



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 09:24 AM UTC

PDB ID : 3BAN / pdb_00003ban
Title : The crystal structure of mannonate dehydratase from *Streptococcus suis* serotype2
Authors : Peng, H.; Zhang, Q.M.; Gao, F.; Liu, Y.W.; Qi, J.X.; Gao, G.F.
Deposited on : 2007-11-08
Resolution : 2.90 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
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

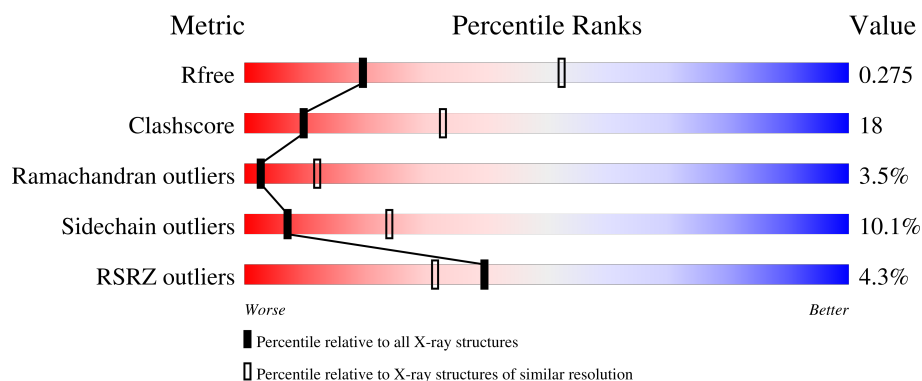
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.90 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	2481 (2.90-2.90)
Clashscore	190562	2690 (2.90-2.90)
Ramachandran outliers	187476	2623 (2.90-2.90)
Sidechain outliers	187428	2625 (2.90-2.90)
RSRZ outliers	180081	2481 (2.90-2.90)

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	386	3% 53% 30% 7% 10%
1	B	386	4% 55% 30% 5% 10%

2 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 5471 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 D-mannonate dehydratase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	349	Total	C	N	O	S	0	0	0
			2738	1745	465	514	14			
1	B	349	Total	C	N	O	S	0	0	0
			2733	1742	465	513	13			

There are 40 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	expression tag	UNP A4VVI4
A	2	GLY	-	expression tag	UNP A4VVI4
A	3	SER	-	expression tag	UNP A4VVI4
A	4	SER	-	expression tag	UNP A4VVI4
A	5	HIS	-	expression tag	UNP A4VVI4
A	6	HIS	-	expression tag	UNP A4VVI4
A	7	HIS	-	expression tag	UNP A4VVI4
A	8	HIS	-	expression tag	UNP A4VVI4
A	9	HIS	-	expression tag	UNP A4VVI4
A	10	HIS	-	expression tag	UNP A4VVI4
A	11	SER	-	expression tag	UNP A4VVI4
A	12	SER	-	expression tag	UNP A4VVI4
A	13	GLY	-	expression tag	UNP A4VVI4
A	14	LEU	-	expression tag	UNP A4VVI4
A	15	VAL	-	expression tag	UNP A4VVI4
A	16	PRO	-	expression tag	UNP A4VVI4
A	17	ARG	-	expression tag	UNP A4VVI4
A	18	GLY	-	expression tag	UNP A4VVI4
A	19	SER	-	expression tag	UNP A4VVI4
A	20	HIS	-	expression tag	UNP A4VVI4
B	1	MET	-	expression tag	UNP A4VVI4
B	2	GLY	-	expression tag	UNP A4VVI4
B	3	SER	-	expression tag	UNP A4VVI4
B	4	SER	-	expression tag	UNP A4VVI4
B	5	HIS	-	expression tag	UNP A4VVI4

