



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 11:02 AM GMT

PDB ID : 3NO9
Title : Crystal Structure of apo fumarate hydratase from Mycobacterium tuberculosis
Authors : Li, H.; Swanson, S.; Yu, M.; Hung, L.-W.; Sacchettini, J.C.; TB Structural Genomics Consortium (TBSGC)
Deposited on : 2010-06-25
Resolution : 2.48 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

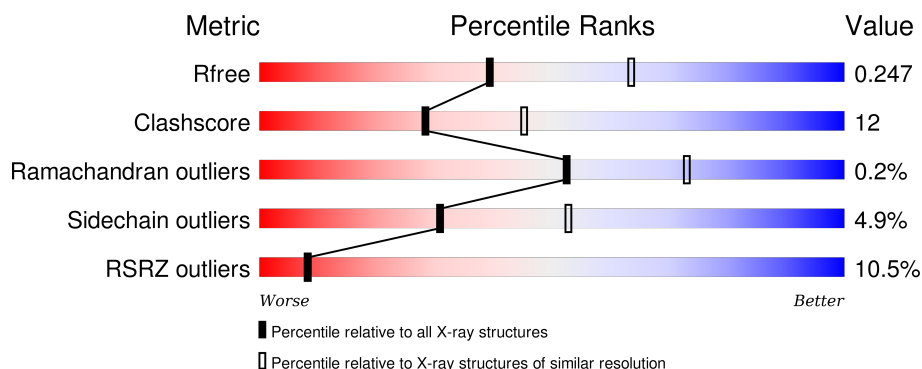
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.48 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	4309 (2.50-2.46)
Clashscore	102246	5050 (2.50-2.46)
Ramachandran outliers	100387	4961 (2.50-2.46)
Sidechain outliers	100360	4963 (2.50-2.46)
RSRZ outliers	91569	4319 (2.50-2.46)

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	475	<div> <div>15%</div> <div>78%</div> <div>15%</div> <div>5%</div> </div>
1	B	475	<div> <div>6%</div> <div>79%</div> <div>14%</div> <div>5%</div> </div>
1	C	475	<div> <div>14%</div> <div>75%</div> <div>17%</div> <div>5%</div> </div>
1	D	475	<div> <div>5%</div> <div>78%</div> <div>14%</div> <div>5%</div> </div>

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 13623 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 Fumarate hydratase class II.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	453	Total	C	N	O	S	38	1	0
			3363	2095	609	648	11			
1	B	452	Total	C	N	O	S	16	1	0
			3357	2092	608	646	11			
1	C	453	Total	C	N	O	S	13	1	0
			3368	2098	611	648	11			
1	D	452	Total	C	N	O	S	13	1	0
			3357	2092	608	646	11			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	SER	-	EXPRESSION TAG	UNP O53446
B	0	SER	-	EXPRESSION TAG	UNP O53446
C	0	SER	-	EXPRESSION TAG	UNP O53446
D	0	SER	-	EXPRESSION TAG	UNP O53446

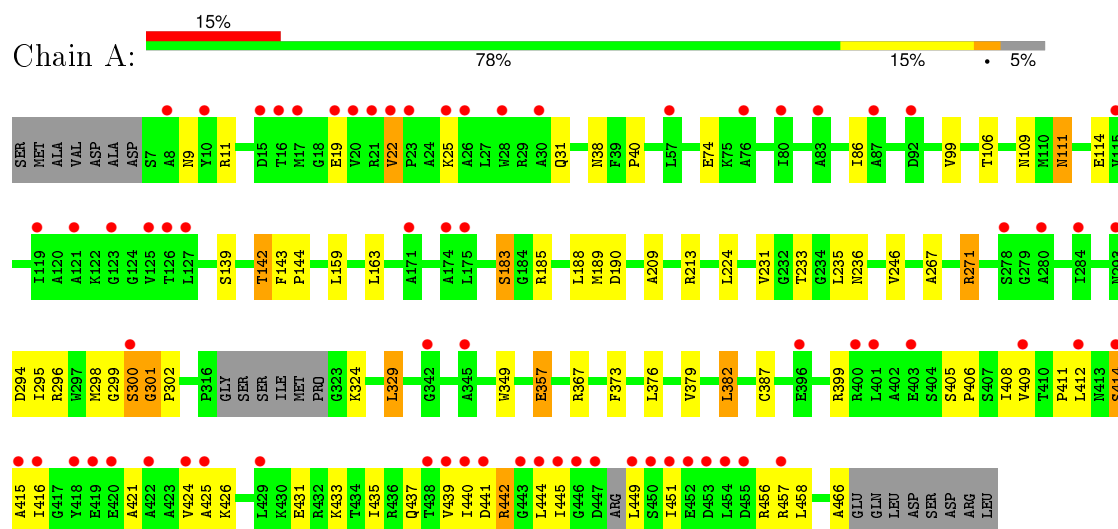
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	37	Total	O	0	0
			37	37		
2	B	55	Total	O	0	0
			55	55		
2	C	38	Total	O	0	0
			38	38		
2	D	48	Total	O	0	0
			48	48		

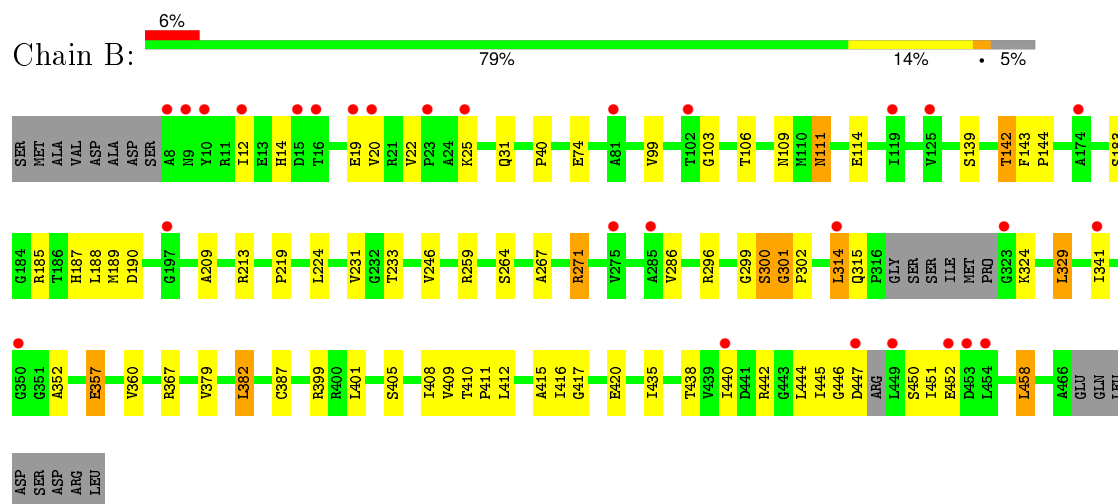
3 Residue-property plots

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.

