136:LYS:O	2.08	0.54
1:C:127:GLN:HG2	1:C:129:GLN:OE1	2.07	0.53
1:C:151:GLN:HG3	3:C:346:HOH:O	2.07	0.53
1:C:312:GLY:O	1:C:313:ASP:HB2	2.08	0.53
1:D:240:ARG:O	1:D:241:ASN:C	2.52	0.53
1:B:307:MSE:HE3	1:B:318:TRP:CE3	2.44	0.53
1:C:86:ASP:O	1:C:90:THR:HG23	2.08	0.53
1:C:118:GLU:C	1:C:120:GLN:H	2.15	0.53
1:D:130:ILE:HD13	1:D:130:ILE:C	2.33	0.53
1:C:62:LYS:H	1:C:62:LYS:CD	2.22	0.53
1:D:136:LYS:HA	1:D:157:LEU:HD21	1.91	0.53
1:B:307:MSE:HE3	1:B:318:TRP:CZ3	2.44	0.53
1:C:189:LEU:HD23	1:C:198:SER:HB2	1.91	0.53
1:D:80:VAL:HB	1:D:84:MSE:HG2	1.91	0.53
1:D:312:GLY:C	1:D:314:SER:H	2.16	0.53
1:C:256:PRO:HD2	1:C:288:VAL:HG11	1.91	0.53
1:B:254:ILE:HD13	1:B:254:ILE:O	2.09	0.52
1:C:250:LEU:H	1:C:250:LEU:HD23	1.75	0.52
1:D:112:LEU:HD22	1:D:126:SER:HB3	1.90	0.52
1:C:131:ASP:O	1:C:134:LYS:HG2	2.10	0.52
1:D:58:SER:OG	1:D:61:LYS:HD3	2.10	0.52
1:A:127:GLN:O	1:A:129:GLN:N	2.43	0.52
1:A:121:PRO:O	1:A:123:GLN:N	2.41	0.52
1:A:306:TYR:CD2	1:A:319:MSE:HG2	2.45	0.52
1:B:249:ARG:HD3	1:B:249:ARG:C	2.34	0.52
1:D:61:LYS:C	1:D:63:ASP:H	2.17	0.52
1:A:73:GLN:HE21	1:A:158:PRO:HB3	1.75	0.51
1:B:151:GLN:HG3	3:D:351:HOH:O	2.08	0.51
1:B:223:GLN:HG3	3:B:357:HOH:O	2.09	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:128:GLU:OE1	1:A:260:ARG:NH2	2.43	0.51
1:D:37:LYS:HE2	1:D:41:GLU:OE2	2.11	0.51
1:C:309:THR:OG1	1:C:316:LYS:HG3	2.11	0.51
1:A:127:GLN:C	1:A:129:GLN:N	2.65	0.51
1:A:305:VAL:HG12	1:A:306:TYR:N	2.26	0.51
1:B:267:VAL:CG2	1:B:268:SER:N	2.73	0.51
1:C:149:HIS:HB2	1:C:150:GLN:HE22	1.74	0.51
1:D:237:GLY:HA2	1:D:287:MSE:SE	2.60	0.51
1:A:238:SER:HB2	1:A:287:MSE:HE2	1.92	0.51
1:B:186:SER:O	1:B:199:ARG:NH2	2.40	0.51
1:B:199:ARG:HD3	1:D:229:ASN:O	2.11	0.51
1:B:202:ASN:OD1	1:B:208:TRP:HA	2.11	0.51
1:B:199:ARG:CZ	1:B:200:GLY:CA	2.88	0.51
1:A:21:LYS:HG2	1:A:26:PHE:CE1	2.46	0.50
1:C:265:ASN:ND2	1:C:310:LYS:O	2.43	0.50
1:B:102:MSE:HE3	1:B:103:ASP:N	2.25	0.50
1:A:114:GLY:C	1:A:121:PRO:HB3	2.36	0.50
1:B:70:ASN:ND2	1:B:162:VAL:H	2.09	0.50
1:C:214:LYS:H	1:C:214:LYS:NZ	2.10	0.50
1:A:306:TYR:HD2	1:A:319:MSE:HG2	1.76	0.50
1:C:98:THR:HB	1:C:101:ALA:HB3	1.93	0.50
1:B:84:MSE:O	1:B:88:VAL:HG23	2.12	0.50
1:B:255:ASP:HB3	1:B:258:THR:HB	1.94	0.50