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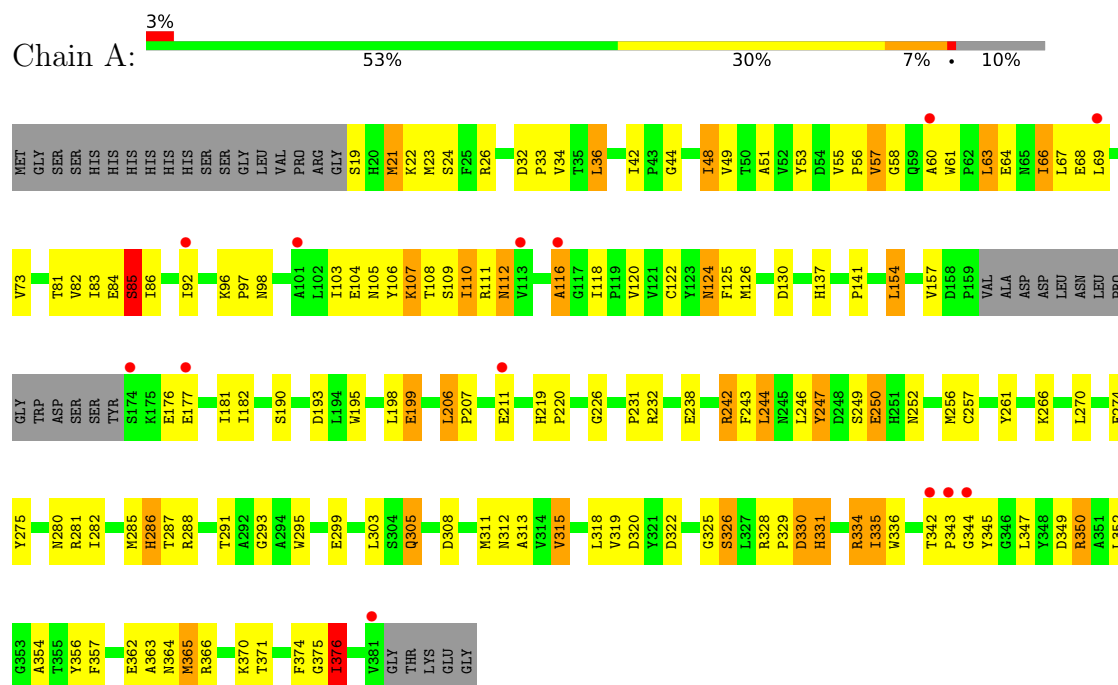
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Chain	Residue	Modelled	Actual	Comment	Reference
B	6	HIS	-	expression tag	UNP A4VVI4
B	7	HIS	-	expression tag	UNP A4VVI4
B	8	HIS	-	expression tag	UNP A4VVI4
B	9	HIS	-	expression tag	UNP A4VVI4
B	10	HIS	-	expression tag	UNP A4VVI4
B	11	SER	-	expression tag	UNP A4VVI4
B	12	SER	-	expression tag	UNP A4VVI4
B	13	GLY	-	expression tag	UNP A4VVI4
B	14	LEU	-	expression tag	UNP A4VVI4
B	15	VAL	-	expression tag	UNP A4VVI4
B	16	PRO	-	expression tag	UNP A4VVI4
B	17	ARG	-	expression tag	UNP A4VVI4
B	18	GLY	-	expression tag	UNP A4VVI4
B	19	SER	-	expression tag	UNP A4VVI4
B	20	HIS	-	expression tag	UNP A4VVI4