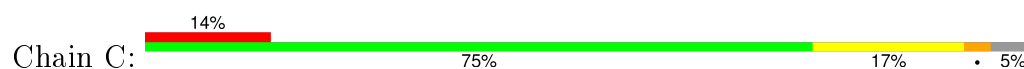
• Molecule 1: Fumarate hydratase class II

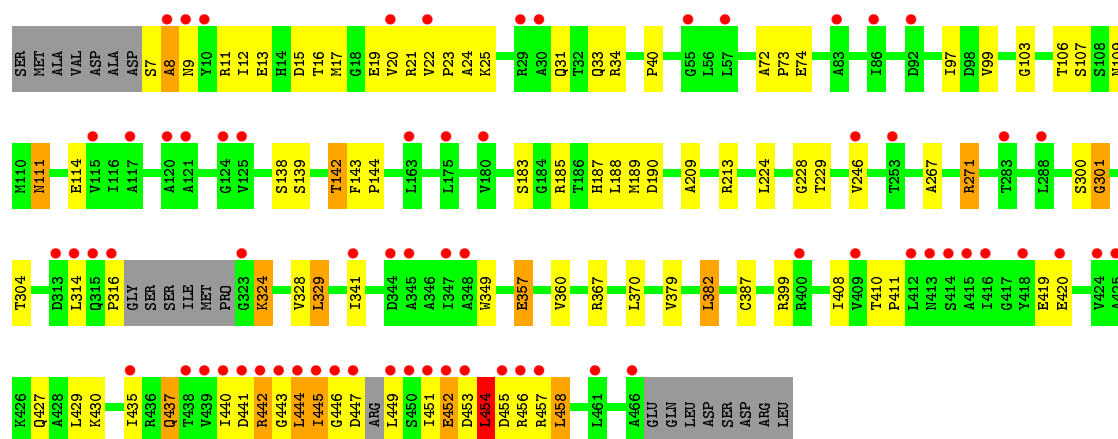


• Molecule 1: Fumarate hydratase class II

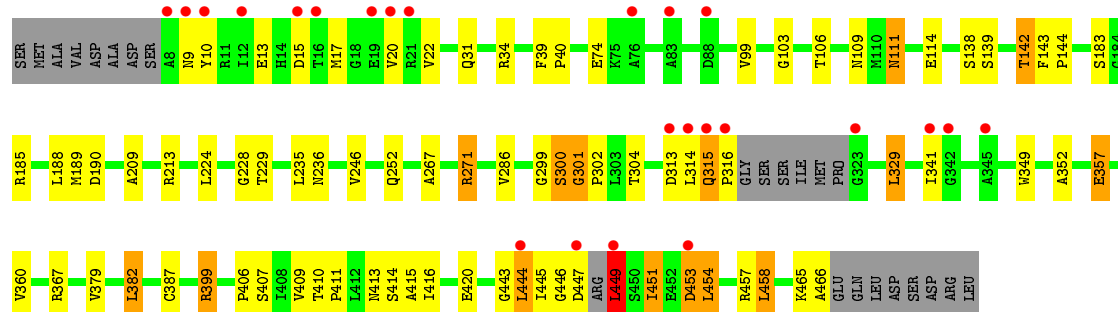
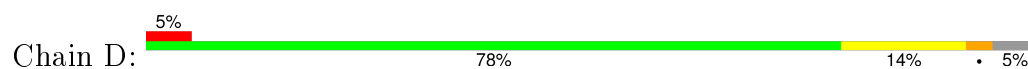


• Molecule 1: Fumarate hydratase class II





• Molecule 1: Fumarate hydratase class II



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	271.22Å 96.56Å 89.89Å 90.00° 102.99° 90.00°	Depositor
Resolution (Å)	48.52 – 2.48 48.52 – 2.48	Depositor EDS
% Data completeness (in resolution range)	88.4 (48.52-2.48) 88.4 (48.52-2.48)	Depositor EDS
R_{merge}	0.15	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.87 (at 2.48Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE: 1.6.1_357)	Depositor
R, R_{free}	0.206 , 0.241 0.213 , 0.247	Depositor DCC
R_{free} test set	3534 reflections (5.26%)	DCC
Wilson B-factor (Å ²)	41.0	Xtriage
Anisotropy	0.341	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 47.2	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	0 of 70733 reflections	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	13623	wwPDB-VP
Average B, all atoms (Å ²)	52.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.10% 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

5.1 Standard geometry

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	A	0.41	0/3411	0.54	1/4635 (0.0%)
1	B	0.42	0/3405	0.56	3/4627 (0.1%)
1	C	0.42	1/3417 (0.0%)	0.58	3/4643 (0.1%)
1	D	0.43	0/3405	0.56	2/4627 (0.0%)
All	All	0.42	1/13638 (0.0%)	0.56	9/18532 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	3
1	B	0	4
1	C	0	3
1	D	0	3
All	All	0	13

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	441	ASP	C-N	-5.83	1.20	1.34

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	12	ILE	CB-CA-C	5.98	123.56	111.60
1	C	452	GLU	CB-CA-C	5.97	122.34	110.40
1	A	456	ARG	N-CA-CB	-5.96	99.88	110.60
1	B	314	LEU	CA-CB-CG	-5.84	101.86	115.30
1	D	449	LEU	CA-CB-CG	-5.78	102.02	115.30
1	C	441	ASP	O-C-N	-5.58	113.77	122.70
1	C	441	ASP	CB-CA-C	5.54	121.48	110.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	12	ILE	N-CA-C	-5.36	96.54	111.00
1	D	449	LEU	CB-CG-CD2	-5.01	102.47	111.00

There are no chirality outliers.