1:A:120:GLN:CB	1:A:122:VAL:HG22	2.42	0.50
1:C:57:LEU:O	1:C:66:LEU:HD23	2.12	0.50
1:D:106:VAL:O	1:D:106:VAL:HG22	2.11	0.50
1:B:137:THR:HG22	1:B:138:GLY:N	2.26	0.50
1:C:109:LEU:O	1:C:112:LEU:HB2	2.12	0.50
1:D:225:VAL:HG12	1:D:328:VAL:HG21	1.93	0.50
1:C:37:LYS:HA	1:D:321:PRO:HB3	1.94	0.50
1:B:199:ARG:HD2	1:B:200:GLY:H	1.72	0.50
1:D:129:GLN:NE2	3:D:357:HOH:O	2.44	0.50
1:C:240:ARG:O	1:C:241:ASN:O	2.30	0.49
1:A:34:ILE:HD11	1:A:38:ARG:HD3	1.93	0.49
1:A:202:ASN:ND2	3:A:345:HOH:O	2.45	0.49
1:A:266:LEU:HA	1:A:309:THR:HG22	1.94	0.49
1:B:21:LYS:HE2	1:B:26:PHE:CE1	2.47	0.49
1:B:199:ARG:CD	1:B:200:GLY:N	2.75	0.49
1:C:247:GLY:O	1:C:249:ARG:N	2.46	0.49
1:A:13:THR:HG22	1:A:14:GLU:N	2.27	0.49
1:C:180:MSE:HE2	1:C:180:MSE:HA	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:43:LYS:HD3	1:A:43:LYS:O	2.13	0.49
1:B:266:LEU:HD23	1:B:287:MSE:HA	1.95	0.49
1:A:114:GLY:HA2	1:A:119:GLN:NE2	2.27	0.49
1:B:204:GLU:C	1:B:206:LEU:H	2.19	0.49
1:C:167:VAL:HG22	1:C:277:LEU:HD12	1.95	0.48
1:D:247:GLY:O	1:D:248:LYS:C	2.56	0.48
1:A:167:VAL:HG22	1:A:277:LEU:HD12	1.95	0.48
1:B:249:ARG:HH22	1:B:287:MSE:HE1	1.77	0.48
1:A:38:ARG:HH12	1:A:183:GLU:HB3	1.78	0.48
1:B:157:LEU:HD11	3:B:347:HOH:O	2.12	0.48
1:B:167:VAL:CG2	1:B:277:LEU:CD1	2.91	0.48
1:C:214:LYS:H	1:C:214:LYS:HE2	1.78	0.48
1:C:264:HIS:CE1	1:C:266:LEU:HB3	2.48	0.48
1:C:133:MSE:HA	1:C:133:MSE:CE	2.36	0.48
1:D:249:ARG:O	1:D:250:LEU:HG	2.13	0.48
1:A:307:MSE:HE3	1:A:318:TRP:CZ3	2.48	0.48
1:B:101:ALA:HB1	1:B:288:VAL:HB	1.94	0.48
1:C:199:ARG:HA	1:C:229:ASN:ND2	2.21	0.48
1:C:265:ASN:OD1	1:C:265:ASN:O	2.32	0.48
1:A:145:ILE:N	1:A:145:ILE:HD12	2.29	0.48
1:B:129:GLN:O	1:B:129:GLN:HG2	2.13	0.48
1:A:106:VAL:O	1:A:106:VAL:HG22	2.14	0.48
1:A:120:GLN:HB3	1:A:122:VAL:HG22	1.96	0.48
1:B:15:VAL:O	1:B:15:VAL:HG12	2.13	0.48
1:B:127:GLN:O	1:B:129:GLN:N	2.46	0.48
1:A:204:GLU:O	1:A:206:LEU:N	2.42	0.47
1:C:255:ASP:HB3	1:C:258:THR:CG2	2.41	0.47
1:C:254:ILE:HD13	1:C:255:ASP:C	2.38	0.47
1:C:254:ILE:HD11	1:C:259:GLY:C	2.39	0.47
1:A:284:THR:O	1:A:288:VAL:HG23	2.15	0.47
1:C:238:SER:C	1:C:240:ARG:N	2.67	0.47
1:A:116:GLY:O	1:A:119:GLN:HB2	2.15	0.47
1:C:148:SER:OG	1:C:149:HIS:HD2	1.97	0.47
