



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 09:13 AM GMT

PDB ID : 3HL9
Title : Simvastatin Synthase (LovD) from *Aspergillus terreus*, unliganded
Authors : Sawaya, M.R.; Yeates, T.O.; Laidman, J.; Pashkov, I.; Gao, X.; Tang, Y.
Deposited on : 2009-05-27
Resolution : 3.40 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

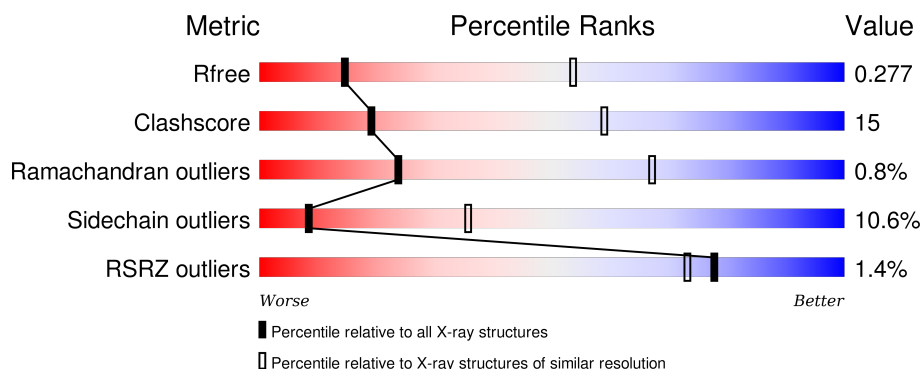
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.40 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	91344	1476 (3.50-3.30)
Clashscore	102246	1611 (3.50-3.30)
Ramachandran outliers	100387	1571 (3.50-3.30)
Sidechain outliers	100360	1571 (3.50-3.30)
RSRZ outliers	91569	1485 (3.50-3.30)

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 $\leq 5\%$. 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	432	<div> <div>62%</div> <div>26%</div> <div>•</div> <div>9%</div> </div>
1	B	432	<div> <div>59%</div> <div>29%</div> <div>•</div> <div>9%</div> </div>
1	C	432	<div> <div>59%</div> <div>29%</div> <div>•</div> <div>9%</div> </div>
1	D	432	<div> <div>60%</div> <div>28%</div> <div>•</div> <div>9%</div> </div>

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 12328 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 Transesterase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	393	Total	C	N	O	S	0	0	0
			3082	1936	560	565	21			
1	B	393	Total	C	N	O	S	0	0	0
			3082	1936	560	565	21			
1	C	393	Total	C	N	O	S	0	0	0
			3082	1936	560	565	21			
1	D	393	Total	C	N	O	S	0	0	0
			3082	1936	560	565	21			

There are 84 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-18	GLY	-	EXPRESSION TAG	UNP Q9Y7D1
A	-17	SER	-	EXPRESSION TAG	UNP Q9Y7D1
A	-16	SER	-	EXPRESSION TAG	UNP Q9Y7D1
A	-15	HIS	-	EXPRESSION TAG	UNP Q9Y7D1
A	-14	HIS	-	EXPRESSION TAG	UNP Q9Y7D1
A	-13	HIS	-	EXPRESSION TAG	UNP Q9Y7D1
A	-12	HIS	-	EXPRESSION TAG	UNP Q9Y7D1
A	-11	HIS	-	EXPRESSION TAG	UNP Q9Y7D1
A	-10	HIS	-	EXPRESSION TAG	UNP Q9Y7D1
A	-9	SER	-	EXPRESSION TAG	UNP Q9Y7D1
A	-8	SER	-	EXPRESSION TAG	UNP Q9Y7D1
A	-7	GLY	-	EXPRESSION TAG	UNP Q9Y7D1
A	-6	LEU	-	EXPRESSION TAG	UNP Q9Y7D1
A	-5	VAL	-	EXPRESSION TAG	UNP Q9Y7D1
A	-4	PRO	-	EXPRESSION TAG	UNP Q9Y7D1
A	-3	ARG	-	EXPRESSION TAG	UNP Q9Y7D1
A	-2	GLY	-	EXPRESSION TAG	UNP Q9Y7D1
A	-1	SER	-	EXPRESSION TAG	UNP Q9Y7D1
A	0	HIS	-	EXPRESSION TAG	UNP Q9Y7D1
A	40	ALA	CYS	ENGINEERED	UNP Q9Y7D1
A	60	ASN	CYS	ENGINEERED	UNP Q9Y7D1

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-18	GLY	-	EXPRESSION TAG	UNP Q9Y7D1
B	-17	SER	-	EXPRESSION TAG	UNP Q9Y7D1
B	-16	SER	-	EXPRESSION TAG	UNP Q9Y7D1
B	-15	HIS	-	EXPRESSION TAG	UNP Q9Y7D1
B	-14	HIS	-	EXPRESSION TAG	UNP Q9Y7D1
B	-13	HIS	-	EXPRESSION TAG	UNP Q9Y7D1
B	-12	HIS	-	EXPRESSION TAG	UNP Q9Y7D1
B	-11	HIS	-	EXPRESSION TAG	UNP Q9Y7D1
B	-10	HIS	-	EXPRESSION TAG	UNP Q9Y7D1
B	-9	SER	-	EXPRESSION TAG	UNP Q9Y7D1
B	-8	SER	-	EXPRESSION TAG	UNP Q9Y7D1
B	-7	GLY	-	EXPRESSION TAG	UNP Q9Y7D1
B	-6	LEU	-	EXPRESSION TAG	UNP Q9Y7D1
B	-5	VAL	-	EXPRESSION TAG	UNP Q9Y7D1
B	-4	PRO	-	EXPRESSION TAG	UNP Q9Y7D1
B	-3	ARG	-	EXPRESSION TAG	UNP Q9Y7D1
B	-2	GLY	-	EXPRESSION TAG	UNP Q9Y7D1
B	-1	SER	-	EXPRESSION TAG	UNP Q9Y7D1
B	0	HIS	-	EXPRESSION TAG	UNP Q9Y7D1
B	40	ALA	CYS	ENGINEERED	UNP Q9Y7D1
B	60	ASN	CYS	ENGINEERED	UNP Q9Y7D1
C	-18	GLY	-	EXPRESSION TAG	UNP Q9Y7D1
C	-17	SER	-	EXPRESSION TAG	UNP Q9Y7D1
C	-16	SER	-	EXPRESSION TAG	UNP Q9Y7D1
C	-15	HIS	-	EXPRESSION TAG	UNP Q9Y7D1
C	-14	HIS	-	EXPRESSION TAG	UNP Q9Y7D1
C	-13	HIS	-	EXPRESSION TAG	UNP Q9Y7D1
C	-12	HIS	-	EXPRESSION TAG	UNP Q9Y7D1
C	-11	HIS	-	EXPRESSION TAG	UNP Q9Y7D1
C	-10	HIS	-	EXPRESSION TAG	UNP Q9Y7D1
C	-9	SER	-	EXPRESSION TAG	UNP Q9Y7D1
C	-8	SER	-	EXPRESSION TAG	UNP Q9Y7D1
C	-7	GLY	-	EXPRESSION TAG	UNP Q9Y7D1
C	-6	LEU	-	EXPRESSION TAG	UNP Q9Y7D1
C	-5	VAL	-	EXPRESSION TAG	UNP Q9Y7D1
C	-4	PRO	-	EXPRESSION TAG	UNP Q9Y7D1
C	-3	ARG	-	EXPRESSION TAG	UNP Q9Y7D1
C	-2	GLY	-	EXPRESSION TAG	UNP Q9Y7D1
C	-1	SER	-	EXPRESSION TAG	UNP Q9Y7D1
C	0	HIS	-	EXPRESSION TAG	UNP Q9Y7D1
C	40	ALA	CYS	ENGINEERED	UNP Q9Y7D1
C	60	ASN	CYS	ENGINEERED	UNP Q9Y7D1