All (13) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	299	GLY	Peptide
1	A	300	SER	Peptide
1	A	301	GLY	Peptide
1	B	299	GLY	Peptide
1	B	300	SER	Peptide
1	B	301	GLY	Peptide
1	B	415	ALA	Peptide
1	C	300	SER	Peptide
1	C	301	GLY	Peptide
1	C	8	ALA	Peptide
1	D	299	GLY	Peptide
1	D	300	SER	Peptide
1	D	301	GLY	Peptide

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	3363	0	3399	100	0
1	B	3357	0	3394	66	0
1	C	3368	0	3403	109	0
1	D	3357	0	3394	91	0
2	A	37	0	0	3	0
2	B	55	0	0	4	0
2	C	38	0	0	2	0
2	D	48	0	0	5	0
All	All	13623	0	13590	313	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 12.

All (313) 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:22:VAL:HG12	1:C:33:GLN:OE1	1.24	1.26
1:C:437:GLN:NE2	1:C:440:ILE:HD12	1.59	1.16
1:C:324:LYS:HB3	1:C:324:LYS:HZ2	1.19	1.05
1:A:415:ALA:HB1	1:A:449:LEU:HD13	1.39	1.04
1:C:22:VAL:CG1	1:C:33:GLN:OE1	2.08	1.02
1:C:324:LYS:HB3	1:C:324:LYS:NZ	1.74	0.99
1:D:449:LEU:HD23	1:D:449:LEU:N	1.72	0.99
1:D:449:LEU:N	1:D:449:LEU:CD2	2.29	0.95
1:C:13:GLU:HB3	1:C:20:VAL:CG2	1.97	0.94
1:C:437:GLN:HE22	1:C:440:ILE:HD12	1.27	0.94
1:C:22:VAL:HB	1:C:23:PRO:HD2	1.49	0.92
1:A:295:ILE:HA	1:A:298:MET:CE	2.01	0.91
1:C:17:MET:SD	1:D:315:GLN:O	2.28	0.91
1:A:295:ILE:HA	1:A:298:MET:HE3	1.53	0.90
1:C:22:VAL:HG12	1:C:33:GLN:CD	1.93	0.89
1:D:449:LEU:O	1:D:449:LEU:HD23	1.72	0.88
1:B:189:MET:CE	1:C:301:GLY:HA2	2.04	0.87
1:A:99:VAL:HG11	1:A:367:ARG:HD2	1.58	0.85
1:A:294:ASP:O	1:A:298:MET:HG3	1.77	0.85
1:D:314:LEU:C	1:D:316:PRO:CD	2.45	0.85
1:C:21:ARG:O	1:C:21:ARG:HG2	1.78	0.84
1:B:99:VAL:HG11	1:B:367:ARG:HD2	1.59	0.82
1:D:99:VAL:HG11	1:D:367:ARG:HD2	1.61	0.82
1:C:446:GLY:N	1:C:449:LEU:O	2.10	0.82
1:D:315:GLN:N	1:D:316:PRO:CD	2.43	0.81
1:D:449:LEU:O	1:D:449:LEU:CD2	2.30	0.80
1:D:314:LEU:C	1:D:316:PRO:HD2	2.00	0.80
1:D:445:ILE:HG21	1:D:451:ILE:HG13	1.64	0.80
1:A:439:VAL:O	1:A:444:LEU:HD13	1.82	0.80
1:C:437:GLN:HA	1:C:437:GLN:HE21	1.48	0.79
1:D:314:LEU:O	1:D:316:PRO:HD2	1.83	0.79
1:B:14:HIS:HA	1:B:19:GLU:HG2	1.65	0.78
1:A:415:ALA:CB	1:A:449:LEU:HD13	2.13	0.78
1:C:445:ILE:HD12	1:C:445:ILE:H	1.49	0.77
1:B:302:PRO:HD2	1:C:190:ASP:OD2	1.85	0.77
1:C:99:VAL:HG11	1:C:367:ARG:HD2	1.67	0.76
1:A:324:LYS:HB3	1:A:324:LYS:NZ	2.02	0.75
1:D:209:ALA:O	1:D:213:ARG:HG2	1.85	0.75
1:B:445:ILE:HD13	1:B:451:ILE:HG12	1.69	0.75
1:C:34:ARG:NE	2:C:497:HOH:O	2.20	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:445:ILE:HD11	1:D:454:LEU:HD12	1.70	0.73
1:A:190:ASP:OD2	1:D:302:PRO:HD2	1.87	0.73
1:A:324:LYS:HB3	1:A:324:LYS:HZ3	1.54	0.72
1:D:106:THR:HA	1:D:139:SER:OG	1.90	0.72
1:B:189:MET:HE1	1:C:301:GLY:HA2	1.71	0.72
1:B:106:THR:HA	1:B:139:SER:OG	1.90	0.72
1:A:324:LYS:CB	1:A:324:LYS:NZ	2.53	0.71
1:A:439:VAL:HG13	1:A:444:LEU:HD22	1.72	0.71
1:A:106:THR:HA	1:A:139:SER:OG	1.89	0.71
1:D:314:LEU:C	1:D:316:PRO:HD3	2.11	0.70
1:A:159:LEU:HD22	1:A:373:PHE:CD1	2.27	0.70
1:C:106:THR:HA	1:C:139:SER:OG	1.91	0.69
1:A:300:SER:HB2	1:D:188:LEU:HB3	1.74	0.69
1:C:209:ALA:O	1:C:213:ARG:HG2	1.91	0.69
1:C:442:ARG:HB3	1:C:444:LEU:HD23	1.73	0.69
1:A:442:ARG:HB2	1:A:444:LEU:HD11	1.75	0.67
1:A:301:GLY:CA	1:D:189:MET:CE	2.72	0.67
1:A:444:LEU:HD12	1:A:444:LEU:N	2.09	0.67
1:C:454:LEU:O	1:C:456:ARG:N	2.29	0.66
1:A:209:ALA:O	1:A:213:ARG:HG2	1.95	0.66
1:B:189:MET:CE	1:C:301:GLY:CA	2.74	0.66
1:B:189:MET:HA	1:C:301:GLY:HA3	1.76	0.65
1:C:442:ARG:HB3	1:C:444:LEU:CD2	2.25	0.65
1:C:7:SER:OG	1:C:8:ALA:N	2.30	0.65
1:C:453:ASP:O	1:C:456:ARG:HB3	1.97	0.64
1:D:313:ASP:O	1:D:316:PRO:HD3	1.97	0.64
1:A:295:ILE:HA	1:A:298:MET:HE2	1.78	0.64
1:D:454:LEU:HD22	1:D:458:LEU:HD22	1.79	0.64
1:C:329:LEU:HD23	1:C:387:CYS:HB2	1.80	0.63