1:A:310:LYS:NZ	1:A:313:ASP:HA	2.30	0.47
1:B:105:THR:O	1:B:108:PRO:HD2	2.15	0.47
1:B:199:ARG:CZ	1:B:200:GLY:HA2	2.44	0.47
1:C:307:MSE:HE3	1:C:318:TRP:CZ3	2.49	0.47
1:A:38:ARG:O	1:A:42:LEU:HG	2.14	0.47
1:A:131:ASP:HA	1:A:134:LYS:HG2	1.95	0.47
1:C:209:ARG:HH11	1:C:209:ARG:HG2	1.79	0.47
1:C:254:ILE:HD13	1:C:255:ASP:O	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:294:ALA:O	1:C:298:VAL:HG23	2.15	0.47
1:C:258:THR:HG23	1:C:260:ARG:H	1.79	0.47
1:D:61:LYS:C	1:D:63:ASP:N	2.72	0.47
1:D:123:GLN:HG3	1:D:124:ILE:N	2.28	0.47
1:B:258:THR:HG22	1:B:260:ARG:N	2.26	0.47
1:C:197:ASN:ND2	1:C:198:SER:N	2.62	0.47
1:D:329:SER:O	1:D:330:GLU:CB	2.62	0.47
1:A:121:PRO:C	1:A:123:GLN:H	2.23	0.47
1:B:112:LEU:CD2	1:B:130:ILE:HG22	2.45	0.47
1:B:204:GLU:O	1:B:206:LEU:N	2.40	0.47
1:B:300:ARG:HB2	1:B:300:ARG:NH1	2.29	0.47
1:D:19:GLU:HG2	1:D:28:ARG:CG	2.38	0.47
1:D:140:GLN:NE2	1:D:140:GLN:N	2.53	0.47
1:A:121:PRO:O	1:A:122:VAL:C	2.57	0.46
1:A:254:ILE:HD13	1:A:254:ILE:C	2.39	0.46
1:B:34:ILE:HD11	1:B:38:ARG:CG	2.44	0.46
1:A:121:PRO:HG2	1:A:122:VAL:H	1.81	0.46
1:B:266:LEU:HB2	1:B:291:PRO:HD3	1.98	0.46
1:C:169:GLU:OE1	1:C:193:GLY:HA3	2.15	0.46
1:A:55:GLN:OE1	1:A:63:ASP:OD1	2.33	0.46
1:B:38:ARG:NH2	1:B:183:GLU:OE1	2.43	0.46
1:B:133:MSE:HE2	1:B:133:MSE:HA	1.96	0.46
1:B:197:ASN:ND2	1:B:198:SER:N	2.61	0.46
1:B:53:ASP:O	1:B:56:LEU:HB3	2.15	0.46
1:B:141:HIS:ND1	1:B:156:ASP:OD1	2.46	0.46
1:C:209:ARG:NH1	1:C:211:ALA:HB2	2.29	0.46
1:C:254:ILE:HD11	1:C:259:GLY:CA	2.46	0.46
1:B:197:ASN:C	1:B:197:ASN:ND2	2.73	0.46
1:A:178:ARG:O	1:A:182:GLN:HG2	2.16	0.46
1:B:137:THR:CG2	1:B:138:GLY:N	2.78	0.46
1:C:136:LYS:HA	1:C:157:LEU:HD21	1.96	0.46
1:B:23:MSE:HE1	1:B:172:ALA:CB	2.45	0.46
1:C:244:GLU:H	1:C:250:LEU:CD2	2.29	0.46
1:C:254:ILE:HD11	1:C:259:GLY:HA2	1.98	0.46
1:D:151:GLN:CD	1:D:151:GLN:N	2.73	0.46
1:D:316:LYS:HB3	3:D:363:HOH:O	2.16	0.46
1:D:70:ASN:ND2	1:D:162:VAL:H	2.14	0.46
1:D:235:THR:CG2	1:D:236:SER:N	2.78	0.46
1:C:258:THR:HG23	1:C:260:ARG:HB2	1.98	0.46
1:D:150:GLN:HG2	1:D:152:TYR:CE1	2.51	0.46
1:C:247:GLY:O	1:C:248:LYS:C	2.58	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:112:LEU:HD12	1:B:112:LEU:C	2.42	0.45
1:D:61:LYS:HD2	1:D:61:LYS:N	2.31	0.45