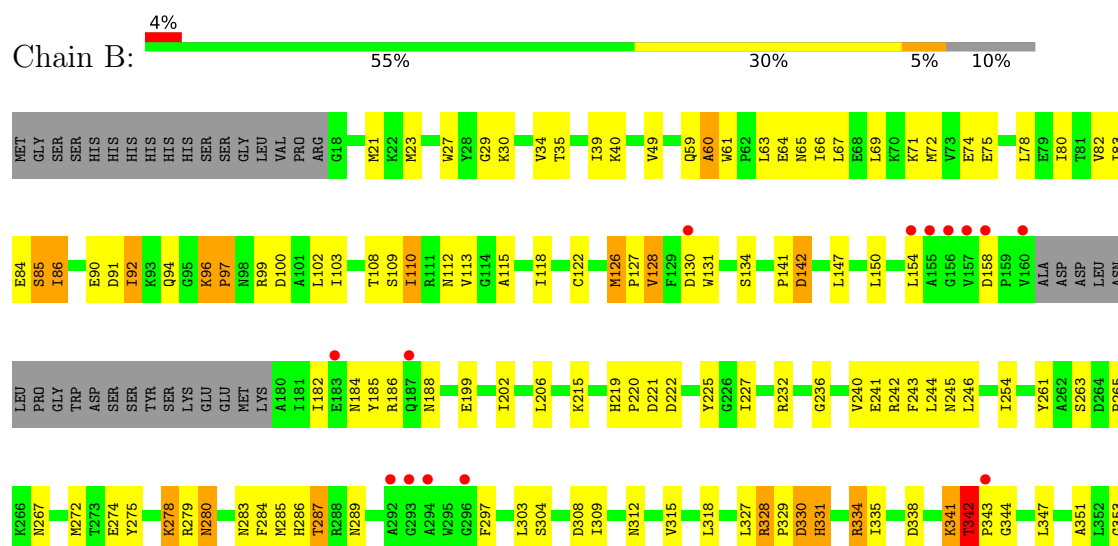
3 Residue-property plots

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: D-mannosate dehydratase



• Molecule 1: D-mannosate dehydratase





4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	105.69Å 105.69Å 159.57Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	44.06 – 2.90 44.06 – 2.90	Depositor EDS
% Data completeness (in resolution range)	99.8 (44.06-2.90) 99.8 (44.06-2.90)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.44 (at 2.90Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.234 , 0.286 0.229 , 0.275	Depositor DCC
R_{free} test set	1063 reflections (5.12%)	wwPDB-VP
Wilson B-factor (Å ²)	51.9	Xtriage
Anisotropy	0.199	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 38.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.43$, $\langle L^2 \rangle = 0.26$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	5471	wwPDB-VP
Average B, all atoms (Å ²)	41.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.48% 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

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	0.83	0/2805	1.13	10/3808 (0.3%)
1	B	0.85	0/2800	1.15	15/3802 (0.4%)
All	All	0.84	0/5605	1.14	25/7610 (0.3%)

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	1

There are no bond length outliers.

All (25) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	B	342	THR	CA-C-N	9.16	131.30	119.84
1	B	342	THR	C-N-CA	9.16	131.30	119.84
1	B	96	LYS	CA-C-N	8.90	130.97	119.84
1	B	96	LYS	C-N-CA	8.90	130.97	119.84
1	A	157	VAL	N-CA-C	7.89	119.76	109.58
1	A	376	ILE	N-CA-C	6.53	117.92	107.73
1	B	328	ARG	CB-CA-C	-6.35	101.97	109.47
1	A	286	HIS	CA-C-N	-6.27	114.63	123.03
1	A	286	HIS	C-N-CA	-6.27	114.63	123.03
1	B	206	LEU	CA-C-N	-6.20	112.25	119.32
1	B	206	LEU	C-N-CA	-6.20	112.25	119.32
1	A	182	ILE	N-CA-C	-6.11	104.79	110.53
1	B	110	ILE	CB-CA-C	-5.85	104.39	111.88
1	A	42	ILE	N-CA-C	-5.72	103.71	108.63
1	B	86	ILE	CA-C-N	5.72	125.65	119.76
1	B	86	ILE	C-N-CA	5.72	125.65	119.76

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	325	GLY	N-CA-C	-5.63	102.55	110.88
1	B	126	MET	CA-C-N	5.61	125.79	119.90
1	B	126	MET	C-N-CA	5.61	125.79	119.90
1	B	84	GLU	N-CA-CB	5.37	118.44	110.49
1	A	342	THR	CA-C-N	5.30	126.47	119.84
1	A	342	THR	C-N-CA	5.30	126.47	119.84
1	B	347	LEU	N-CA-C	5.23	116.67	111.07
1	A	112	ASN	N-CA-C	5.06	116.79	111.28
1	B	86	ILE	N-CA-C	-5.02	98.04	108.88

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	85	SER	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	2738	0	2676	105	0
1	B	2733	0	2679	91	0
All	All	5471	0	5355	191	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 18.