1:B:209:ALA:O	1:B:213:ARG:HG2	1.98	0.63
1:A:382:LEU:HD21	1:B:40:PRO:HD2	1.80	0.63
1:A:301:GLY:HA2	1:D:189:MET:CE	2.29	0.63
1:B:267:ALA:O	1:B:271:ARG:NH2	2.32	0.62
1:A:445:ILE:HG23	1:A:449:LEU:O	2.00	0.62
1:C:9:ASN:OD1	1:C:9:ASN:C	2.34	0.62
1:C:437:GLN:CA	1:C:437:GLN:HE21	2.13	0.62
1:C:440:ILE:HA	1:C:445:ILE:HD11	1.82	0.62
1:D:449:LEU:O	1:D:449:LEU:CG	2.48	0.62
1:D:267:ALA:O	1:D:271:ARG:NH2	2.31	0.62
1:D:9:ASN:OD1	1:D:10:TYR:CE2	2.53	0.61
1:C:437:GLN:HA	1:C:437:GLN:NE2	2.16	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:185:ARG:O	1:D:357:GLU:HG2	2.01	0.61
1:A:267:ALA:O	1:A:271:ARG:NH2	2.34	0.60
1:C:437:GLN:HE22	1:C:440:ILE:CD1	2.08	0.60
1:C:13:GLU:HB3	1:C:20:VAL:HG23	1.83	0.60
1:A:442:ARG:C	1:A:444:LEU:HD12	2.21	0.60
1:A:442:ARG:HG3	1:A:444:LEU:HD11	1.83	0.59
1:B:187:HIS:O	1:B:188:LEU:HB2	2.02	0.59
1:B:189:MET:SD	1:C:301:GLY:CA	2.91	0.59
1:A:301:GLY:N	1:D:189:MET:SD	2.75	0.59
1:A:440:ILE:HG12	1:A:445:ILE:HD12	1.84	0.59
1:B:219:PRO:HA	2:B:527:HOH:O	2.02	0.59
1:A:442:ARG:CB	1:A:444:LEU:HD11	2.31	0.59
1:D:444:LEU:O	1:D:449:LEU:HD21	2.03	0.59
1:B:357:GLU:HG2	1:D:185:ARG:O	2.03	0.59
1:D:446:GLY:O	1:D:447:ASP:HB2	2.03	0.58
1:C:453:ASP:HA	1:C:456:ARG:HE	1.67	0.58
1:A:426:LYS:O	1:A:426:LYS:HD3	2.04	0.58
1:D:329:LEU:HD23	1:D:387:CYS:HB2	1.86	0.58
1:D:454:LEU:CD2	1:D:458:LEU:HD22	2.34	0.58
1:C:324:LYS:CB	1:C:324:LYS:NZ	2.49	0.57
1:A:444:LEU:H	1:A:444:LEU:CD1	2.17	0.57
1:A:302:PRO:HD2	1:D:190:ASP:OD2	2.04	0.57
1:C:454:LEU:C	1:C:456:ARG:H	2.08	0.57
1:C:382:LEU:HD21	1:D:40:PRO:HD2	1.86	0.57
1:C:17:MET:HG3	1:C:34:ARG:NH1	2.19	0.57
1:B:213:ARG:NH1	2:B:478:HOH:O	2.37	0.57
1:D:20:VAL:CG1	1:D:34:ARG:HE	2.16	0.57
1:A:301:GLY:HA2	1:D:189:MET:HE1	1.85	0.57
1:B:329:LEU:HD23	1:B:387:CYS:HB2	1.86	0.57
1:A:444:LEU:HD12	1:A:444:LEU:H	1.69	0.56
1:D:315:GLN:N	1:D:316:PRO:HD3	2.20	0.56
1:C:349:TRP:CZ3	1:D:341:ILE:HD13	2.40	0.56
1:C:328:VAL:HG11	1:D:39:PHE:HZ	1.71	0.56
1:A:142:THR:HG22	1:A:143:PHE:N	2.19	0.56
1:A:301:GLY:HA3	1:D:189:MET:HE3	1.86	0.56
1:A:189:MET:HE1	1:D:301:GLY:HA2	1.87	0.56
1:B:408:ILE:O	1:B:411:PRO:HD2	2.05	0.56
1:A:324:LYS:CB	1:A:324:LYS:HZ2	2.16	0.56
1:C:454:LEU:C	1:C:456:ARG:N	2.59	0.56
1:B:31:GLN:HB2	1:B:114:GLU:OE2	2.06	0.56
1:A:295:ILE:CG1	1:A:298:MET:HE2	2.36	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:21:ARG:CG	1:C:21:ARG:O	2.51	0.56
1:D:9:ASN:OD1	1:D:10:TYR:CD2	2.59	0.56
1:C:267:ALA:O	1:C:271:ARG:NH2	2.39	0.55
1:D:224:LEU:HD12	1:D:246:VAL:HG22	1.87	0.55
1:C:411:PRO:HB2	1:C:457:ARG:HB3	1.87	0.55
1:D:31:GLN:HB2	1:D:114:GLU:OE2	2.07	0.54
1:A:295:ILE:HG12	1:A:298:MET:CE	2.37	0.54
1:C:12:ILE:HA	1:C:21:ARG:HA	1.89	0.54
1:B:445:ILE:HG21	1:B:451:ILE:HG12	1.88	0.54
1:A:442:ARG:CG	1:A:444:LEU:HD11	2.38	0.54
1:D:406:PRO:O	1:D:409:VAL:HG22	2.08	0.54
1:B:324:LYS:HG2	1:B:324:LYS:O	2.06	0.54
1:A:11:ARG:HH21	1:A:22:VAL:HG21	1.73	0.54
1:A:31:GLN:HB2	1:A:114:GLU:OE2	2.07	0.54
1:A:329:LEU:HD23	1:A:387:CYS:HB2	1.88	0.54
1:D:315:GLN:NE2	2:D:513:HOH:O	2.40	0.54
1:A:349:TRP:CZ3	1:B:341:ILE:HD13	2.43	0.54
1:D:449:LEU:HD22	1:D:449:LEU:N	2.22	0.54
1:B:189:MET:SD	1:C:301:GLY:N	2.81	0.54
1:B:25:LYS:O	1:B:25:LYS:HD2	2.08	0.53
1:A:189:MET:CE	1:D:301:GLY:HA2	2.38	0.53
1:B:264:SER:HB2	2:B:492:HOH:O	2.08	0.53
1:A:411:PRO:HB2	1:A:457:ARG:HB3	1.91	0.53
1:A:159:LEU:HD22	1:A:373:PHE:HD1	1.69	0.53
1:A:440:ILE:HG13	1:A:445:ILE:HD11	1.91	0.53
1:C:19:GLU:HG3	1:C:19:GLU:O	2.09	0.53
1:C:15:ASP:OD2	1:C:16:THR:N	2.39	0.53
1:A:349:TRP:CH2	1:B:341:ILE:HD13	2.44	0.52
1:C:408:ILE:O	1:C:411:PRO:HD2	2.09	0.52
1:C:31:GLN:HB2	1:C:114:GLU:OE2	2.10	0.52
1:B:224:LEU:HD12	1:B:246:VAL:HG22	1.92	0.52