1:A:249:ARG:HD3	1:A:249:ARG:C	2.42	0.45
1:C:197:ASN:C	1:C:197:ASN:ND2	2.75	0.45
1:A:260:ARG:HB2	1:A:261:PRO:CD	2.47	0.45
1:A:283:ASP:OD1	1:A:284:THR:N	2.49	0.45
1:C:31:ILE:CG1	1:C:185:ILE:HG21	2.46	0.45
1:C:254:ILE:HG12	1:C:260:ARG:O	2.17	0.45
1:D:54:ASP:OD1	1:D:58:SER:HB2	2.17	0.45
1:D:124:ILE:O	1:D:125:PRO:C	2.59	0.45
1:A:212:ILE:O	1:A:212:ILE:HG13	2.16	0.45
1:C:244:GLU:H	1:C:250:LEU:HD21	1.81	0.45
1:A:176:LEU:HD23	1:A:190:VAL:CG2	2.42	0.45
1:C:120:GLN:O	1:C:122:VAL:N	2.50	0.45
1:D:149:HIS:HB2	1:D:150:GLN:OE1	2.16	0.45
1:D:212:ILE:HD11	1:D:224:ALA:CB	2.43	0.45
1:D:250:LEU:HD12	1:D:252:HIS:CD2	2.51	0.45
1:A:198:SER:HB3	1:A:228:ILE:HG13	1.99	0.45
1:D:38:ARG:NH2	1:D:183:GLU:O	2.50	0.45
1:B:30:SER:HB3	3:B:368:HOH:O	2.17	0.44
1:C:241:ASN:HD22	1:C:243:TYR:N	2.13	0.44
1:D:273:ALA:HB1	1:D:274:PRO:CD	2.46	0.44
1:B:45:LYS:NZ	1:B:183:GLU:OE2	2.41	0.44
1:B:189:LEU:HD22	3:B:370:HOH:O	2.17	0.44
1:C:196:LEU:HB2	1:C:233:ILE:HG22	1.99	0.44
1:D:250:LEU:HD12	1:D:252:HIS:NE2	2.32	0.44
1:A:87:ILE:HG21	1:A:164:LEU:HD13	1.98	0.44
1:A:112:LEU:CD2	1:A:126:SER:HB3	2.37	0.44
1:C:129:GLN:HE21	1:C:129:GLN:HB3	1.52	0.44
1:D:140:GLN:HE21	1:D:140:GLN:N	2.06	0.44
1:D:312:GLY:C	1:D:314:SER:N	2.75	0.44
1:A:88:VAL:HG21	1:A:153:LEU:HD21	1.99	0.44
1:C:118:GLU:O	1:C:120:GLN:N	2.46	0.44
1:A:73:GLN:NE2	1:A:158:PRO:HB3	2.32	0.44
1:A:264:HIS:CE1	1:A:266:LEU:HB3	2.52	0.44
1:B:242:TYR:HA	3:B:371:HOH:O	2.17	0.44
1:D:87:ILE:HD11	1:D:171:TYR:CG	2.53	0.44
1:A:127:GLN:HG3	1:A:129:GLN:HB3	2.00	0.44
1:A:254:ILE:HD11	1:A:259:GLY:CA	2.46	0.44
1:B:242:TYR:OH	1:B:265:ASN:HA	2.17	0.44
1:A:110:VAL:HG22	1:A:254:ILE:HG21	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:17:VAL:O	1:B:17:VAL:HG23	2.17	0.43
1:B:244:GLU:HB2	1:B:245:LEU:H	1.57	0.43
1:D:225:VAL:HG12	1:D:328:VAL:CG2	2.48	0.43
1:A:292:GLU:O	1:A:296:GLU:HG3	2.18	0.43
1:B:267:VAL:HG23	1:B:268:SER:N	2.31	0.43
1:C:153:LEU:HD23	1:C:153:LEU:HA	1.83	0.43
1:A:32:PRO:HD2	1:A:187:ARG:O	2.19	0.43
1:A:102:MSE:HG3	1:A:281:ALA:O	2.18	0.43
1:B:267:VAL:HG22	1:B:308:ILE:O	2.17	0.43
1:C:32:PRO:O	1:C:33:GLY:C	2.61	0.43
1:C:133:MSE:CE	1:C:136:LYS:HD3	2.49	0.43
1:D:59:THR:HG22	1:D:60:TYR:CD1	2.53	0.43
