



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 07:35 AM GMT

PDB ID : 3BAN
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
<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

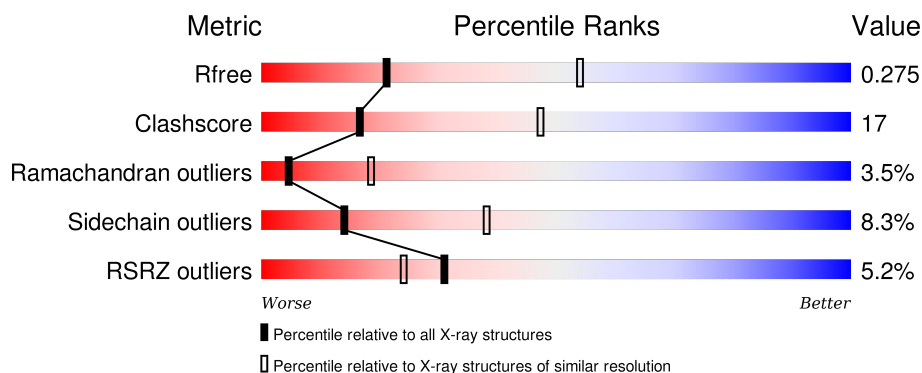
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.90 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}	91344	1451 (2.90-2.90)
Clashscore	102246	1668 (2.90-2.90)
Ramachandran outliers	100387	1630 (2.90-2.90)
Sidechain outliers	100360	1632 (2.90-2.90)
RSRZ outliers	91569	1456 (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 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	386	<div> <div>4%</div> <div>56%</div> <div>28%</div> <div>6%</div> <div>10%</div> </div>
1	B	386	<div> <div>5%</div> <div>59%</div> <div>28%</div> <div>•</div> <div>10%</div> </div>

2 Entry composition

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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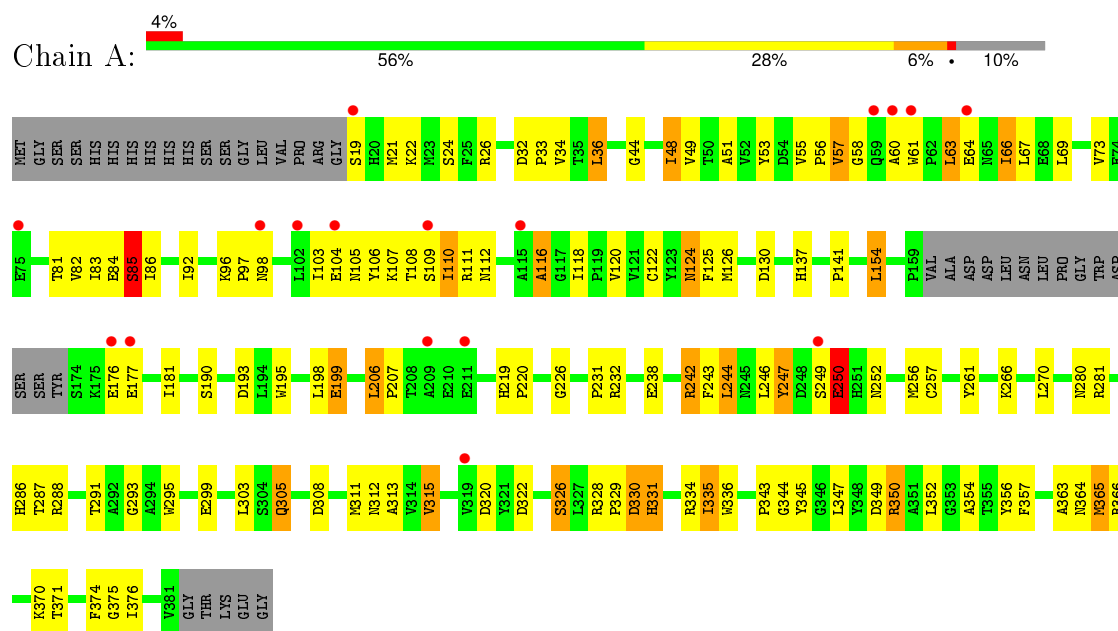
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Chain	Residue	Modelled	Actual	Comment	Reference
B	6	HIS	-	EXPRESSION TAG	UNP A4VVI4
B	7	HIS	-	EXPRESSION TAG	UNP A4VVI4
B	8	HIS	-	EXPRESSION TAG	UNP A4VVI4
B	9	HIS	-	EXPRESSION TAG	UNP A4VVI4
B	10	HIS	-	EXPRESSION TAG	UNP A4VVI4
B	11	SER	-	EXPRESSION 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