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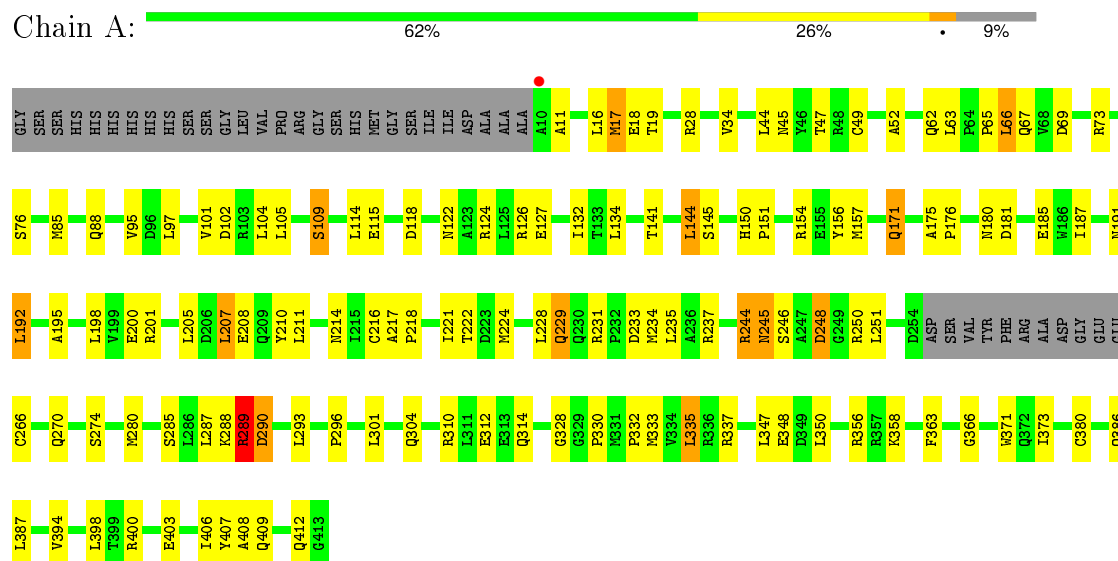
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Chain	Residue	Modelled	Actual	Comment	Reference
D	-18	GLY	-	EXPRESSION TAG	UNP Q9Y7D1
D	-17	SER	-	EXPRESSION TAG	UNP Q9Y7D1
D	-16	SER	-	EXPRESSION TAG	UNP Q9Y7D1
D	-15	HIS	-	EXPRESSION TAG	UNP Q9Y7D1
D	-14	HIS	-	EXPRESSION TAG	UNP Q9Y7D1
D	-13	HIS	-	EXPRESSION TAG	UNP Q9Y7D1
D	-12	HIS	-	EXPRESSION TAG	UNP Q9Y7D1
D	-11	HIS	-	EXPRESSION TAG	UNP Q9Y7D1
D	-10	HIS	-	EXPRESSION TAG	UNP Q9Y7D1
D	-9	SER	-	EXPRESSION TAG	UNP Q9Y7D1
D	-8	SER	-	EXPRESSION TAG	UNP Q9Y7D1
D	-7	GLY	-	EXPRESSION TAG	UNP Q9Y7D1
D	-6	LEU	-	EXPRESSION TAG	UNP Q9Y7D1
D	-5	VAL	-	EXPRESSION TAG	UNP Q9Y7D1
D	-4	PRO	-	EXPRESSION TAG	UNP Q9Y7D1
D	-3	ARG	-	EXPRESSION TAG	UNP Q9Y7D1
D	-2	GLY	-	EXPRESSION TAG	UNP Q9Y7D1
D	-1	SER	-	EXPRESSION TAG	UNP Q9Y7D1
D	0	HIS	-	EXPRESSION TAG	UNP Q9Y7D1
D	40	ALA	CYS	ENGINEERED	UNP Q9Y7D1
D	60	ASN	CYS	ENGINEERED	UNP Q9Y7D1