1:D:415:ALA:HB2	1:D:457:ARG:CZ	2.40	0.52
1:D:252:GLN:NE2	2:D:515:HOH:O	2.23	0.52
1:B:143:PHE:N	1:B:144:PRO:HD2	2.24	0.52
1:C:11:ARG:N	1:C:22:VAL:O	2.42	0.51
1:C:143:PHE:N	1:C:144:PRO:HD2	2.25	0.51
1:C:22:VAL:HB	1:C:23:PRO:CD	2.31	0.51
1:A:231:VAL:HG23	1:A:233:THR:HG23	1.91	0.51
1:A:406:PRO:O	1:A:409:VAL:HG22	2.11	0.51
1:A:444:LEU:N	1:A:444:LEU:CD1	2.72	0.51
1:C:349:TRP:CH2	1:D:341:ILE:HD13	2.46	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:111:ASN:C	1:D:111:ASN:HD22	2.13	0.51
1:B:416:ILE:HB	1:B:420:GLU:HB2	1.93	0.51
1:A:301:GLY:HA3	1:D:189:MET:CE	2.39	0.51
1:A:301:GLY:CA	1:D:189:MET:SD	2.99	0.51
1:B:259:ARG:NH2	2:B:527:HOH:O	2.42	0.51
1:B:111:ASN:HD22	1:B:111:ASN:C	2.14	0.51
1:A:224:LEU:HD12	1:A:246:VAL:HG22	1.91	0.51
1:C:13:GLU:HB3	1:C:20:VAL:HG22	1.88	0.50
1:C:109:ASN:OD1	1:C:142:THR:HG21	2.11	0.50
1:C:111:ASN:HD22	1:C:111:ASN:C	2.12	0.50
1:B:442:ARG:HB2	1:B:444:LEU:CD2	2.41	0.50
1:D:413:ASN:O	1:D:416:ILE:O	2.29	0.50
1:D:445:ILE:HD13	1:D:451:ILE:HG13	1.93	0.50
1:A:405:SER:O	1:A:408:ILE:HG12	2.11	0.50
1:A:189:MET:CE	1:D:301:GLY:CA	2.90	0.50
1:C:34:ARG:CZ	2:C:497:HOH:O	2.58	0.49
1:A:367:ARG:HG2	1:A:367:ARG:HH11	1.77	0.49
1:C:446:GLY:O	1:C:447:ASP:HB2	2.12	0.49
1:B:187:HIS:O	1:B:188:LEU:CB	2.60	0.49
1:D:142:THR:HG22	1:D:143:PHE:N	2.26	0.49
1:A:440:ILE:HG12	1:A:445:ILE:CD1	2.42	0.49
1:A:301:GLY:CA	1:D:189:MET:HE3	2.41	0.49
1:B:438:THR:O	1:B:442:ARG:HG3	2.13	0.49
1:D:143:PHE:N	1:D:144:PRO:HD2	2.27	0.49
1:B:109:ASN:OD1	1:B:142:THR:HG21	2.13	0.49
1:A:445:ILE:HD13	1:A:451:ILE:HG12	1.95	0.48
1:D:449:LEU:O	1:D:449:LEU:HG	2.12	0.48
1:B:301:GLY:HA2	1:C:189:MET:CE	2.42	0.48
1:A:40:PRO:HD2	1:B:382:LEU:HD21	1.93	0.48
1:C:138:SER:HB3	1:C:229:THR:HA	1.94	0.48
1:A:445:ILE:HG21	1:A:451:ILE:HG13	1.95	0.48
1:C:410:THR:N	1:C:411:PRO:CD	2.77	0.48
1:A:295:ILE:HG13	1:A:298:MET:HE2	1.95	0.47
1:A:185:ARG:O	1:C:357:GLU:HG2	2.14	0.47
1:B:352:ALA:HA	1:D:286:VAL:HG13	1.96	0.47
1:D:329:LEU:HA	1:D:329:LEU:HD12	1.80	0.47
1:D:20:VAL:HG13	1:D:34:ARG:HE	1.79	0.47
1:C:420:GLU:OE2	1:C:444:LEU:HD21	2.14	0.47
1:A:143:PHE:N	1:A:144:PRO:HD2	2.30	0.47
1:C:224:LEU:HD12	1:C:246:VAL:HG22	1.95	0.47
1:D:315:GLN:O	1:D:316:PRO:C	2.51	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:367:ARG:HG2	1:C:367:ARG:HH11	1.80	0.46
1:A:409:VAL:O	1:A:412:LEU:HB2	2.14	0.46
1:A:466:ALA:N	2:A:495:HOH:O	2.47	0.46
1:B:324:LYS:CG	1:B:324:LYS:O	2.63	0.46
1:C:20:VAL:HB	1:C:33:GLN:HG2	1.98	0.46
1:A:295:ILE:CG1	1:A:298:MET:CE	2.94	0.46
1:C:103:GLY:HA3	1:C:360:VAL:HB	1.97	0.46
1:D:109:ASN:OD1	1:D:142:THR:HG21	2.16	0.46
1:D:410:THR:OG1	1:D:411:PRO:HD3	2.16	0.46
1:B:296:ARG:HG3	1:C:188:LEU:HD12	1.96	0.46
1:A:433:LYS:HE2	1:A:441:ASP:OD2	2.16	0.46
1:D:235:LEU:O	1:D:236:ASN:HB2	2.15	0.46
1:C:451:ILE:H	1:C:451:ILE:HG13	1.51	0.46
1:B:409:VAL:O	1:B:412:LEU:HB2	2.16	0.46
1:B:440:ILE:HG12	1:B:445:ILE:HD12	1.97	0.45
1:C:187:HIS:O	1:C:188:LEU:HB2	2.15	0.45
1:C:454:LEU:O	1:C:457:ARG:N	2.49	0.45
1:D:445:ILE:CG2	1:D:451:ILE:HG13	2.42	0.45
1:A:440:ILE:CG1	1:A:445:ILE:HD11	2.47	0.45
1:A:235:LEU:O	1:A:236:ASN:HB2	2.15	0.45
1:D:15:ASP:OD1	1:D:34:ARG:NH1	2.49	0.45
1:B:142:THR:HG22	1:B:143:PHE:N	2.31	0.45
1:B:367:ARG:HG2	1:B:367:ARG:HH11	1.81	0.45
1:D:453:ASP:O	1:D:457:ARG:HG3	2.17	0.45
1:A:433:LYS:HE3	1:A:437:GLN:HG3	1.98	0.45
1:A:38:ASN:HD21	1:B:315:GLN:HG3	1.82	0.45
1:A:412:LEU:O	1:A:416:ILE:HG12	2.17	0.45
1:B:301:GLY:HA2	1:C:189:MET:HE1	1.99	0.45
1:D:414:SER:OG	1:D:457:ARG:NH2	2.50	0.44
1:C:22:VAL:CB	1:C:23:PRO:HD2	2.24	0.44
1:C:328:VAL:HG11	1:D:39:PHE:CZ	2.51	0.44
1:A:439:VAL:HG13	1:A:444:LEU:HB2	1.99	0.44