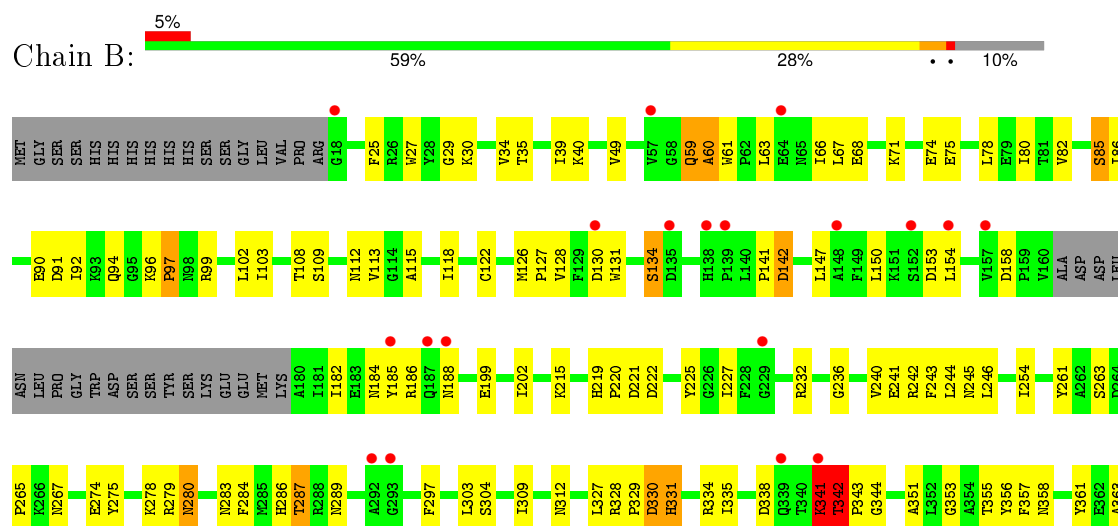
3 Residue-property plots

These plots are drawn for all protein, RNA 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: D-mannonate dehydratase



• Molecule 1: D-mannonate dehydratase



K364	K365	K366	A367	T371	A376	T383	K384	E385	GLY
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4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	105.69 Å 105.69 Å 159.57 Å 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 2.90 Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.234 , 0.286 0.230 , 0.275	Depositor DCC
R_{free} test set	1063 reflections (5.42%)	DCC
Wilson B-factor (Å ²)	51.9	Xtriage
Anisotropy	0.199	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 38.2	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.43$, $\langle L^2 \rangle = 0.26$	Xtriage
Outliers	1 of 20698 reflections (0.005%)	Xtriage
F_o, F_c correlation	0.89	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, 0.375 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	0.68	2/2805 (0.1%)	0.77	0/3808
1	B	0.68	0/2800	0.81	0/3802
All	All	0.68	2/5605 (0.0%)	0.79	0/7610

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

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	250	GLU	CG-CD	6.01	1.60	1.51
1	A	250	GLU	CB-CG	5.46	1.62	1.52

There are no bond angle outliers.

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	100	0
1	B	2733	0	2679	83	0
All	All	5471	0	5355	179	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 17.