All (191) 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:250:GLU:HG2	1:A:280:ASN:HD22	1.16	1.06
1:B:199:GLU:HB2	1:B:246:LEU:CD2	1.92	0.98
1:B:182:ILE:HG22	1:B:186:ARG:HD2	1.49	0.94
1:A:57:VAL:HG13	1:A:58:GLY:H	1.37	0.90
1:B:61:TRP:O	1:B:112:ASN:ND2	2.06	0.88

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:250:GLU:HG3	1:A:281:ARG:NH1	1.87	0.87
1:B:284:PHE:CE1	1:B:286:HIS:HE1	1.93	0.87
1:A:250:GLU:HG3	1:A:281:ARG:HH12	1.40	0.86
1:B:287:THR:HG23	1:B:357:PHE:CZ	2.13	0.83
1:B:199:GLU:HB2	1:B:246:LEU:HD22	1.58	0.82
1:B:199:GLU:HB2	1:B:246:LEU:HD21	1.60	0.80
1:A:63:LEU:HD22	1:A:67:LEU:HG	1.64	0.79
1:A:220:PRO:HB3	1:A:261:TYR:CZ	2.20	0.76
1:B:312:ASN:ND2	1:B:364:ASN:HD21	1.82	0.76
1:A:85:SER:HA	1:A:122:CYS:O	1.85	0.75
1:A:334:ARG:HH11	1:A:334:ARG:HG3	1.52	0.74
1:A:126:MET:HE1	1:A:130:ASP:O	1.86	0.74
1:B:287:THR:HG23	1:B:287:THR:O	1.87	0.72
1:A:250:GLU:HG2	1:A:280:ASN:ND2	2.00	0.71
1:B:59:GLN:O	1:B:60:ALA:HB3	1.91	0.70
1:A:106:TYR:O	1:A:110:ILE:HG12	1.92	0.70
1:B:287:THR:O	1:B:287:THR:CG2	2.38	0.70
1:A:82:VAL:HG22	1:A:120:VAL:HB	1.75	0.69
1:B:334:ARG:HG2	1:B:338:ASP:HB3	1.75	0.68
1:A:311:MET:O	1:A:315:VAL:HG12	1.93	0.68
1:A:288:ARG:HD3	1:A:331:HIS:HB2	1.76	0.67
1:A:24:SER:OG	1:A:81:THR:HG21	1.95	0.67
1:B:85:SER:HA	1:B:122:CYS:O	1.95	0.66
1:A:226:GLY:HA2	1:A:232:ARG:HD3	1.78	0.65
1:A:334:ARG:HG3	1:A:334:ARG:NH1	2.11	0.65
1:A:57:VAL:HG13	1:A:58:GLY:N	2.10	0.64
1:B:287:THR:CG2	1:B:357:PHE:CZ	2.80	0.64
1:B:126:MET:HE1	1:B:130:ASP:O	1.97	0.64
1:A:293:GLY:HA3	1:A:295:TRP:CD1	2.33	0.63
1:B:94:GLN:OE1	1:B:184:ASN:ND2	2.32	0.63
1:B:284:PHE:CE1	1:B:286:HIS:CE1	2.83	0.63
1:A:331:HIS:HA	1:A:344:GLY:O	1.99	0.62
1:A:366:ARG:NH1	1:A:371:THR:HG22	2.14	0.62
1:A:312:ASN:ND2	1:A:364:ASN:HD21	1.96	0.62
1:A:51:ALA:HB3	1:A:53:TYR:CZ	2.35	0.62
1:A:125:PHE:CG	1:A:198:LEU:HD13	2.34	0.62
1:B:353:GLY:O	1:B:357:PHE:HD2	1.83	0.61
1:A:61:TRP:O	1:A:112:ASN:ND2	2.30	0.61
1:B:109:SER:O	1:B:113:VAL:HG23	2.00	0.61
1:A:330:ASP:O	1:A:331:HIS:C	2.45	0.60
1:A:19:SER:HB2	1:A:322:ASP:OD2	2.02	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:334:ARG:HD3	1:B:338:ASP:O	2.01	0.60