1:C:454:LEU:HD23	1:C:454:LEU:HA	1.75	0.44
1:C:329:LEU:HD12	1:C:329:LEU:HA	1.79	0.44
1:A:38:ASN:ND2	1:B:315:GLN:HE21	2.16	0.44
1:B:286:VAL:HG13	1:D:352:ALA:HA	2.00	0.44
1:C:40:PRO:HD2	1:D:382:LEU:HD21	2.00	0.44
1:A:111:ASN:HD22	1:A:111:ASN:C	2.21	0.44
1:D:13:GLU:HB3	1:D:20:VAL:HG23	1.99	0.44
1:D:410:THR:N	1:D:411:PRO:CD	2.81	0.44
1:A:25:LYS:O	1:A:25:LYS:HD2	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:231:VAL:HG23	1:B:233:THR:HG23	1.99	0.44
1:B:435:ILE:HG22	1:B:458:LEU:HD21	1.99	0.44
1:D:443:GLY:O	2:D:518:HOH:O	2.21	0.44
1:D:213:ARG:NH1	2:D:477:HOH:O	2.51	0.43
1:A:424:VAL:CG1	1:A:435:ILE:HG23	2.48	0.43
1:B:189:MET:HE3	1:C:301:GLY:HA2	1.90	0.43
1:A:424:VAL:HG11	1:A:435:ILE:HG23	1.99	0.43
1:A:86:ILE:HA	2:A:476:HOH:O	2.19	0.43
1:A:109:ASN:OD1	1:A:142:THR:HG21	2.18	0.43
1:B:329:LEU:HA	1:B:329:LEU:HD12	1.80	0.43
1:A:431:GLU:OE1	1:A:433:LYS:HD2	2.18	0.43
1:B:446:GLY:O	1:B:447:ASP:HB2	2.19	0.43
1:D:103:GLY:HA3	1:D:360:VAL:HB	2.01	0.43
1:C:22:VAL:CB	1:C:23:PRO:CD	2.93	0.43
1:C:17:MET:HG3	1:C:34:ARG:HH12	1.83	0.43
1:B:300:SER:HB2	1:C:188:LEU:HB3	2.01	0.43
1:B:452:GLU:HA	1:B:452:GLU:OE1	2.18	0.43
1:C:341:ILE:HD13	1:D:349:TRP:CZ3	2.54	0.43
1:D:314:LEU:HD21	1:D:329:LEU:HD22	2.01	0.43
1:A:414:SER:OG	1:A:457:ARG:NH2	2.52	0.43
1:C:445:ILE:H	1:C:445:ILE:CD1	2.11	0.43
1:A:367:ARG:NH1	2:A:475:HOH:O	2.52	0.43
1:A:296:ARG:O	1:A:300:SER:HB3	2.19	0.43
1:C:419:GLU:HA	1:C:419:GLU:OE2	2.18	0.42
1:C:443:GLY:C	1:C:445:ILE:HD12	2.39	0.42
1:D:453:ASP:OD2	1:D:457:ARG:NH1	2.51	0.42
1:B:103:GLY:HA3	1:B:360:VAL:HB	2.01	0.42
1:C:11:ARG:NH1	1:C:24:ALA:O	2.53	0.42
1:B:417:GLY:N	1:B:420:GLU:OE1	2.43	0.42
1:A:159:LEU:O	1:A:163:LEU:HG	2.19	0.42
1:C:452:GLU:O	1:C:456:ARG:HB2	2.20	0.42
1:C:142:THR:HG22	1:C:143:PHE:N	2.33	0.42
1:C:429:LEU:HD23	1:C:429:LEU:HA	1.81	0.42
1:D:367:ARG:HH11	1:D:367:ARG:HG2	1.84	0.42
1:B:301:GLY:CA	1:C:189:MET:CE	2.98	0.42
1:A:376:LEU:HD23	1:A:376:LEU:HA	1.92	0.42
1:C:22:VAL:CG1	1:C:33:GLN:CD	2.72	0.41
1:A:440:ILE:CG1	1:A:445:ILE:CD1	2.98	0.41
1:A:424:VAL:HG12	1:A:435:ILE:HD12	2.01	0.41
1:D:138:SER:HB3	1:D:229:THR:HA	2.02	0.41
1:A:9:ASN:OD1	1:A:9:ASN:N	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:399:ARG:NH1	2:D:503:HOH:O	2.49	0.41
1:C:454:LEU:HD22	1:C:458:LEU:HD22	2.02	0.41
1:C:228:GLY:O	1:C:229:THR:OG1	2.30	0.41
1:C:314:LEU:C	1:C:316:PRO:HD3	2.41	0.41
1:C:435:ILE:HG22	1:C:458:LEU:HD21	2.02	0.41
1:C:341:ILE:HD13	1:D:349:TRP:CH2	2.56	0.41
1:B:190:ASP:OD1	1:C:304:THR:HG23	2.21	0.41
1:A:357:GLU:HG2	1:C:185:ARG:O	2.20	0.41
1:A:406:PRO:HB3	1:A:425:ALA:HB1	2.02	0.41
1:C:97:ILE:HD13	1:C:107:SER:HB3	2.01	0.41
1:D:465:LYS:O	1:D:466:ALA:C	2.57	0.41
1:C:445:ILE:N	1:C:445:ILE:HD12	2.27	0.41
1:B:401:LEU:HA	1:B:401:LEU:HD23	1.92	0.41
1:D:15:ASP:C	1:D:17:MET:H	2.23	0.41
1:A:183:SER:HB3	1:D:304:THR:HG21	2.04	0.41
1:A:295:ILE:CA	1:A:298:MET:HE2	2.49	0.40
1:C:430:LYS:HE3	1:C:430:LYS:HB2	1.65	0.40
1:A:188:LEU:HB3	1:D:300:SER:HB2	2.03	0.40
1:A:324:LYS:HZ2	1:A:324:LYS:HB2	1.86	0.40
1:B:405:SER:O	1:B:408:ILE:HG12	2.22	0.40
1:B:442:ARG:HB2	1:B:444:LEU:HD23	2.02	0.40
1:A:421:ALA:O	1:A:424:VAL:N	2.55	0.40
1:C:370:LEU:HD23	1:C:370:LEU:HA	1.96	0.40
1:B:296:ARG:HG3	1:C:188:LEU:CD1	2.52	0.40
1:D:228:GLY:O	1:D:229:THR:OG1	2.30	0.40
1:B:189:MET:HE3	1:C:301:GLY:CA	2.47	0.40
1:C:72:ALA:HA	1:C:73:PRO:HD2	1.90	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	448/475 (94%)	427 (95%)	21 (5%)	0	100	100
1	B	447/475 (94%)	432 (97%)	15 (3%)	0	100	100
1	C	448/475 (94%)	433 (97%)	12 (3%)	3 (1%)	26	43
1	D	447/475 (94%)	434 (97%)	12 (3%)	1 (0%)	52	73
All	All	1790/1900 (94%)	1726 (96%)	60 (3%)	4 (0%)	52	73