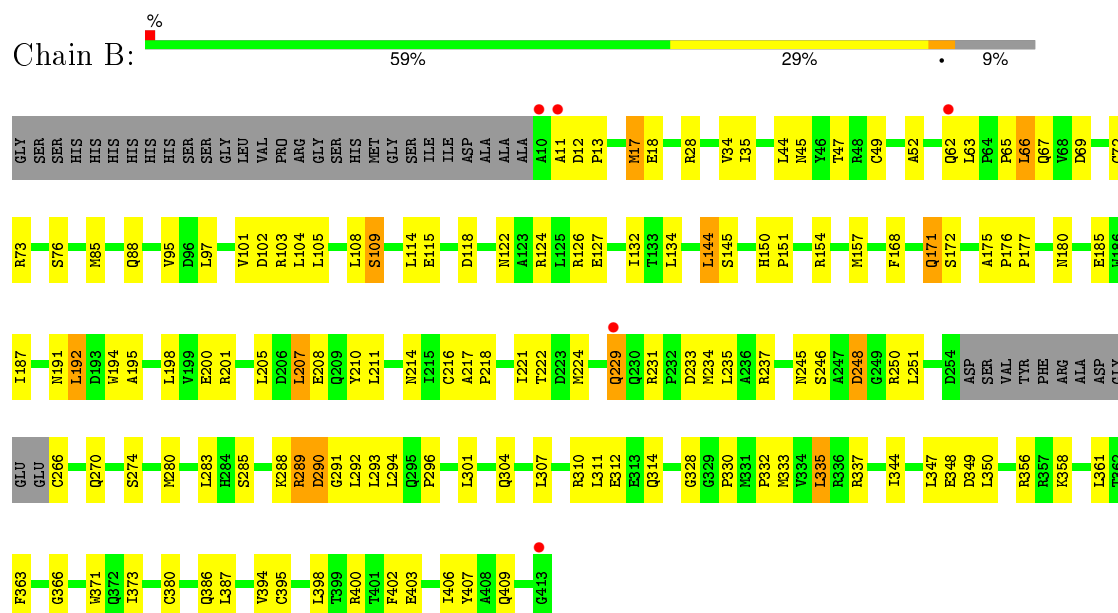
3 Residue-property plots

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

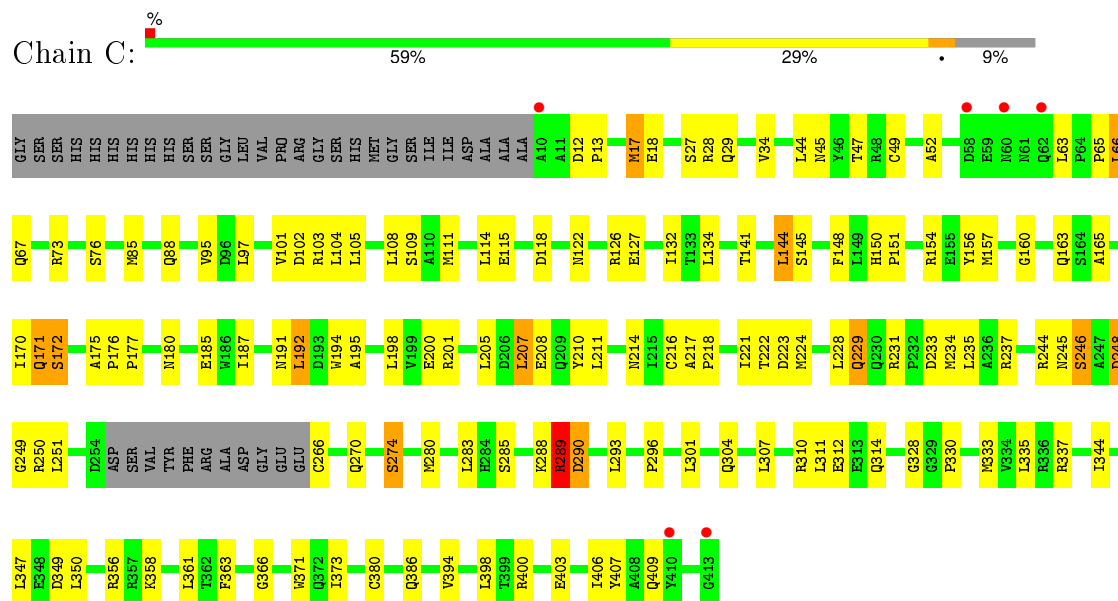
• Molecule 1: Transesterase



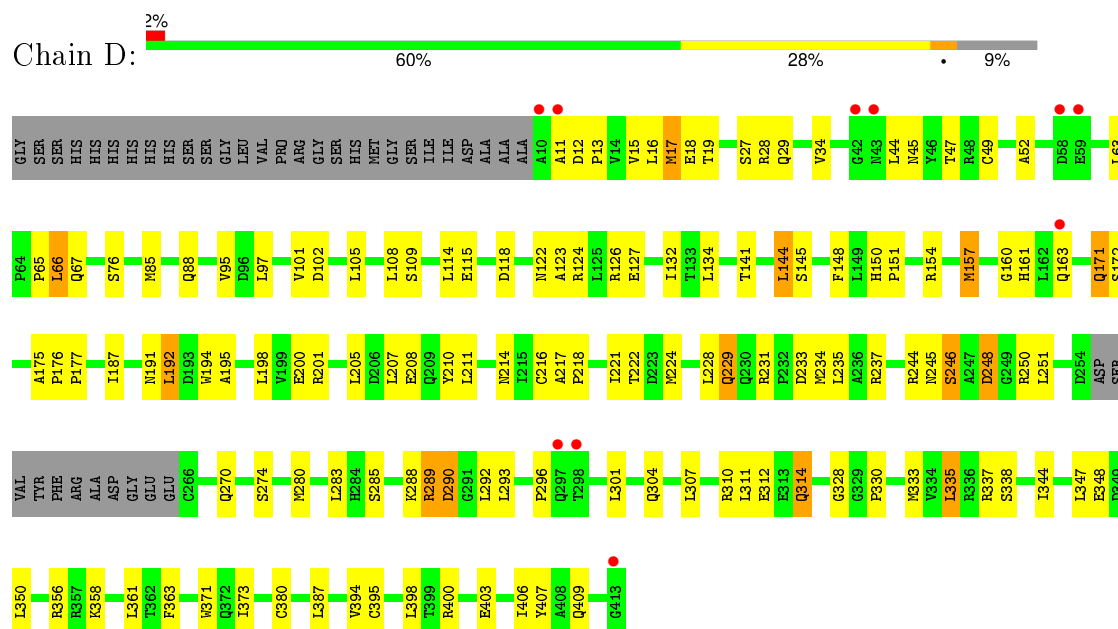
• Molecule 1: Transesterase



- Molecule 1: Transesterase



- Molecule 1: Transesterase



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	56.72Å 79.74Å 104.11Å 94.11° 91.56° 106.79°	Depositor
Resolution (Å)	76.03 – 3.40 76.08 – 3.40	Depositor EDS
% Data completeness (in resolution range)	98.9 (76.03-3.40) 96.2 (76.08-3.40)	Depositor EDS
R_{merge}	0.23	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.00 (at 3.41Å)	Xtriage
Refinement program	REFMAC 5.5.0072	Depositor
R, R_{free}	0.231 , 0.275 0.237 , 0.277	Depositor DCC
R_{free} test set	1216 reflections (5.42%)	DCC
Wilson B-factor (Å ²)	31.0	Xtriage
Anisotropy	0.105	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 13.8	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.44$, $\langle L^2 \rangle = 0.27$	Xtriage
Outliers	0 of 23672 reflections	Xtriage
F_o, F_c correlation	0.84	EDS
Total number of atoms	12328	wwPDB-VP
Average B, all atoms (Å ²)	6.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.94% 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, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

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	0.57	0/3147	0.70	1/4261 (0.0%)
1	B	0.56	1/3147 (0.0%)	0.68	0/4261
1	C	0.56	0/3147	0.69	0/4261
1	D	0.54	0/3147	0.68	0/4261
All	All	0.56	1/12588 (0.0%)	0.69	1/17044 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	72	CYS	CB-SG	-5.06	1.73	1.81

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	244	ARG	NE-CZ-NH1	5.07	122.84	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	3082	0	3060	91	0
1	B	3082	0	3060	90	0
1	C	3082	0	3060	107	0
1	D	3082	0	3060	114	0
All	All	12328	0	12240	373	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 15.