1:A:120:GLN:HB2	1:A:121:PRO:HA	1.99	0.43
1:A:301:GLU:HB2	1:A:303:LEU:HG	2.00	0.43
1:B:254:ILE:C	1:B:254:ILE:CD1	2.81	0.43
1:C:149:HIS:C	1:C:150:GLN:NE2	2.77	0.43
1:D:31:ILE:HG21	1:D:34:ILE:CD1	2.46	0.43
1:D:62:LYS:HZ3	1:D:62:LYS:CB	2.21	0.43
1:A:128:GLU:CD	1:A:260:ARG:NH2	2.77	0.43
1:B:258:THR:HG22	1:B:260:ARG:HB2	2.00	0.43
1:D:62:LYS:H	1:D:62:LYS:HZ2	1.66	0.43
1:A:149:HIS:C	1:A:150:GLN:HG2	2.44	0.43
1:A:214:LYS:O	1:A:215:PRO:C	2.61	0.43
1:A:290:GLY:O	1:A:294:ALA:CB	2.67	0.43
1:D:202:ASN:C	1:D:202:ASN:ND2	2.74	0.43
1:C:115:PHE:CD1	1:C:252:HIS:HA	2.54	0.42
1:D:239:TYR:O	1:D:240:ARG:C	2.61	0.42
1:B:199:ARG:HE	1:D:231:HIS:CE1	2.32	0.42
1:A:107:GLY:N	1:A:108:PRO:HD2	2.35	0.42
1:C:212:ILE:HB	1:C:224:ALA:HB3	2.01	0.42
1:C:16:THR:HB	1:C:31:ILE:HG22	2.01	0.42
1:A:119:GLN:O	1:A:120:GLN:C	2.63	0.42
1:B:267:VAL:HG22	1:B:308:ILE:HB	2.00	0.42
1:D:191:SER:HB2	1:D:196:LEU:HG	1.98	0.42
1:D:265:ASN:ND2	1:D:265:ASN:N	2.57	0.42
1:C:110:VAL:HG22	1:C:254:ILE:CG2	2.50	0.42
1:C:250:LEU:HD23	1:C:250:LEU:N	2.34	0.42
1:B:32:PRO:O	1:B:33:GLY:C	2.62	0.42
1:D:297:VAL:HG22	1:D:300:ARG:NH2	2.35	0.42
1:D:297:VAL:HG22	1:D:300:ARG:HH22	1.85	0.42
1:A:116:GLY:O	1:A:117:PRO:C	2.60	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:91:SER:HB3	1:B:104:ILE:CG2	2.50	0.42
1:B:258:THR:CG2	1:B:260:ARG:HB2	2.50	0.42
1:A:257:GLN:NE2	3:A:347:HOH:O	2.44	0.41
1:C:200:GLY:H	1:C:229:ASN:ND2	2.17	0.41
1:C:291:PRO:O	1:C:295:LYS:HG3	2.19	0.41
1:D:68:ARG:HG3	1:D:78:TRP:HZ2	1.85	0.41
1:B:27:TRP:CZ3	1:B:46:ILE:HG21	2.55	0.41
1:B:106:VAL:O	1:B:106:VAL:HG22	2.20	0.41
1:B:134:LYS:O	1:B:137:THR:HB	2.20	0.41
1:C:42:LEU:O	1:C:43:LYS:C	2.63	0.41
1:D:176:LEU:HD12	1:D:176:LEU:HA	1.89	0.41
1:C:176:LEU:O	1:C:179:LEU:HB3	2.21	0.41
1:C:198:SER:HB3	1:C:228:ILE:HG13	2.03	0.41
1:D:268:SER:HB3	1:D:308:ILE:HB	2.03	0.41
1:A:55:GLN:HA	1:A:55:GLN:NE2	2.35	0.41
1:A:127:GLN:OE1	1:A:128:GLU:N	2.54	0.41
1:C:212:ILE:HD11	1:C:226:VAL:CG1	2.49	0.41
1:C:212:ILE:HD11	1:C:226:VAL:HG13	2.02	0.41
1:C:171:TYR:HB2	1:C:277:LEU:HD13	2.03	0.41
1:C:239:TYR:HA	1:C:267:VAL:HG11	2.02	0.41
1:C:196:LEU:N	1:C:196:LEU:HD12	2.35	0.41
1:D:44:GLU:C	1:D:44:GLU:CD	2.88	0.41