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	455	ASP
1	C	454	LEU
1	C	444	LEU
1	D	315	GLN

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	346/365 (95%)	331 (96%)	15 (4%)	35	59
1	B	345/365 (94%)	329 (95%)	16 (5%)	33	56
1	C	347/365 (95%)	329 (95%)	18 (5%)	29	50
1	D	345/365 (94%)	326 (94%)	19 (6%)	27	46
All	All	1383/1460 (95%)	1315 (95%)	68 (5%)	31	53

All (68) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	19	GLU
1	A	22	VAL
1	A	74	GLU
1	A	111	ASN
1	A	142	THR
1	A	183	SER
1	A	271	ARG

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Mol	Chain	Res	Type
1	A	329	LEU
1	A	357	GLU
1	A	379	VAL
1	A	382	LEU
1	A	399	ARG
1	A	414	SER
1	A	442	ARG
1	A	458	LEU
1	B	20	VAL
1	B	22	VAL
1	B	74	GLU
1	B	111	ASN
1	B	142	THR
1	B	183	SER
1	B	271	ARG
1	B	314	LEU
1	B	329	LEU
1	B	357	GLU
1	B	379	VAL
1	B	382	LEU
1	B	399	ARG
1	B	410	THR
1	B	450	SER
1	B	458	LEU
1	C	25	LYS
1	C	74	GLU
1	C	111	ASN
1	C	142	THR
1	C	183	SER
1	C	271	ARG
1	C	324	LYS
1	C	329	LEU
1	C	357	GLU
1	C	379	VAL
1	C	382	LEU
1	C	399	ARG
1	C	427	GLN
1	C	437	GLN
1	C	442	ARG
1	C	445	ILE
1	C	454	LEU
1	C	458	LEU

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Mol	Chain	Res	Type
1	D	22	VAL
1	D	74	GLU
1	D	111	ASN
1	D	142	THR
1	D	183	SER
1	D	271	ARG
1	D	329	LEU
1	D	357	GLU
1	D	379	VAL
1	D	382	LEU
1	D	399	ARG
1	D	407	SER
1	D	420	GLU
1	D	444	LEU
1	D	449	LEU
1	D	451	ILE
1	D	453	ASP
1	D	454	LEU
1	D	458	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	38	ASN
1	B	38	ASN
1	C	38	ASN
1	C	353	ASN
1	C	437	GLN
1	D	38	ASN

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 [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 ⓘ

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	450/475 (94%)	0.84	70 (15%) 3 2	20, 48, 93, 125	17 (3%)
1	B	452/475 (95%)	0.44	28 (6%) 24 26	20, 46, 77, 113	24 (5%)
1	C	453/475 (95%)	0.86	67 (14%) 3 3	20, 49, 98, 122	18 (3%)
1	D	452/475 (95%)	0.45	24 (5%) 30 34	20, 46, 76, 128	24 (5%)
All	All	1807/1900 (95%)	0.65	189 (10%) 8 8	20, 47, 89, 128	83 (4%)

All (189) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	8	ALA	11.4
1	C	449	LEU	10.3
1	C	314	LEU	10.2
1	D	316	PRO	8.0
1	B	8	ALA	8.0
1	C	439	VAL	6.9
1	D	16	THR	6.8
1	C	447	ASP	6.7
1	A	439	VAL	6.6
1	C	409	VAL	6.1
1	C	20	VAL	5.8
1	D	323	GLY	5.6
1	A	447	ASP	5.5
1	C	412	LEU	5.5
1	C	124	GLY	5.5
1	C	8	ALA	5.4
1	A	453	ASP	5.4
1	C	425	ALA	5.3
1	D	314	LEU	5.3
1	A	449	LEU	5.2
1	D	10	TYR	5.2