All (373) 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:11:ALA:HB2	1:A:409:GLN:HG3	1.19	1.16
1:B:11:ALA:HB2	1:B:409:GLN:HG3	1.43	0.99
1:A:95:VAL:HG11	1:A:198:LEU:HD21	1.58	0.85
1:A:11:ALA:CB	1:A:409:GLN:HG3	2.07	0.83
1:C:148:PHE:CZ	1:D:244:ARG:HD3	2.15	0.81
1:C:95:VAL:HG11	1:C:198:LEU:HD21	1.62	0.81
1:B:95:VAL:HG11	1:B:198:LEU:HD21	1.60	0.81
1:C:244:ARG:HD3	1:D:148:PHE:CZ	2.15	0.80
1:C:172:SER:HB2	1:D:250:ARG:HD3	1.62	0.80
1:C:280:MET:HE3	1:C:280:MET:O	1.82	0.79
1:A:19:THR:HG21	1:D:16:LEU:HD21	1.64	0.78
1:C:246:SER:HA	1:D:148:PHE:CD2	2.18	0.78
1:B:217:ALA:HB3	1:B:218:PRO:HD3	1.64	0.78
1:A:280:MET:HE3	1:A:280:MET:O	1.85	0.75
1:D:95:VAL:HG11	1:D:198:LEU:HD21	1.68	0.74
1:B:114:LEU:C	1:B:114:LEU:HD23	2.08	0.74
1:A:217:ALA:HB3	1:A:218:PRO:HD3	1.67	0.73
1:C:250:ARG:HD3	1:D:172:SER:HB2	1.71	0.73
1:C:217:ALA:HB3	1:C:218:PRO:HD3	1.71	0.72
1:A:44:LEU:HD12	1:A:45:ASN:N	2.05	0.72
1:D:217:ALA:HB3	1:D:218:PRO:HD3	1.72	0.71
1:D:101:VAL:HG12	1:D:132:ILE:HG23	1.72	0.70
1:D:280:MET:O	1:D:280:MET:HE3	1.90	0.70
1:C:148:PHE:CD2	1:D:246:SER:HA	2.26	0.70
1:A:145:SER:HB2	1:A:187:ILE:HG21	1.73	0.70
1:B:101:VAL:HG22	1:B:105:LEU:HB2	1.73	0.70
1:C:163:GLN:NE2	1:D:27:SER:OG	2.25	0.70
1:A:406:ILE:HD12	1:A:407:TYR:N	2.07	0.70
1:C:101:VAL:HG12	1:C:132:ILE:HG23	1.73	0.69
1:B:101:VAL:HG12	1:B:132:ILE:HG23	1.74	0.69
1:D:101:VAL:HG22	1:D:105:LEU:HB2	1.75	0.68
1:A:101:VAL:HG22	1:A:105:LEU:HB2	1.75	0.67
1:B:145:SER:HB2	1:B:187:ILE:HG21	1.78	0.66
1:A:102:ASP:HB3	1:A:109:SER:CB	2.26	0.66
1:C:148:PHE:HE2	1:D:244:ARG:HG2	1.61	0.65
1:B:44:LEU:HD12	1:B:45:ASN:N	2.11	0.65
1:A:52:ALA:HA	1:A:65:PRO:HA	1.78	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:11:ALA:HB2	1:A:409:GLN:CG	2.13	0.65
1:C:101:VAL:HG22	1:C:105:LEU:HB2	1.78	0.65
1:A:101:VAL:HG12	1:A:132:ILE:HG23	1.79	0.65
1:C:114:LEU:HD23	1:C:114:LEU:C	2.17	0.65
1:B:97:LEU:HD23	1:B:134:LEU:HD12	1.80	0.64
1:C:246:SER:HA	1:D:148:PHE:HD2	1.61	0.64
1:C:244:ARG:HG2	1:D:148:PHE:HE2	1.62	0.64
1:D:403:GLU:HA	1:D:406:ILE:HD11	1.80	0.64
1:D:52:ALA:HA	1:D:65:PRO:HA	1.80	0.64
1:D:102:ASP:HB3	1:D:109:SER:CB	2.28	0.63
1:D:34:VAL:CG2	1:D:66:LEU:HD13	2.29	0.63
1:C:102:ASP:HB3	1:C:109:SER:CB	2.29	0.63
1:D:145:SER:HB2	1:D:187:ILE:HG21	1.80	0.62
1:C:145:SER:HB2	1:C:187:ILE:HG21	1.80	0.62
1:C:52:ALA:HA	1:C:65:PRO:HA	1.80	0.62
1:A:114:LEU:HD23	1:A:114:LEU:C	2.20	0.62
1:C:27:SER:OG	1:D:163:GLN:NE2	2.33	0.62
1:C:172:SER:CB	1:D:250:ARG:HD3	2.30	0.61
1:C:403:GLU:HA	1:C:406:ILE:HD11	1.82	0.60
1:C:244:ARG:HG2	1:D:148:PHE:CE2	2.37	0.60
1:A:285:SER:HB2	1:A:290:ASP:OD1	2.01	0.60
1:B:403:GLU:HA	1:B:406:ILE:HD11	1.84	0.60
1:A:380:CYS:SG	1:A:380:CYS:O	2.60	0.60
1:C:406:ILE:HD12	1:C:407:TYR:N	2.17	0.60
1:B:52:ALA:HA	1:B:65:PRO:HA	1.83	0.59
1:C:328:GLY:O	1:C:330:PRO:HD2	2.02	0.59
1:A:34:VAL:CG2	1:A:66:LEU:HD13	2.31	0.59
1:B:333:MET:CE	1:B:333:MET:HA	2.33	0.59
1:B:102:ASP:HB3	1:B:109:SER:CB	2.31	0.59
1:D:101:VAL:CG1	1:D:132:ILE:HG23	2.33	0.58
1:C:160:GLY:HA2	1:D:29:GLN:NE2	2.18	0.58
1:C:148:PHE:HZ	1:D:244:ARG:HD3	1.64	0.58
1:C:244:ARG:HD3	1:D:148:PHE:HZ	1.67	0.58
1:C:34:VAL:CG2	1:C:66:LEU:HD13	2.33	0.58
1:D:344:ILE:O	1:D:361:LEU:HD12	2.04	0.58
1:C:101:VAL:CG1	1:C:132:ILE:HG23	2.34	0.58
1:D:328:GLY:O	1:D:330:PRO:HD2	2.04	0.58
1:C:148:PHE:CE2	1:D:244:ARG:HG2	2.39	0.57
1:C:97:LEU:HD23	1:C:134:LEU:HD12	1.87	0.57
1:A:333:MET:CE	1:A:333:MET:HA	2.33	0.57
1:B:66:LEU:O	1:B:66:LEU:HD12	2.03	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:333:MET:CE	1:C:333:MET:HA	2.35	0.57
1:B:73:ARG:H	1:B:386:GLN:HE22	1.53	0.57
1:A:85:MET:CE	1:A:210:TYR:HD1	2.18	0.57
1:D:114:LEU:C	1:D:114:LEU:HD23	2.24	0.57
1:D:406:ILE:HD12	1:D:407:TYR:N	2.19	0.57
1:A:192:LEU:HD13	1:A:195:ALA:HB3	1.87	0.57
1:A:406:ILE:HD12	1:A:407:TYR:H	1.68	0.56
1:B:216:CYS:SG	1:B:224:MET:HB3	2.45	0.56
1:C:216:CYS:SG	1:C:224:MET:HB3	2.45	0.56
1:D:44:LEU:HD12	1:D:45:ASN:N	2.21	0.56
1:B:280:MET:O	1:B:280:MET:HE3	2.06	0.55
1:C:221:ILE:HD13	1:C:224:MET:CE	2.37	0.55
1:B:328:GLY:O	1:B:330:PRO:HD2	2.05	0.55
1:C:148:PHE:HD2	1:D:246:SER:HA	1.67	0.55
1:B:11:ALA:CB	1:B:409:GLN:HG3	2.26	0.55
1:A:216:CYS:SG	1:A:224:MET:HB3	2.47	0.55