1:C:20:GLY:HA3	1:C:27:TRP:NE1	2.35	0.41
1:B:100:GLY:O	1:B:256:PRO:HG3	2.21	0.41
1:B:199:ARG:HD3	1:D:230:GLY:HA3	2.02	0.41
1:C:116:GLY:HA3	1:C:117:PRO:HD2	1.95	0.41
1:C:214:LYS:NZ	3:C:363:HOH:O	2.53	0.41
1:D:249:ARG:O	1:D:250:LEU:CG	2.68	0.41
1:D:301:GLU:HB2	1:D:303:LEU:HG	2.02	0.41
1:D:112:LEU:CD2	1:D:126:SER:HB3	2.51	0.41
1:C:243:TYR:HA	1:C:250:LEU:CD2	2.51	0.40
1:D:169:GLU:OE1	1:D:193:GLY:HA3	2.21	0.40
1:B:296:GLU:HG2	1:B:300:ARG:HH12	1.87	0.40
1:C:199:ARG:HB3	1:C:230:GLY:H	1.86	0.40
1:B:167:VAL:CG2	1:B:277:LEU:HD12	2.51	0.40
1:B:282:TRP:CH2	1:B:301:GLU:HG3	2.57	0.40
1:A:76:SER:HB2	3:A:389:HOH:O	2.22	0.40
1:A:106:VAL:C	1:A:108:PRO:HD2	2.47	0.40
1:C:235:THR:HG22	1:C:236:SER:N	2.36	0.40
1:D:226:VAL:HG12	1:D:327:LEU:HD23	2.04	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	301/340 (88%)	275 (91%)	18 (6%)	8 (3%)	4	2
1	B	294/340 (86%)	268 (91%)	21 (7%)	5 (2%)	7	5
1	C	309/340 (91%)	273 (88%)	24 (8%)	12 (4%)	2	1
1	D	300/340 (88%)	273 (91%)	20 (7%)	7 (2%)	5	3
All	All	1204/1360 (88%)	1089 (90%)	83 (7%)	32 (3%)	4	2

All (32) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	123	GLN
1	C	35	ASP
1	C	117	PRO
1	C	241	ASN
1	C	242	TYR
1	C	245	LEU
1	C	248	LYS
1	D	127	GLN
1	D	330	GLU
1	A	128	GLU
1	A	240	ARG
1	B	33	GLY
1	B	244	GLU
1	C	33	GLY
1	C	244	GLU
1	C	247	GLY
1	D	241	ASN
1	A	214	LYS
1	A	215	PRO
1	B	14	GLU
1	B	258	THR
1	C	119	GLN

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Mol	Chain	Res	Type
1	C	121	PRO
1	D	329	SER
1	D	248	LYS
1	D	291	PRO
1	A	311	GLU
1	A	120	GLN
1	B	128	GLU
1	C	122	VAL
1	D	202	ASN
1	A	122	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	254/277 (92%)	239 (94%)	15 (6%)	18	22
1	B	248/277 (90%)	230 (93%)	18 (7%)	13	15
1	C	253/277 (91%)	235 (93%)	18 (7%)	13	16
1	D	246/277 (89%)	226 (92%)	20 (8%)	11	12
All	All	1001/1108 (90%)	930 (93%)	71 (7%)	13	16

All (71) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	13	THR
1	A	38	ARG
1	A	62	LYS
1	A	112	LEU
1	A	126	SER
1	A	127	GLN
1	A	128	GLU
1	A	167	VAL
1	A	176	LEU
1	A	189	LEU
1	A	190	VAL

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Mol	Chain	Res	Type
1	A	191	SER
1	A	223	GLN
1	A	254	ILE
1	A	286	LEU
1	B	15	VAL