All (179) 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
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:HG3	1:A:334:ARG:HH11	1.52	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:B:287:THR:CG2	1:B:287:THR:O	2.38	0.70
1:A:106:TYR:O	1:A:110:ILE:HG12	1.92	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:A:293:GLY:HA3	1:A:295:TRP:CD1	2.33	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:125:PHE:CG	1:A:198:LEU:HD13	2.34	0.62
1:A:51:ALA:HB3	1:A:53:TYR:CZ	2.35	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:19:SER:HB2	1:A:322:ASP:OD2	2.02	0.60
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:250:GLU:CG	1:A:280:ASN:HD22	2.05	0.59
1:A:57:VAL:CG1	1:A:58:GLY:H	2.14	0.59
1:A:365:MET:HE2	1:A:370:LYS:HB2	1.84	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:243:PHE:O	1:B:246:LEU:HB2	2.05	0.57
1:B:240:VAL:HG13	1:B:254:ILE:HG21	1.86	0.57
1:B:355:THR:HA	1:B:358:ASN:ND2	2.20	0.57
1:A:126:MET:HE1	1:A:130:ASP:O	2.06	0.56
1:A:63:LEU:CD2	1:A:67:LEU:HG	2.36	0.55
1:A:330:ASP:O	1:A:331:HIS:C	2.45	0.55
1:A:365:MET:HE2	1:A:370:LYS:CB	2.36	0.55
1:A:206:LEU:HD11	1:A:252:ASN:HB2	1.89	0.55
1:A:34:VAL:HG22	1:A:347:LEU:HB2	1.87	0.55
1:B:134:SER:HG	1:B:150:LEU:H	1.51	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:48:ILE:HG21	1:A:73:VAL:HG21	1.88	0.54
1:A:32:ASP:OD1	1:A:33:PRO:HD2	2.08	0.54
1:B:312:ASN:HD21	1:B:364:ASN:HD21	1.55	0.54
1:A:312:ASN:HD21	1:A:364:ASN:HD21	1.56	0.54
1:A:231:PRO:O	1:A:232:ARG:HD2	2.08	0.54
1:A:365:MET:HE1	1:A:370:LYS:HD2	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:257:CYS:HA	1:A:286:HIS:HB2	1.89	0.53
1:A:104:GLU:O	1:A:107:LYS:HB2	2.09	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:O	1:A:376:ILE:HG22	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:B:303:LEU:O	1:B:304:SER:C	2.48	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: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:244:LEU:HG	1:A:281:ARG:HG3	1.94	0.50
1:A:44:GLY:HA2	1:A:374:PHE:HB3	1.92	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:361:TYR:O	1:B:365:MET:HG2	2.13	0.49
1:A:86:ILE:HD13	1:A:109:SER:HB3	1.95	0.49
1:A:291:THR:HA	1:A:308:ASP:CG	2.33	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:B:142:ASP:C	1:B:142:ASP:OD1	2.50	0.49
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:96:LYS:HA	1:B:97:PRO:HD2	1.56	0.47
1:B:126:MET:CE	1:B:130:ASP:O	2.62	0.47
1:A:26:ARG:HA	1:A:49:VAL:HB	1.96	0.47
1:B:341:LYS:O	1:B:342:THR:C	2.52	0.47
1:B:27:TRP:CH2	1:B:29:GLY:HA2	2.49	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: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: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:A:83:ILE:HG13	1:A:118:ILE:HG21	1.97	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:225:TYR:O	1:B:232:ARG:HD3	2.16	0.45
1:B:35:THR:O	1:B:39:ILE:HG13	2.16	0.45
1:B:265:PRO:C	1:B:267:ASN:N	2.69	0.45
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: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:B:91:ASP:HB2	1:B:102:LEU:CD1	2.47	0.44
1:A:108:THR:HG22	1:A:111:ARG:HH11	1.83	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:A:124:ASN:OD1	1:A:124:ASN:C	2.55	0.44
1:B:27:TRP:CZ3	1:B:29:GLY:HA2	2.53	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:A:141:PRO:HG2	1:B:378:ALA: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:335:ILE:HG12	1:A:336:TRP:CG	2.54	0.43
1:A:287:THR:HG23	1:A:357:PHE:CE2	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:274:GLU:O	1:B:275:TYR:C	2.57	0.43
1:B:330:ASP:O	1:B:331:HIS:O	2.37	0.43
1:B:245:ASN:ND2	1:B:279:ARG:HH22	2.16	0.43
1:B:86:ILE:HD11	1:B:113:VAL:HG21	2.02	0.42
1:B:274:GLU:HG2	1:B:278:LYS:HE3	2.01	0.42
1:A:22:LYS:O	1:A:326:SER:HB3	2.18	0.42
1:A:190:SER:O	1:A:193:ASP:HB2	2.19	0.42
1:A:249:SER:N	1:A:281:ARG:HH21	2.18	0.42
1:A:195:TRP:CZ3	1:A:242:ARG:HD2	2.55	0.42
1:A:231:PRO:C	1:A:232:ARG:HD2	2.40	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:B:312:ASN:HD22	1:B:364:ASN:HD21	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:92:ILE:HD13	1:B:103:ILE:HG12	2.01	0.42
1:A:243:PHE:O	1:A:244:LEU:C	2.59	0.41
1:A:104:GLU:OE2	1:A:107:LYS:NZ	2.52	0.41
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:B:127:PRO:HB3	1:B:185:TYR:CZ	2.55	0.41
1:A:363:ALA:HB3	1:B:363:ALA:HB3	2.03	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:B:90:GLU:O	1:B:94:GLN:HG3	2.20	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: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:A:48:ILE:O	1:A:81:THR:HG22	2.21	0.40
1:B:150:LEU:HD23	1:B:150:LEU:HA	1.86	0.40
1:A:270:LEU:HD21	1:A:313:ALA:HB3	2.02	0.40
1:A:154:LEU:HA	1:A:154:LEU:HD12	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%)	6 23