1:B:350:LEU:HD22	1:B:356:ARG:HB2	1.89	0.55
1:C:350:LEU:HD13	1:C:356:ARG:HB2	1.87	0.55
1:B:114:LEU:CD2	1:B:114:LEU:C	2.75	0.54
1:B:406:ILE:HD12	1:B:407:TYR:N	2.22	0.54
1:D:144:LEU:HD12	1:D:145:SER:N	2.23	0.54
1:B:285:SER:HB2	1:B:290:ASP:OD1	2.07	0.54
1:B:229:GLN:HA	1:B:235:LEU:HD12	1.89	0.54
1:D:192:LEU:HD13	1:D:195:ALA:HB3	1.88	0.54
1:C:221:ILE:HD13	1:C:224:MET:HE1	1.89	0.54
1:A:97:LEU:HD23	1:A:134:LEU:HD12	1.88	0.54
1:C:307:LEU:HD12	1:C:311:LEU:HB3	1.88	0.54
1:C:34:VAL:HG22	1:C:66:LEU:HD13	1.90	0.54
1:D:101:VAL:CG2	1:D:105:LEU:HD12	2.38	0.53
1:D:34:VAL:HG22	1:D:66:LEU:HD13	1.88	0.53
1:D:97:LEU:HD23	1:D:134:LEU:HD12	1.90	0.53
1:B:380:CYS:SG	1:B:380:CYS:O	2.64	0.53
1:B:17:MET:HE1	1:B:18:GLU:HA	1.90	0.53
1:A:17:MET:HE1	1:A:18:GLU:HA	1.91	0.53
1:D:350:LEU:HD13	1:D:356:ARG:HB2	1.89	0.53
1:D:285:SER:HB2	1:D:290:ASP:OD1	2.09	0.53
1:C:250:ARG:HD3	1:D:172:SER:CB	2.38	0.53
1:D:333:MET:HA	1:D:333:MET:CE	2.39	0.53
1:C:73:ARG:H	1:C:386:GLN:HE22	1.57	0.53
1:B:101:VAL:CG1	1:B:132:ILE:HG23	2.38	0.53
1:B:118:ASP:OD1	1:B:122:ASN:N	2.42	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:85:MET:CE	1:B:210:TYR:HD1	2.21	0.52
1:A:180:ASN:ND2	1:A:185:GLU:HG3	2.25	0.52
1:C:44:LEU:HD12	1:C:45:ASN:N	2.23	0.52
1:A:16:LEU:HD21	1:D:19:THR:HG21	1.91	0.52
1:A:328:GLY:O	1:A:330:PRO:HD2	2.08	0.52
1:D:88:GLN:OE1	1:D:214:ASN:HB3	2.10	0.52
1:B:192:LEU:HD13	1:B:195:ALA:HB3	1.92	0.52
1:B:114:LEU:HD23	1:B:115:GLU:N	2.25	0.52
1:A:221:ILE:HD13	1:A:224:MET:HE1	1.92	0.52
1:A:350:LEU:HD13	1:A:356:ARG:HB2	1.90	0.52
1:A:280:MET:HE1	1:A:380:CYS:SG	2.50	0.52
1:A:44:LEU:HD12	1:A:45:ASN:H	1.75	0.52
1:C:350:LEU:HD22	1:C:356:ARG:HB2	1.93	0.51
1:C:301:LEU:HA	1:C:304:GLN:HG2	1.93	0.51
1:D:350:LEU:HD22	1:D:356:ARG:HB2	1.93	0.51
1:C:200:GLU:HA	1:C:205:LEU:O	2.10	0.51
1:C:192:LEU:HD13	1:C:195:ALA:HB3	1.92	0.51
1:A:333:MET:HE2	1:A:333:MET:HA	1.92	0.51
1:D:301:LEU:HA	1:D:304:GLN:HG2	1.92	0.51
1:A:144:LEU:HD12	1:A:145:SER:N	2.26	0.51
1:C:285:SER:HB2	1:C:290:ASP:OD1	2.11	0.51
1:D:363:PHE:HB3	1:D:371:TRP:CZ2	2.46	0.51
1:D:102:ASP:HB3	1:D:109:SER:HB2	1.93	0.51
1:B:150:HIS:O	1:B:154:ARG:HG2	2.10	0.51
1:D:280:MET:CE	1:D:380:CYS:SG	2.99	0.50
1:C:102:ASP:HB3	1:C:109:SER:HB2	1.93	0.50
1:C:104:LEU:O	1:C:105:LEU:HD23	2.12	0.50
1:A:101:VAL:CG1	1:A:132:ILE:HG23	2.41	0.50
1:C:208:GLU:HA	1:C:208:GLU:OE1	2.10	0.50
1:C:280:MET:CE	1:C:380:CYS:SG	2.99	0.50
1:C:85:MET:CE	1:C:210:TYR:HD1	2.24	0.50
1:D:288:LYS:O	1:D:290:ASP:N	2.45	0.50
1:D:101:VAL:HG21	1:D:105:LEU:HD12	1.93	0.50
1:A:16:LEU:CD2	1:D:19:THR:HG21	2.42	0.50
1:D:221:ILE:HD13	1:D:224:MET:HE1	1.94	0.50
1:C:229:GLN:HA	1:C:235:LEU:HD12	1.94	0.50
1:A:150:HIS:O	1:A:154:ARG:HG2	2.12	0.50
1:B:104:LEU:O	1:B:105:LEU:HD23	2.11	0.49
1:C:144:LEU:HD12	1:C:145:SER:N	2.27	0.49
1:D:406:ILE:HD12	1:D:407:TYR:H	1.77	0.49
1:B:101:VAL:CG2	1:B:105:LEU:HD12	2.42	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:34:VAL:CG2	1:B:66:LEU:HD13	2.42	0.49
1:A:350:LEU:HD22	1:A:356:ARG:HB2	1.94	0.49
1:D:85:MET:HE1	1:D:211:LEU:HB2	1.94	0.49
1:D:280:MET:HE1	1:D:380:CYS:SG	2.52	0.49
1:A:102:ASP:HB3	1:A:109:SER:HB2	1.94	0.49
1:B:144:LEU:HD12	1:B:145:SER:N	2.28	0.49
1:A:85:MET:HE2	1:A:210:TYR:HD1	1.75	0.49
1:A:17:MET:CE	1:A:18:GLU:HA	2.42	0.49
1:B:85:MET:HE1	1:B:211:LEU:HB2	1.94	0.49
1:A:245:ASN:ND2	1:A:250:ARG:O	2.38	0.49
1:D:66:LEU:HD12	1:D:66:LEU:O	2.12	0.49
1:D:200:GLU:HA	1:D:205:LEU:O	2.13	0.49
1:B:101:VAL:HG21	1:B:105:LEU:HD12	1.94	0.49
1:B:333:MET:HE2	1:B:333:MET:HA	1.95	0.49
1:B:34:VAL:HG22	1:B:66:LEU:HD13	1.95	0.49
1:A:229:GLN:HA	1:A:235:LEU:HD12	1.95	0.48
1:B:126:ARG:HG2	1:B:127:GLU:O	2.12	0.48
1:A:403:GLU:HA	1:A:406:ILE:HD11	1.94	0.48
1:A:17:MET:HE2	1:A:17:MET:C	2.33	0.48
1:C:344:ILE:O	1:C:361:LEU:HD12	2.13	0.48
1:D:380:CYS:O	1:D:380:CYS:SG	2.71	0.48
1:C:406:ILE:HD12	1:C:407:TYR:H	1.78	0.48
1:A:288:LYS:O	1:A:290:ASP:N	2.47	0.48
1:B:280:MET:CE	1:B:380:CYS:SG	3.02	0.48
1:C:333:MET:HE2	1:C:333:MET:HA	1.94	0.48
1:C:288:LYS:O	1:C:290:ASP:N	2.46	0.48
1:C:363:PHE:HB3	1:C:371:TRP:CZ2	2.49	0.48
1:C:347:LEU:O	1:C:358:LYS:HG3	2.14	0.48
1:A:221:ILE:HD13	1:A:224:MET:CE	2.44	0.48