1	B	57	LEU
1	B	75	LEU
1	B	112	LEU
1	B	115	PHE
1	B	127	GLN
1	B	129	GLN
1	B	150	GLN
1	B	176	LEU
1	B	197	ASN
1	B	199	ARG
1	B	209	ARG
1	B	254	ILE
1	B	267	VAL
1	B	286	LEU
1	B	311	GLU
1	B	313	ASP
1	B	330	GLU
1	C	31	ILE
1	C	34	ILE
1	C	43	LYS
1	C	44	GLU
1	C	62	LYS
1	C	90	THR
1	C	112	LEU
1	C	115	PHE
1	C	129	GLN
1	C	131	ASP
1	C	136	LYS
1	C	150	GLN
1	C	189	LEU
1	C	197	ASN
1	C	214	LYS
1	C	254	ILE
1	C	258	THR
1	C	286	LEU
1	D	62	LYS
1	D	112	LEU

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Mol	Chain	Res	Type
1	D	125	PRO
1	D	126	SER
1	D	130	ILE
1	D	134	LYS
1	D	137	THR
1	D	140	GLN
1	D	142	LEU
1	D	159	ASP
1	D	167	VAL
1	D	189	LEU
1	D	190	VAL
1	D	202	ASN
1	D	227	ASP
1	D	250	LEU
1	D	254	ILE
1	D	257	GLN
1	D	265	ASN
1	D	278	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (32) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	55	GLN
1	A	70	ASN
1	A	73	GLN
1	A	120	GLN
1	A	147	GLN
1	A	150	GLN
1	A	154	GLN
1	A	182	GLN
1	A	223	GLN
1	B	70	ASN
1	B	127	GLN
1	B	146	ASN
1	B	147	GLN
1	B	149	HIS
1	B	150	GLN
1	B	154	GLN
1	B	197	ASN
1	B	241	ASN
1	C	55	GLN
1	C	70	ASN

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Mol	Chain	Res	Type
1	C	147	GLN
1	C	149	HIS
1	C	150	GLN
1	C	197	ASN
1	C	223	GLN
1	C	229	ASN
1	C	241	ASN
1	D	70	ASN
1	D	140	GLN
1	D	202	ASN
1	D	231	HIS
1	D	265	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

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

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	297/340 (87%)	0.40	27 (9%) 15 12	7, 20, 52, 61	0
1	B	290/340 (85%)	0.65	28 (9%) 13 10	9, 25, 52, 73	0
1	C	303/340 (89%)	0.63	32 (10%) 11 8	9, 22, 56, 72	0
1	D	296/340 (87%)	0.62	35 (11%) 9 7	6, 22, 54, 67	0
All	All	1186/1360 (87%)	0.57	122 (10%) 12 9	6, 22, 53, 73	0

All (122) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	246	ASP	7.4
1	A	122	VAL	7.0
1	B	115	PHE	6.6
1	C	116	GLY	6.5
1	D	122	VAL	6.1
1	C	246	ASP	5.4
1	B	199	ARG	5.1
1	D	250	LEU	5.0
1	B	116	GLY	4.9
1	C	117	PRO	4.9
1	D	331	LYS	4.9
1	D	241	ASN	4.8
1	B	245	LEU	4.7
1	D	247	GLY	4.6
1	D	244	GLU	4.5
1	C	122	VAL	4.5
1	B	127	GLN	4.5
1	C	222	VAL	4.4
1	D	243	TYR	4.4
1	C	121	PRO	4.3
1	A	241	ASN	4.3