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	345/386 (89%)	290 (84%)	41 (12%)	14 (4%)	3	14
All	All	690/772 (89%)	585 (85%)	81 (12%)	24 (4%)	4	18

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%)	260 (90%)	28 (10%)	10	30
1	B	288/321 (90%)	268 (93%)	20 (7%)	19	48
All	All	576/642 (90%)	528 (92%)	48 (8%)	14	38

All (48) 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	69	LEU
1	A	85	SER
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	238	GLU
1	A	242	ARG
1	A	244	LEU
1	A	250	GLU
1	A	256	MET
1	A	266	LYS
1	A	305	GLN
1	A	315	VAL
1	A	326	SER
1	A	330	ASP
1	A	335	ILE
1	A	350	ARG
1	A	365	MET
1	B	25	PHE
1	B	34	VAL
1	B	59	GLN
1	B	66	ILE
1	B	68	GLU
1	B	108	THR
1	B	134	SER

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Mol	Chain	Res	Type
1	B	147	LEU
1	B	153	ASP
1	B	158	ASP
1	B	188	ASN
1	B	227	ILE
1	B	242	ARG
1	B	244	LEU
1	B	280	ASN
1	B	287	THR
1	B	341	LYS
1	B	342	THR
1	B	371	THR
1	B	383	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (20) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	94	GLN
1	A	105	ASN
1	A	137	HIS
1	A	184	ASN
1	A	219	HIS
1	A	251	HIS
1	A	280	ASN
1	A	298	GLN
1	A	312	ASN
1	A	324	GLN
1	A	358	ASN
1	B	105	ASN
1	B	138	HIS
1	B	219	HIS
1	B	280	ASN
1	B	283	ASN
1	B	286	HIS
1	B	298	GLN
1	B	312	ASN
1	B	324	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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%)	0.17	17 (4%) 33 27	21, 42, 62, 69	0
1	B	349/386 (90%)	0.14	19 (5%) 29 23	19, 38, 64, 82	0
All	All	698/772 (90%)	0.15	36 (5%) 31 24	19, 40, 62, 82	0

All (36) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	293	GLY	9.9
1	B	339	GLN	4.1
1	B	187	GLN	3.9
1	B	138	HIS	3.8
1	A	60	ALA	3.7
1	B	139	PRO	3.6
1	B	292	ALA	3.4
1	A	61	TRP	3.1
1	B	341	LYS	3.1
1	B	154	LEU	3.1
1	A	249	SER	3.0
1	A	104	GLU	3.0
1	A	211	GLU	3.0
1	A	98	ASN	2.9
1	A	177	GLU	2.9
1	B	64	GLU	2.9
1	A	109	SER	2.8
1	B	157	VAL	2.6
1	A	319	VAL	2.6
1	A	75	GLU	2.6
1	B	185	TYR	2.5
1	A	176	GLU	2.5
1	A	64	GLU	2.5
1	A	102	LEU	2.5

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Mol	Chain	Res	Type	RSRZ
1	B	229	GLY	2.4
1	B	188	ASN	2.4
1	B	18	GLY	2.3
1	B	57	VAL	2.3
1	B	148	ALA	2.3
1	A	19	SER	2.2
1	A	209	ALA	2.2
1	B	130	ASP	2.2
1	A	115	ALA	2.1
1	A	59	GLN	2.1
1	B	135	ASP	2.0
1	B	152	SER	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.