1:C:85:MET:HE1	1:C:211:LEU:HB2	1.96	0.48
1:C:234:MET:HA	1:C:237:ARG:HG2	1.96	0.48
1:C:150:HIS:O	1:C:154:ARG:HG2	2.14	0.48
1:C:171:GLN:HE21	1:C:171:GLN:HA	1.79	0.47
1:B:180:ASN:ND2	1:B:185:GLU:HG3	2.29	0.47
1:C:163:GLN:NE2	1:D:29:GLN:OE1	2.47	0.47
1:C:280:MET:HE1	1:C:380:CYS:SG	2.54	0.47
1:D:229:GLN:HA	1:D:235:LEU:HD12	1.94	0.47
1:D:248:ASP:HB2	1:D:250:ARG:H	1.79	0.47
1:A:114:LEU:HD12	1:A:156:TYR:CD1	2.49	0.47
1:D:126:ARG:HG2	1:D:127:GLU:O	2.15	0.47
1:A:280:MET:CE	1:A:380:CYS:SG	3.02	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:34:VAL:HG22	1:A:66:LEU:HD13	1.96	0.47
1:B:17:MET:CE	1:B:18:GLU:HA	2.45	0.47
1:D:280:MET:HE1	1:D:283:LEU:HB2	1.97	0.47
1:B:288:LYS:O	1:B:290:ASP:N	2.48	0.47
1:A:394:VAL:O	1:A:398:LEU:HD13	2.15	0.47
1:C:126:ARG:HG2	1:C:127:GLU:O	2.15	0.47
1:A:104:LEU:O	1:A:105:LEU:HD23	2.14	0.47
1:B:44:LEU:HD12	1:B:45:ASN:H	1.78	0.47
1:C:394:VAL:O	1:C:398:LEU:HD13	2.15	0.47
1:C:244:ARG:CD	1:D:148:PHE:CZ	2.95	0.47
1:C:114:LEU:C	1:C:114:LEU:CD2	2.83	0.47
1:B:85:MET:HE3	1:B:210:TYR:HD1	1.79	0.47
1:C:114:LEU:HD23	1:C:115:GLU:N	2.30	0.46
1:D:221:ILE:HD13	1:D:224:MET:CE	2.45	0.46
1:D:11:ALA:O	1:D:15:VAL:HG22	2.16	0.46
1:A:118:ASP:OD1	1:A:122:ASN:N	2.48	0.46
1:A:244:ARG:NH1	1:A:387:LEU:HD21	2.30	0.46
1:A:231:ARG:HB3	1:A:234:MET:HG2	1.98	0.46
1:A:114:LEU:CD2	1:A:114:LEU:C	2.84	0.46
1:D:49:CYS:SG	1:D:67:GLN:HA	2.56	0.46
1:B:406:ILE:HD12	1:B:407:TYR:H	1.81	0.46
1:A:301:LEU:HA	1:A:304:GLN:HG2	1.96	0.46
1:A:126:ARG:HG2	1:A:127:GLU:O	2.15	0.46
1:A:175:ALA:N	1:A:176:PRO:HD2	2.31	0.46
1:D:171:GLN:HE21	1:D:171:GLN:HA	1.80	0.46
1:B:200:GLU:HA	1:B:205:LEU:O	2.16	0.46
1:C:88:GLN:OE1	1:C:214:ASN:HB3	2.15	0.46
1:B:248:ASP:HB2	1:B:250:ARG:H	1.81	0.46
1:D:85:MET:CE	1:D:210:TYR:HD1	2.29	0.46
1:B:171:GLN:HE21	1:B:171:GLN:HA	1.80	0.46
1:A:85:MET:HE1	1:A:211:LEU:HB2	1.97	0.46
1:C:307:LEU:CD1	1:C:311:LEU:HB3	2.45	0.46
1:A:248:ASP:HB2	1:A:250:ARG:H	1.80	0.46
1:B:363:PHE:HB3	1:B:371:TRP:CZ2	2.50	0.46
1:B:350:LEU:HD13	1:B:356:ARG:HB2	1.98	0.46
1:A:49:CYS:SG	1:A:67:GLN:HA	2.55	0.46
1:B:88:GLN:OE1	1:B:214:ASN:HB3	2.16	0.46
1:D:150:HIS:O	1:D:154:ARG:HG2	2.15	0.45
1:B:102:ASP:HB3	1:B:109:SER:HB2	1.97	0.45
1:C:85:MET:HE2	1:C:210:TYR:HD1	1.81	0.45
1:D:216:CYS:SG	1:D:224:MET:HB3	2.56	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:280:MET:HE1	1:B:283:LEU:HB2	1.98	0.45
1:D:114:LEU:HD23	1:D:115:GLU:N	2.32	0.45
1:D:17:MET:HE1	1:D:18:GLU:HA	1.99	0.45
1:C:223:ASP:O	1:C:274:SER:HA	2.17	0.45
1:D:118:ASP:OD1	1:D:122:ASN:N	2.50	0.45
1:B:288:LYS:C	1:B:289:ARG:HD3	2.37	0.45
1:B:207:LEU:HD11	1:B:266:CYS:O	2.16	0.45
1:C:17:MET:CE	1:C:18:GLU:HA	2.47	0.45
1:D:333:MET:HA	1:D:333:MET:HE2	1.99	0.45
1:A:234:MET:HA	1:A:237:ARG:HG2	1.98	0.45
1:C:12:ASP:HB2	1:C:13:PRO:HD3	1.98	0.45
1:C:266:CYS:SG	1:C:266:CYS:O	2.75	0.45
1:A:200:GLU:HA	1:A:205:LEU:O	2.17	0.45
1:A:34:VAL:HG23	1:A:66:LEU:HD13	1.97	0.45
1:B:151:PRO:O	1:B:154:ARG:HB2	2.16	0.45
1:C:180:ASN:ND2	1:C:185:GLU:HG3	2.32	0.45
1:B:234:MET:HA	1:B:237:ARG:HG2	1.98	0.45
1:D:394:VAL:O	1:D:398:LEU:HD13	2.17	0.45
1:D:234:MET:HA	1:D:237:ARG:HG2	1.98	0.45
1:B:175:ALA:N	1:B:176:PRO:HD2	2.32	0.45
1:A:114:LEU:HD23	1:A:115:GLU:N	2.32	0.44
1:D:231:ARG:HB3	1:D:234:MET:HG2	1.99	0.44
1:D:307:LEU:HD12	1:D:311:LEU:HB3	1.98	0.44
1:B:347:LEU:O	1:B:358:LYS:HG3	2.17	0.44
1:D:12:ASP:HB2	1:D:13:PRO:HD3	1.98	0.44
1:A:288:LYS:C	1:A:289:ARG:HD3	2.37	0.44
1:C:228:LEU:HD11	1:C:235:LEU:HA	1.98	0.44
1:D:17:MET:CE	1:D:18:GLU:HA	2.47	0.44
1:A:88:GLN:OE1	1:A:214:ASN:HB3	2.18	0.44
1:A:171:GLN:HE21	1:A:171:GLN:HA	1.82	0.44
1:C:248:ASP:HB2	1:C:250:ARG:H	1.82	0.44
1:B:221:ILE:HD13	1:B:224:MET:CE	2.47	0.44
1:B:235:LEU:HD23	1:B:235:LEU:O	2.17	0.44
1:D:11:ALA:HB2	1:D:409:GLN:HG3	1.98	0.44
1:B:49:CYS:SG	1:B:67:GLN:HA	2.58	0.44
1:D:175:ALA:N	1:D:176:PRO:HD2	2.32	0.44
1:C:114:LEU:HD12	1:C:156:TYR:CD1	2.53	0.44
1:A:85:MET:HE3	1:A:211:LEU:HA	2.00	0.44
1:B:208:GLU:OE1	1:B:208:GLU:HA	2.18	0.44
1:A:73:ARG:H	1:A:386:GLN:HE22	1.64	0.44
1:B:115:GLU:OE2	1:B:124:ARG:NH1	2.50	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:266:CYS:SG	1:B:266:CYS:O	2.76	0.44
1:B:168:PHE:HB3	1:C:111:MET:HE1	2.00	0.44