1:B:71:LYS:O	1:B:75:GLU:HG3	2.02	0.59
1:A:57:VAL:CG1	1:A:58:GLY:H	2.14	0.59
1:A:250:GLU:CG	1:A:280:ASN:HD22	2.05	0.59
1:A:177:GLU:O	1:A:181:ILE:HG13	2.02	0.59
1:A:219:HIS:HE1	1:A:286:HIS:CE1	2.22	0.58
1:B:236:GLY:O	1:B:240:VAL:HG23	2.04	0.58
1:B:202:ILE:HD11	1:B:246:LEU:HB3	1.86	0.57
1:B:240:VAL:HG13	1:B:254:ILE:HG21	1.86	0.57
1:B:243:PHE:O	1:B:246:LEU:HB2	2.05	0.57
1:B:303:LEU:O	1:B:304:SER:C	2.48	0.57
1:B:355:THR:HA	1:B:358:ASN:ND2	2.20	0.57
1:A:365:MET:HE2	1:A:370:LYS:HB2	1.86	0.56
1:A:63:LEU:CD2	1:A:67:LEU:HG	2.36	0.55
1:B:285:MET:HE2	1:B:318:LEU:HD11	1.88	0.55
1:A:34:VAL:HG22	1:A:347:LEU:HB2	1.87	0.55
1:A:206:LEU:HD11	1:A:252:ASN:HB2	1.89	0.55
1:A:56:PRO:O	1:A:57:VAL:HB	2.05	0.55
1:A:66:ILE:HG13	1:A:67:LEU:N	2.21	0.55
1:A:60:ALA:HB2	1:A:105:ASN:HD22	1.71	0.55
1:B:63:LEU:HG	1:B:67:LEU:CD1	2.38	0.54
1:B:40:LYS:HD3	1:B:78:LEU:HD21	1.89	0.54
1:A:32:ASP:OD1	1:A:33:PRO:HD2	2.08	0.54
1:A:48:ILE:HG21	1:A:73:VAL:HG21	1.88	0.54
1:A:365:MET:HE1	1:A:370:LYS:HD2	1.89	0.54
1:A:291:THR:HA	1:A:308:ASP:CG	2.33	0.54
1:A:312:ASN:HD21	1:A:364:ASN:HD21	1.56	0.54
1:B:312:ASN:HD21	1:B:364:ASN:HD21	1.55	0.54
1:A:231:PRO:O	1:A:232:ARG:HD2	2.08	0.54
1:B:142:ASP:OD1	1:B:142:ASP:C	2.50	0.53
1:A:104:GLU:O	1:A:107:LYS:HB2	2.09	0.53
1:A:257:CYS:HA	1:A:286:HIS:HB2	1.89	0.53
1:A:66:ILE:HD11	1:A:116:ALA:CB	2.39	0.53
1:B:59:GLN:O	1:B:60:ALA:CB	2.54	0.53
1:A:376:ILE:HG22	1:A:376:ILE:O	2.08	0.53
1:B:199:GLU:CB	1:B:246:LEU:HD22	2.32	0.53
1:B:355:THR:O	1:B:358:ASN:HB2	2.09	0.52
1:A:365:MET:HE2	1:A:370:LYS:CB	2.40	0.52
1:A:352:LEU:HD21	1:B:351:ALA:HB1	1.91	0.52
1:A:335:ILE:HD12	1:A:349:ASP:HB2	1.91	0.52
1:B:341:LYS:O	1:B:342:THR:C	2.52	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:137:HIS:CE1	1:A:334:ARG:HE	2.28	0.51
1:B:303:LEU:HA	1:B:356:TYR:CZ	2.45	0.51
1:A:328:ARG:NH2	1:A:345:TYR:OH	2.44	0.51
1:B:287:THR:HG21	1:B:327:LEU:HD21	1.93	0.51
1:B:287:THR:HG22	1:B:329:PRO:HA	1.92	0.51
1:A:44:GLY:HA2	1:A:374:PHE:HB3	1.92	0.50
1:A:244:LEU:HG	1:A:281:ARG:HG3	1.94	0.50
1:B:126:MET:HG3	1:B:221:ASP:OD2	2.12	0.50
1:A:36:LEU:H	1:A:36:LEU:HD12	1.76	0.49