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Mol	Chain	Res	Type	RSRZ
1	C	418	TYR	5.1
1	A	422	ALA	5.1
1	D	12	ILE	5.0
1	C	440	ILE	4.8
1	C	446	GLY	4.8
1	A	444	LEU	4.8
1	C	450	SER	4.7
1	C	121	ALA	4.7
1	B	453	ASP	4.6
1	A	119	ILE	4.5
1	A	19	GLU	4.5
1	D	315	GLN	4.5
1	D	313	ASP	4.4
1	A	429	LEU	4.4
1	B	449	LEU	4.4
1	A	418	TYR	4.4
1	C	413	ASN	4.3
1	C	453	ASP	4.2
1	A	125	VAL	4.2
1	A	451	ILE	4.2
1	B	25	LYS	4.1
1	C	441	ASP	4.1
1	B	10	TYR	4.0
1	B	440	ILE	3.8
1	A	10	TYR	3.7
1	C	445	ILE	3.7
1	A	92	ASP	3.7
1	C	416	ILE	3.7
1	C	29	ARG	3.7
1	C	315	GLN	3.7
1	A	455	ASP	3.6
1	C	451	ILE	3.6
1	D	15	ASP	3.6
1	D	9	ASN	3.6
1	B	16	THR	3.6
1	A	415	ALA	3.5
1	A	175	LEU	3.5
1	A	174	ALA	3.4
1	A	21	ARG	3.4
1	C	466	ALA	3.4
1	A	446	GLY	3.4
1	A	127	LEU	3.3

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Mol	Chain	Res	Type	RSRZ
1	D	19	GLU	3.3
1	C	9	ASN	3.3
1	A	445	ILE	3.3
1	B	19	GLU	3.3
1	C	415	ALA	3.3
1	D	447	ASP	3.3
1	A	424	VAL	3.3
1	A	76	ALA	3.3
1	C	83	ALA	3.3
1	A	452	GLU	3.3
1	B	323	GLY	3.3
1	D	342	GLY	3.2
1	C	400	ARG	3.2
1	D	453	ASP	3.2
1	B	12	ILE	3.2
1	C	452	GLU	3.2
1	A	409	VAL	3.2
1	C	10	TYR	3.2
1	A	30	ALA	3.2
1	C	55	GLY	3.1
1	A	121	ALA	3.1
1	C	438	THR	3.1
1	B	23	PRO	3.0
1	D	83	ALA	3.0
1	C	323	GLY	3.0
1	C	22	VAL	3.0
1	C	125	VAL	3.0
1	A	8	ALA	3.0
1	A	342	GLY	2.9
1	B	314	LEU	2.9
1	C	455	ASP	2.9
1	A	412	LEU	2.9
1	A	440	ILE	2.9
1	A	420	GLU	2.8
1	A	126	THR	2.8
1	B	341	ILE	2.8
1	C	414	SER	2.8
1	C	120	ALA	2.8
1	B	275	VAL	2.7
1	C	180	VAL	2.7
1	A	438	THR	2.7
1	A	20	VAL	2.7

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Mol	Chain	Res	Type	RSRZ
1	A	345	ALA	2.7
1	A	28	TRP	2.7
1	A	26	ALA	2.7
1	A	23	PRO	2.6
1	A	414	SER	2.6
1	A	454	LEU	2.6
1	D	449	LEU	2.6
1	A	425	ALA	2.6
1	C	92	ASP	2.5
1	C	345	ALA	2.5
1	C	442	ARG	2.5
1	A	401	LEU	2.5
1	A	278	SER	2.5
1	B	15	ASP	2.5
1	D	21	ARG	2.5
1	A	25	LYS	2.5
1	A	123	GLY	2.5
1	A	87	ALA	2.5
1	D	444	LEU	2.4
1	C	348	ALA	2.4
1	A	115	VAL	2.4
1	A	83	ALA	2.4
1	D	341	ILE	2.4
1	C	57	LEU	2.4
1	A	300	SER	2.4
1	B	447	ASP	2.4
1	B	20	VAL	2.4
1	C	313	ASP	2.4
1	C	288	LEU	2.4
1	A	17	MET	2.4
1	C	435	ILE	2.4
1	C	444	LEU	2.3
1	D	20	VAL	2.3
1	C	253	THR	2.3
1	D	88	ASP	2.3
1	A	15	ASP	2.3
1	A	80	ILE	2.3
1	C	117	ALA	2.3
1	C	420	GLU	2.3
1	C	456	ARG	2.3
1	C	344	ASP	2.3
1	C	246	VAL	2.3

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Mol	Chain	Res	Type	RSRZ
1	C	424	VAL	2.3
1	A	419	GLU	2.2
1	D	76	ALA	2.2
1	A	443	GLY	2.2
1	B	454	LEU	2.2
1	B	452	GLU	2.2
1	C	316	PRO	2.2
1	A	450	SER	2.2
1	A	293	ASN	2.2
1	A	457	ARG	2.2
1	C	175	LEU	2.2
1	C	283	THR	2.2
1	A	22	VAL	2.2
1	A	171	ALA	2.2
1	A	280	ALA	2.2
1	B	9	ASN	2.2
1	B	197	GLY	2.2
1	C	115	VAL	2.2
1	C	30	ALA	2.2
1	D	345	ALA	2.2
1	A	400	ARG	2.2
1	C	457	ARG	2.1
1	B	81	ALA	2.1
1	B	119	ILE	2.1
1	B	125	VAL	2.1
1	A	441	ASP	2.1
1	B	285	ALA	2.1
1	C	461	LEU	2.1
1	B	174	ALA	2.1
1	C	341	ILE	2.1
1	C	443	GLY	2.1
1	B	102	THR	2.1
1	A	396	GLU	2.0
1	A	284	ILE	2.0
1	B	350	GLY	2.0
1	A	403	GLU	2.0
1	A	416	ILE	2.0
1	C	347	ILE	2.0
1	C	163	LEU	2.0
1	A	16	THR	2.0
1	C	86	ILE	2.0
1	A	57	LEU	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.