1:B:12:ASP:HB2	1:B:13:PRO:HD3	1.99	0.44
1:B:301:LEU:HA	1:B:304:GLN:HG2	1.99	0.44
1:D:403:GLU:O	1:D:406:ILE:HD12	2.18	0.43
1:C:221:ILE:HG21	1:C:224:MET:HB2	1.99	0.43
1:A:301:LEU:HD23	1:A:301:LEU:HA	1.91	0.43
1:B:344:ILE:O	1:B:361:LEU:HD12	2.17	0.43
1:C:29:GLN:NE2	1:D:160:GLY:HA2	2.33	0.43
1:D:151:PRO:O	1:D:154:ARG:HB2	2.17	0.43
1:D:115:GLU:OE2	1:D:124:ARG:NH1	2.50	0.43
1:C:207:LEU:HD11	1:C:266:CYS:O	2.18	0.43
1:D:311:LEU:O	1:D:314:GLN:HG3	2.18	0.43
1:C:66:LEU:HD12	1:C:66:LEU:O	2.18	0.43
1:B:231:ARG:HB3	1:B:234:MET:HG2	2.00	0.43
1:D:208:GLU:HA	1:D:208:GLU:OE1	2.17	0.43
1:D:141:THR:HG22	1:D:141:THR:O	2.18	0.43
1:D:290:ASP:OD2	1:D:292:LEU:HD13	2.17	0.43
1:C:231:ARG:HB3	1:C:234:MET:HG2	2.00	0.43
1:A:69:ASP:OD1	1:A:237:ARG:NH2	2.52	0.43
1:B:108:LEU:HD13	1:B:194:TRP:CE2	2.54	0.43
1:A:347:LEU:O	1:A:358:LYS:HG3	2.18	0.43
1:D:335:LEU:HD23	1:D:348:GLU:OE2	2.19	0.43
1:D:108:LEU:HD13	1:D:194:TRP:CE2	2.53	0.43
1:B:387:LEU:HD23	1:B:395:CYS:SG	2.59	0.43
1:C:350:LEU:HD13	1:C:356:ARG:CB	2.48	0.42
1:C:288:LYS:C	1:C:289:ARG:HD3	2.39	0.42
1:B:394:VAL:O	1:B:398:LEU:HD13	2.19	0.42
1:D:347:LEU:O	1:D:358:LYS:HG3	2.19	0.42
1:D:66:LEU:HD12	1:D:66:LEU:C	2.40	0.42
1:C:141:THR:HG22	1:C:141:THR:O	2.19	0.42
1:C:118:ASP:OD1	1:C:122:ASN:N	2.52	0.42
1:A:101:VAL:HG13	1:A:102:ASP:N	2.34	0.42
1:C:49:CYS:SG	1:C:67:GLN:HA	2.59	0.42
1:A:228:LEU:HD11	1:A:235:LEU:HA	2.01	0.42
1:D:228:LEU:HD11	1:D:235:LEU:HA	2.02	0.42
1:D:221:ILE:HG21	1:D:224:MET:HB2	2.02	0.42
1:B:97:LEU:CD2	1:B:134:LEU:HD12	2.49	0.42
1:C:403:GLU:O	1:C:406:ILE:HD12	2.20	0.42
1:B:280:MET:HE1	1:B:380:CYS:SG	2.60	0.42
1:D:387:LEU:HD23	1:D:395:CYS:SG	2.60	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:17:MET:HE2	1:C:17:MET:C	2.40	0.42
1:A:363:PHE:HB3	1:A:371:TRP:CZ2	2.54	0.42
1:C:108:LEU:HD13	1:C:194:TRP:CE2	2.54	0.42
1:D:394:VAL:HG23	1:D:395:CYS:N	2.34	0.41
1:C:301:LEU:HA	1:C:301:LEU:HD23	1.79	0.41
1:A:235:LEU:O	1:A:235:LEU:HD23	2.20	0.41
1:B:307:LEU:HD12	1:B:311:LEU:HB3	2.02	0.41
1:C:280:MET:HE1	1:C:283:LEU:HB2	2.01	0.41
1:A:217:ALA:HB3	1:A:218:PRO:CD	2.44	0.41
1:C:175:ALA:N	1:C:176:PRO:HD2	2.35	0.41
1:D:148:PHE:HA	1:D:154:ARG:HD3	2.02	0.41
1:A:287:LEU:HD22	1:A:380:CYS:HB3	2.02	0.41
1:A:350:LEU:HD13	1:A:356:ARG:CB	2.49	0.41
1:B:176:PRO:HA	1:B:177:PRO:HD3	1.89	0.41
1:A:207:LEU:HD11	1:A:266:CYS:O	2.21	0.41
1:A:266:CYS:O	1:A:266:CYS:SG	2.79	0.41
1:D:114:LEU:CD2	1:D:114:LEU:C	2.87	0.41
1:B:280:MET:HE2	1:B:380:CYS:SG	2.60	0.41
1:A:221:ILE:HG21	1:A:224:MET:HB2	2.03	0.41
1:D:335:LEU:CD2	1:D:348:GLU:HG2	2.51	0.41
1:C:244:ARG:HH21	1:D:157:MET:HE3	1.85	0.41
1:B:291:GLY:HA2	1:B:294:LEU:O	2.21	0.41
1:A:208:GLU:HA	1:A:208:GLU:OE1	2.21	0.41
1:C:249:GLY:O	1:D:157:MET:HE3	2.20	0.41
1:B:217:ALA:HB3	1:B:218:PRO:CD	2.42	0.41
1:D:235:LEU:O	1:D:235:LEU:HD23	2.21	0.41
1:C:17:MET:HE1	1:C:18:GLU:HA	2.01	0.41
1:C:148:PHE:HZ	1:D:244:ARG:CD	2.33	0.41
1:D:244:ARG:NH1	1:D:387:LEU:HD21	2.36	0.41
1:B:290:ASP:OD2	1:B:292:LEU:HD13	2.21	0.41
1:C:151:PRO:O	1:C:154:ARG:HB2	2.21	0.41
1:C:176:PRO:HA	1:C:177:PRO:HD3	1.91	0.41
1:C:165:ALA:HB1	1:C:170:ILE:HB	2.03	0.41
1:B:103:ARG:CZ	1:B:104:LEU:HD21	2.51	0.41
1:D:350:LEU:HD13	1:D:356:ARG:CB	2.49	0.41
1:A:335:LEU:HD23	1:A:348:GLU:OE2	2.20	0.41
1:A:115:GLU:OE2	1:A:124:ARG:NH1	2.55	0.40
1:B:66:LEU:C	1:B:66:LEU:CD1	2.90	0.40
1:A:180:ASN:OD1	1:A:181:ASP:N	2.47	0.40
1:A:150:HIS:HA	1:A:151:PRO:HD3	1.95	0.40
1:B:335:LEU:HD23	1:B:348:GLU:OE2	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:141:THR:O	1:A:141:THR:HG22	2.21	0.40
1:B:69:ASP:OD1	1:B:237:ARG:NH2	2.54	0.40
1:D:307:LEU:HB2	1:D:338:SER:OG	2.22	0.40
1:D:123:ALA:HB2	1:D:161:HIS:CD2	2.56	0.40
1:D:176:PRO:HA	1:D:177:PRO:HD3	1.90	0.40
1:B:335:LEU:CD2	1:B:348:GLU:HG2	2.51	0.40
1:B:35:ILE:HD12	1:B:402:PHE:CD1	2.57	0.40
1:A:408:ALA:HA	1:A:412:GLN:NE2	2.36	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	389/432 (90%)	354 (91%)	31 (8%)	4 (1%)	19	63
1	B	389/432 (90%)	354 (91%)	32 (8%)	3 (1%)	24	67
1	C	389/432 (90%)	359 (92%)	27 (7%)	3 (1%)	24	67
1	D	389/432 (90%)	357 (92%)	30 (8%)	2 (0%)	34	75
All	All	1556/1728 (90%)	1424 (92%)	120 (8%)	12 (1%)	24	67