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Mol	Chain	Res	Type	RSRZ
1	C	247	GLY	4.2
1	B	312	GLY	4.2
1	D	242	TYR	4.2
1	C	124	ILE	4.0
1	A	214	LYS	3.9
1	C	242	TYR	3.9
1	C	115	PHE	3.7
1	C	241	ASN	3.7
1	B	252	HIS	3.6
1	B	114	GLY	3.6
1	B	247	GLY	3.6
1	C	119	GLN	3.6
1	D	123	GLN	3.6
1	D	116	GLY	3.5
1	C	248	LYS	3.4
1	C	313	ASP	3.4
1	C	252	HIS	3.4
1	C	159	ASP	3.3
1	D	248	LYS	3.3
1	D	313	ASP	3.2
1	D	245	LEU	3.2
1	D	314	SER	3.2
1	A	125	PRO	3.2
1	A	218	LYS	3.1
1	D	223	GLN	3.1
1	C	216	THR	3.1
1	B	330	GLU	3.0
1	A	60	TYR	3.0
1	B	239	TYR	3.0
1	B	130	ILE	3.0
1	D	34	ILE	3.0
1	A	123	GLN	3.0
1	B	129	GLN	3.0
1	D	125	PRO	2.9
1	C	243	TYR	2.9
1	A	315	PHE	2.9
1	D	127	GLN	2.8
1	B	244	GLU	2.8
1	C	35	ASP	2.8
1	A	121	PRO	2.8
1	B	243	TYR	2.8
1	D	13	THR	2.8

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Mol	Chain	Res	Type	RSRZ
1	C	329	SER	2.8
1	D	312	GLY	2.8
1	A	215	PRO	2.8
1	C	312	GLY	2.7
1	D	329	SER	2.7
1	B	246	ASP	2.7
1	D	330	GLU	2.7
1	D	124	ILE	2.7
1	B	242	TYR	2.6
1	A	202	ASN	2.6
1	B	241	ASN	2.6
1	B	26	PHE	2.6
1	D	315	PHE	2.6
1	B	31	ILE	2.6
1	C	245	LEU	2.6
1	B	159	ASP	2.6
1	A	120	GLN	2.5
1	B	113	TRP	2.5
1	C	130	ILE	2.5
1	D	249	ARG	2.5
1	A	217	ASP	2.5
1	B	202	ASN	2.5
1	C	265	ASN	2.5
1	A	254	ILE	2.5
1	C	63	ASP	2.5
1	D	224	ALA	2.5
1	D	63	ASP	2.4
1	C	125	PRO	2.4
1	B	13	THR	2.4
1	C	114	GLY	2.4
1	A	330	GLU	2.4
1	B	311	GLU	2.4
1	D	214	LYS	2.4
1	A	329	SER	2.4
1	B	329	SER	2.4
1	D	296	GLU	2.3
1	D	60	TYR	2.3
1	A	316	LYS	2.3
1	D	205	GLY	2.3
1	A	311	GLU	2.3
1	C	118	GLU	2.3
1	D	130	ILE	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	250	LEU	2.2
1	D	68	ARG	2.2
1	A	249	ARG	2.2
1	A	118	GLU	2.2
1	C	127	GLN	2.2
1	B	328	VAL	2.1
1	A	134	LYS	2.1
1	A	117	PRO	2.1
1	B	15	VAL	2.1
1	C	120	GLN	2.1
1	A	126	SER	2.1
1	A	128	GLU	2.1
1	C	244	GLU	2.1
1	A	124	ILE	2.1
1	C	330	GLU	2.0
1	A	314	SER	2.0
1	D	213	GLN	2.0

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q<0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	CA	A	341	1/1	0.83	0.15	23,23,23,23	0
2	CA	D	341	1/1	0.91	0.12	20,20,20,20	0
2	CA	B	341	1/1	0.92	0.21	24,24,24,24	0
2	CA	C	341	1/1	0.95	0.22	13,13,13,13	0

6.5 Other polymers [i](#)

There are no such residues in this entry.