1:B:21:MET:SD	1:B:23:MET:HE1	2.52	0.49
1:B:265:PRO:C	1:B:267:ASN:N	2.69	0.49
1:B:361:TYR:O	1:B:365:MET:HG2	2.13	0.49
1:A:21:MET:SD	1:A:23:MET:HE1	2.52	0.49
1:B:261:TYR:HB3	1:B:272:MET:HE1	1.95	0.49
1:A:86:ILE:HD13	1:A:109:SER:HB3	1.95	0.49
1:B:112:ASN:O	1:B:115:ALA:HB3	2.13	0.49
1:A:96:LYS:HB3	1:A:97:PRO:CD	2.43	0.49
1:B:99:ARG:O	1:B:102:LEU:N	2.46	0.49
1:A:124:ASN:OD1	1:A:124:ASN:C	2.55	0.48
1:A:63:LEU:HD22	1:A:67:LEU:CG	2.41	0.48
1:B:113:VAL:HG12	1:B:118:ILE:HB	1.95	0.48
1:B:274:GLU:O	1:B:275:TYR:C	2.57	0.48
1:A:285:MET:HE2	1:A:318:LEU:HD11	1.95	0.47
1:B:96:LYS:HA	1:B:97:PRO:HD2	1.56	0.47
1:A:26:ARG:HA	1:A:49:VAL:HB	1.96	0.47
1:B:27:TRP:CH2	1:B:29:GLY:HA2	2.49	0.47
1:A:231:PRO:C	1:A:232:ARG:HD2	2.40	0.47
1:A:49:VAL:CG1	1:A:84:GLU:HB2	2.45	0.47
1:B:49:VAL:HG11	1:B:328:ARG:HD2	1.95	0.47
1:A:362:GLU:OE2	1:B:304:SER:OG	2.32	0.46
1:A:243:PHE:O	1:A:244:LEU:C	2.59	0.46
1:A:328:ARG:HH21	1:A:345:TYR:HE2	1.63	0.46
1:B:331:HIS:HA	1:B:344:GLY:O	2.14	0.46
1:B:126:MET:CE	1:B:130:ASP:O	2.62	0.46
1:A:195:TRP:CH2	1:A:242:ARG:HD2	2.51	0.46
1:A:288:ARG:HB2	1:A:330:ASP:HB3	1.97	0.46
1:B:220:PRO:HB3	1:B:261:TYR:CZ	2.51	0.46
1:B:69:LEU:HA	1:B:72:MET:HE3	1.98	0.46
1:A:83:ILE:HG13	1:A:118:ILE:HG21	1.97	0.45
1:B:35:THR:O	1:B:39:ILE:HG13	2.16	0.45
1:B:225:TYR:O	1:B:232:ARG:HD3	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:335:ILE:O	1:B:338:ASP:HB2	2.16	0.45
1:B:113:VAL:CG1	1:B:118:ILE:HB	2.46	0.45
1:A:199:GLU:HG3	1:A:246:LEU:HD22	1.99	0.45
1:A:274:GLU:O	1:A:275:TYR:C	2.60	0.44
1:A:329:PRO:HG3	1:A:354:ALA:HB2	1.99	0.44
1:B:241:GLU:HG3	1:B:275:TYR:OH	2.18	0.44
1:A:22:LYS:O	1:A:23:MET:C	2.59	0.44
1:A:108:THR:HG22	1:A:111:ARG:HH11	1.83	0.44
1:B:91:ASP:HB2	1:B:102:LEU:CD1	2.47	0.44
1:A:110:ILE:HG12	1:A:110:ILE:H	1.60	0.44
1:A:206:LEU:HD12	1:A:247:TYR:CD1	2.52	0.44
1:B:82:VAL:HG11	1:B:284:PHE:CE1	2.52	0.44
1:B:27:TRP:CZ3	1:B:29:GLY:HA2	2.53	0.44
1:A:141:PRO:HG2	1:B:378:ALA:O	2.17	0.44
1:A:374:PHE:C	1:A:376:ILE:H	2.25	0.44
1:B:63:LEU:HG	1:B:67:LEU:HD11	2.00	0.44
1:B:74:GLU:HA	1:B:78:LEU:O	2.17	0.44
1:B:383:THR:OG1	1:B:384:LYS:N	2.47	0.43