All (12) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	289	ARG
1	D	289	ARG
1	A	296	PRO
1	C	289	ARG
1	D	296	PRO
1	A	332	PRO
1	B	296	PRO

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Mol	Chain	Res	Type
1	A	366	GLY
1	C	296	PRO
1	C	366	GLY
1	B	332	PRO
1	B	366	GLY

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	326/356 (92%)	292 (90%)	34 (10%)	9	37
1	B	326/356 (92%)	290 (89%)	36 (11%)	8	34
1	C	326/356 (92%)	290 (89%)	36 (11%)	8	34
1	D	326/356 (92%)	294 (90%)	32 (10%)	10	40
All	All	1304/1424 (92%)	1166 (89%)	138 (11%)	8	36

All (138) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	17	MET
1	A	28	ARG
1	A	47	THR
1	A	62	GLN
1	A	63	LEU
1	A	66	LEU
1	A	76	SER
1	A	109	SER
1	A	144	LEU
1	A	157	MET
1	A	171	GLN
1	A	191	ASN
1	A	192	LEU
1	A	201	ARG
1	A	207	LEU
1	A	222	THR

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Mol	Chain	Res	Type
1	A	229	GLN
1	A	233	ASP
1	A	245	ASN
1	A	246	SER
1	A	248	ASP
1	A	251	LEU
1	A	270	GLN
1	A	274	SER
1	A	289	ARG
1	A	290	ASP
1	A	293	LEU
1	A	310	ARG
1	A	312	GLU
1	A	314	GLN
1	A	335	LEU
1	A	337	ARG
1	A	373	ILE
1	A	400	ARG
1	B	17	MET
1	B	28	ARG
1	B	47	THR
1	B	62	GLN
1	B	63	LEU
1	B	66	LEU
1	B	76	SER
1	B	109	SER
1	B	144	LEU
1	B	157	MET
1	B	171	GLN
1	B	172	SER
1	B	191	ASN
1	B	192	LEU
1	B	201	ARG
1	B	207	LEU
1	B	222	THR
1	B	229	GLN
1	B	233	ASP
1	B	245	ASN
1	B	246	SER
1	B	248	ASP
1	B	251	LEU
1	B	270	GLN

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Mol	Chain	Res	Type
1	B	274	SER
1	B	289	ARG
1	B	290	ASP
1	B	293	LEU
1	B	310	ARG
1	B	312	GLU
1	B	314	GLN
1	B	335	LEU
1	B	337	ARG
1	B	349	ASP
1	B	373	ILE
1	B	400	ARG
1	C	17	MET
1	C	28	ARG
1	C	47	THR
1	C	63	LEU
1	C	66	LEU
1	C	76	SER
1	C	103	ARG
1	C	144	LEU
1	C	157	MET
1	C	171	GLN
1	C	172	SER
1	C	191	ASN
1	C	192	LEU
1	C	201	ARG
1	C	207	LEU
1	C	222	THR
1	C	229	GLN
1	C	233	ASP
1	C	245	ASN
1	C	246	SER
1	C	248	ASP
1	C	251	LEU
1	C	270	GLN
1	C	274	SER
1	C	289	ARG
1	C	290	ASP
1	C	293	LEU
1	C	310	ARG
1	C	312	GLU
1	C	314	GLN

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Mol	Chain	Res	Type
1	C	335	LEU
1	C	337	ARG
1	C	349	ASP
1	C	373	ILE
1	C	400	ARG
1	C	409	GLN
1	D	17	MET
1	D	28	ARG
1	D	47	THR
1	D	63	LEU
1	D	66	LEU
1	D	76	SER
1	D	144	LEU
1	D	157	MET
1	D	171	GLN
1	D	191	ASN
1	D	192	LEU
1	D	201	ARG
1	D	207	LEU
1	D	222	THR
1	D	229	GLN
1	D	233	ASP
1	D	245	ASN
1	D	246	SER
1	D	248	ASP
1	D	251	LEU
1	D	270	GLN
1	D	274	SER
1	D	289	ARG
1	D	290	ASP
1	D	293	LEU
1	D	310	ARG
1	D	312	GLU
1	D	314	GLN
1	D	335	LEU
1	D	337	ARG
1	D	373	ILE
1	D	400	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (30) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	150	HIS
1	A	171	GLN
1	A	229	GLN
1	A	270	GLN
1	A	284	HIS
1	A	314	GLN
1	A	386	GLN
1	A	412	GLN
1	B	150	HIS
1	B	171	GLN
1	B	229	GLN
1	B	270	GLN
1	B	284	HIS
1	B	314	GLN
1	B	386	GLN
1	C	29	GLN
1	C	163	GLN
1	C	171	GLN
1	C	229	GLN
1	C	270	GLN
1	C	284	HIS
1	C	314	GLN
1	C	386	GLN
1	D	29	GLN
1	D	163	GLN
1	D	171	GLN
1	D	229	GLN
1	D	284	HIS
1	D	314	GLN
1	D	386	GLN

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

There are no ligands in this entry.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	393/432 (90%)	0.01	1 (0%) 94 92	4, 6, 7, 36	0
1	B	393/432 (90%)	0.14	5 (1%) 79 74	4, 6, 7, 49	0
1	C	393/432 (90%)	0.19	6 (1%) 76 71	5, 6, 7, 66	0
1	D	393/432 (90%)	0.36	10 (2%) 61 55	5, 6, 7, 71	0
All	All	1572/1728 (90%)	0.17	22 (1%) 78 73	4, 6, 7, 71	0

All (22) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	10	ALA	5.6
1	C	10	ALA	5.0
1	B	413	GLY	3.5
1	B	10	ALA	3.5
1	C	60	ASN	3.4
1	C	413	GLY	3.4
1	D	42	GLY	2.9
1	C	62	GLN	2.8
1	D	59	GLU	2.7
1	D	297	GLN	2.6
1	D	43	ASN	2.6
1	D	298	THR	2.3
1	D	413	GLY	2.2
1	C	410	TYR	2.2
1	A	10	ALA	2.2
1	B	11	ALA	2.2
1	D	58	ASP	2.1
1	D	11	ALA	2.1
1	D	163	GLN	2.1
1	B	229	GLN	2.1
1	B	62	GLN	2.0
1	C	58	ASP	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 carbohydrates in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.