1:B:80:ILE:HG21	1:B:118:ILE:HD13	1.99	0.43
1:B:353:GLY:O	1:B:357:PHE:CD2	2.66	0.43
1:A:287:THR:HG23	1:A:357:PHE:CE2	2.54	0.43
1:A:335:ILE:HG12	1:A:336:TRP:CG	2.54	0.43
1:A:81:THR:O	1:A:82:VAL:HG23	2.19	0.43
1:B:263:SER:HB3	1:B:297:PHE:CD1	2.54	0.43
1:B:245:ASN:ND2	1:B:279:ARG:HH22	2.16	0.43
1:B:330:ASP:O	1:B:331:HIS:O	2.37	0.43
1:B:265:PRO:C	1:B:267:ASN:H	2.25	0.43
1:B:86:ILE:HD11	1:B:113:VAL:HG21	2.02	0.42
1:A:22:LYS:O	1:A:326:SER:HB3	2.18	0.42
1:B:64:GLU:O	1:B:65:ASN:C	2.60	0.42
1:B:274:GLU:HG2	1:B:278:LYS:HE3	2.01	0.42
1:A:190:SER:O	1:A:193:ASP:HB2	2.19	0.42
1:A:195:TRP:CZ3	1:A:242:ARG:HD2	2.55	0.42
1:A:249:SER:N	1:A:281:ARG:HH21	2.18	0.42
1:A:92:ILE:CD1	1:A:103:ILE:HG13	2.49	0.42
1:A:299:GLU:OE1	1:A:331:HIS:HB3	2.20	0.42
1:B:280:ASN:HD22	1:B:280:ASN:HA	1.60	0.42
1:A:206:LEU:N	1:A:207:PRO:HD2	2.35	0.42
1:A:345:TYR:HA	1:A:350:ARG:NE	2.35	0.42
1:B:92:ILE:HD13	1:B:103:ILE:HG12	2.01	0.42
1:B:312:ASN:HD22	1:B:364:ASN:HD21	1.60	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:250:GLU:CG	1:A:281:ARG:HH12	2.23	0.41
1:A:334:ARG:HH11	1:A:334:ARG:CG	2.27	0.41
1:B:131:TRP:HA	1:B:222:ASP:O	2.20	0.41
1:A:363:ALA:HB3	1:B:363:ALA:HB3	2.03	0.41
1:B:127:PRO:HB3	1:B:185:TYR:CZ	2.55	0.41
1:A:220:PRO:HB3	1:A:261:TYR:CE1	2.55	0.41
1:B:219:HIS:HD2	1:B:220:PRO:O	2.03	0.41
1:A:125:PHE:CE2	1:A:198:LEU:HB2	2.56	0.41
1:A:303:LEU:HA	1:A:356:TYR:CZ	2.55	0.41
1:B:90:GLU:O	1:B:94:GLN:HG3	2.20	0.41
1:A:219:HIS:CE1	1:A:286:HIS:CE1	3.06	0.41
1:A:374:PHE:O	1:A:376:ILE:N	2.50	0.41
1:B:215:LYS:HD2	1:B:283:ASN:ND2	2.36	0.41
1:A:49:VAL:HG12	1:A:84:GLU:HB2	2.02	0.40
1:A:352:LEU:HB3	1:B:355:THR:HG21	2.03	0.40
1:B:99:ARG:O	1:B:100:ASP:C	2.63	0.40
1:A:48:ILE:O	1:A:81:THR:HG22	2.21	0.40
1:A:154:LEU:HD12	1:A:154:LEU:HA	1.86	0.40
1:A:270:LEU:HD21	1:A:313:ALA:HB3	2.02	0.40
1:B:150:LEU:HD23	1:B:150:LEU:HA	1.86	0.40
1:A:137:HIS:HE1	1:A:334:ARG:HE	1.70	0.40
1:B:289:ASN:HA	1:B:309:ILE:HD12	2.04	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	345/386 (89%)	295 (86%)	40 (12%)	10 (3%)	3	15
1	B	345/386 (89%)	290 (84%)	41 (12%)	14 (4%)	2	9
All	All	690/772 (89%)	585 (85%)	81 (12%)	24 (4%)	3	12

All (24) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	57	VAL
1	A	116	ALA
1	A	343	PRO
1	B	97	PRO
1	B	128	VAL
1	B	331	HIS
1	B	343	PRO
1	A	98	ASN
1	A	331	HIS
1	B	85	SER
1	B	142	ASP
1	B	154	LEU
1	B	341	LYS
1	B	367	ALA
1	A	85	SER
1	A	305	GLN
1	A	320	ASP
1	B	60	ALA
1	B	330	ASP
1	A	375	GLY
1	B	30	LYS
1	A	247	TYR
1	B	342	THR
1	B	141	PRO

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	288/321 (90%)	253 (88%)	35 (12%)	5	16
1	B	288/321 (90%)	265 (92%)	23 (8%)	11	34
All	All	576/642 (90%)	518 (90%)	58 (10%)	7	24

All (58) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	21	MET
1	A	36	LEU
1	A	48	ILE
1	A	55	VAL
1	A	63	LEU
1	A	64	GLU
1	A	66	ILE
1	A	68	GLU
1	A	69	LEU
1	A	85	SER
1	A	107	LYS
1	A	110	ILE
1	A	124	ASN
1	A	154	LEU
1	A	176	GLU
1	A	199	GLU
1	A	206	LEU
1	A	211	GLU
1	A	238	GLU
1	A	242	ARG
1	A	244	LEU
1	A	250	GLU
1	A	256	MET
1	A	266	LYS
1	A	282	ILE
1	A	305	GLN
1	A	315	VAL
1	A	319	VAL
1	A	326	SER
1	A	330	ASP
1	A	334	ARG
1	A	335	ILE
1	A	350	ARG
1	A	365	MET
1	A	376	ILE
1	B	34	VAL
1	B	66	ILE
1	B	83	ILE
1	B	92	ILE
1	B	108	THR
1	B	110	ILE
1	B	128	VAL
1	B	134	SER

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Mol	Chain	Res	Type
1	B	147	LEU
1	B	158	ASP
1	B	188	ASN
1	B	227	ILE
1	B	242	ARG
1	B	244	LEU
1	B	278	LYS
1	B	280	ASN
1	B	287	THR
1	B	308	ASP
1	B	315	VAL
1	B	334	ARG
1	B	342	THR
1	B	371	THR
1	B	383	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (24) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	59	GLN
1	A	105	ASN
1	A	137	HIS
1	A	184	ASN
1	A	219	HIS
1	A	280	ASN
1	A	283	ASN
1	A	298	GLN
1	A	312	ASN
1	A	324	GLN
1	B	46	GLN
1	B	105	ASN
1	B	138	HIS
1	B	219	HIS
1	B	237	GLN
1	B	245	ASN
1	B	267	ASN
1	B	280	ASN
1	B	283	ASN
1	B	286	HIS
1	B	298	GLN
1	B	312	ASN
1	B	324	GLN

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Mol	Chain	Res	Type
1	B	358	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](#)

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	349/386 (90%)	0.33	13 (3%) 45 37	21, 42, 62, 69	0
1	B	349/386 (90%)	0.28	17 (4%) 35 27	19, 38, 64, 82	0
All	All	698/772 (90%)	0.30	30 (4%) 40 31	19, 40, 62, 82	0

All (30) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	293	GLY	11.5
1	A	343	PRO	5.8
1	A	342	THR	5.5
1	B	160	VAL	4.9
1	B	154	LEU	4.7
1	B	292	ALA	4.6
1	A	211	GLU	3.7
1	A	174	SER	3.4
1	B	383	THR	3.1
1	B	157	VAL	3.0
1	A	177	GLU	2.9
1	B	158	ASP	2.8
1	A	60	ALA	2.8
1	A	92	ILE	2.6
1	B	155	ALA	2.6
1	B	294	ALA	2.6
1	A	69	LEU	2.6
1	A	116	ALA	2.5
1	B	130	ASP	2.5
1	A	381	VAL	2.5
1	B	296	GLY	2.4
1	A	101	ALA	2.3
1	A	344	GLY	2.3
1	B	183	GLU	2.3

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Mol	Chain	Res	Type	RSRZ
1	B	187	GLN	2.1
1	A	113	VAL	2.1
1	B	384	LYS	2.1
1	B	382	GLY	2.1
1	B	343	PRO	2.0
1	B	156	GLY	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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.