Full wwPDB X-ray Structure Validation Report ⓘ

May 29, 2020 – 01:42 am BST

PDB ID	:	2X03
Title	:	The X-ray structure of the Streptomyces coelicolor A3 Chondroitin AC Lyase Y253A mutant
Authors	:	Elmabrouk, Z.H.; Taylor, E.J.; Vincent, F.; Smith, N.L.; Turkenburg, J.P.; Davies, G.J.; Black, G.W.
Deposited on	:	2009-12-04
Resolution	:	2.30 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 following versions of software and data (see references ①) were used in the production of this report:

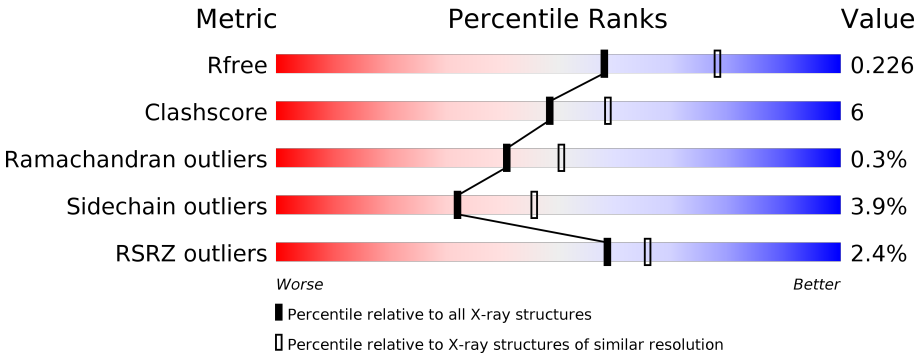
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

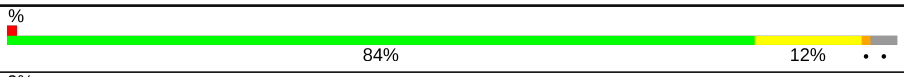
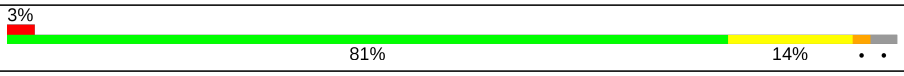
The reported resolution of this entry is 2.30 Å.

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}	130704	5042 (2.30-2.30)
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)
RSRZ outliers	127900	4938 (2.30-2.30)

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 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 <=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	765	
1	B	765	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 12283 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 PUTATIVE SECRETED LYASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	742	Total	C	N	O	S	0	5	0
			5719	3587	1064	1048	20			
1	B	743	Total	C	N	O	S	0	4	0
			5722	3587	1065	1050	20			

There are 44 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	expression tag	UNP O86516
A	2	GLY	-	expression tag	UNP O86516
A	3	SER	-	expression tag	UNP O86516
A	4	SER	-	expression tag	UNP O86516
A	5	HIS	-	expression tag	UNP O86516
A	6	HIS	-	expression tag	UNP O86516
A	7	HIS	-	expression tag	UNP O86516
A	8	HIS	-	expression tag	UNP O86516
A	9	HIS	-	expression tag	UNP O86516
A	10	HIS	-	expression tag	UNP O86516
A	11	SER	-	expression tag	UNP O86516
A	12	SER	-	expression tag	UNP O86516
A	13	GLY	-	expression tag	UNP O86516
A	14	LEU	-	expression tag	UNP O86516
A	15	VAL	-	expression tag	UNP O86516
A	16	PRO	-	expression tag	UNP O86516
A	17	ARG	-	expression tag	UNP O86516
A	18	GLY	-	expression tag	UNP O86516
A	19	SER	-	expression tag	UNP O86516
A	20	HIS	-	expression tag	UNP O86516
A	21	MET	-	expression tag	UNP O86516
B	1	MET	-	expression tag	UNP O86516
B	2	GLY	-	expression tag	UNP O86516
B	3	SER	-	expression tag	UNP O86516
B	4	SER	-	expression tag	UNP O86516

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Chain	Residue	Modelled	Actual	Comment	Reference
B	5	HIS	-	expression tag	UNP O86516
B	6	HIS	-	expression tag	UNP O86516
B	7	HIS	-	expression tag	UNP O86516
B	8	HIS	-	expression tag	UNP O86516
B	9	HIS	-	expression tag	UNP O86516
B	10	HIS	-	expression tag	UNP O86516
B	11	SER	-	expression tag	UNP O86516
B	12	SER	-	expression tag	UNP O86516
B	13	GLY	-	expression tag	UNP O86516
B	14	LEU	-	expression tag	UNP O86516
B	15	VAL	-	expression tag	UNP O86516
B	16	PRO	-	expression tag	UNP O86516
B	17	ARG	-	expression tag	UNP O86516
B	18	GLY	-	expression tag	UNP O86516
B	19	SER	-	expression tag	UNP O86516
B	20	HIS	-	expression tag	UNP O86516
B	21	MET	-	expression tag	UNP O86516
A	253	ALA	TYR	engineered mutation	UNP O86516
B	253	ALA	TYR	engineered mutation	UNP O86516

- Molecule 2 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	B	1	Total Mg 1 1	0	0

- Molecule 3 is water.

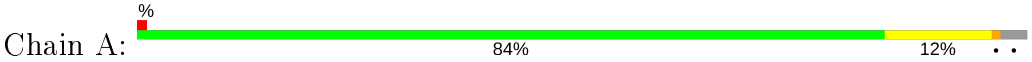
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	419	Total O 419 419	0	0
3	B	422	Total O 422 422	0	0

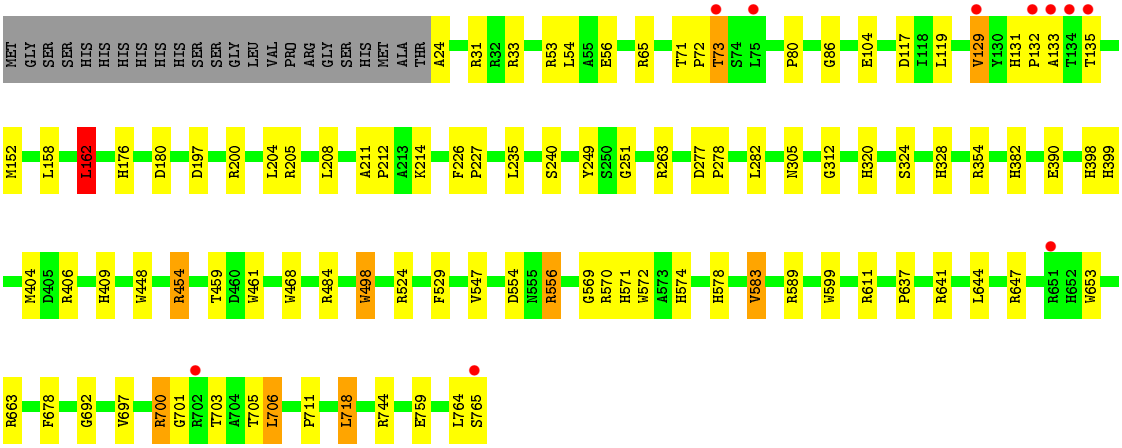
3 Residue-property plots (i)

These plots are drawn for all protein, RNA and DNA 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: PUTATIVE SECRETED LYASE

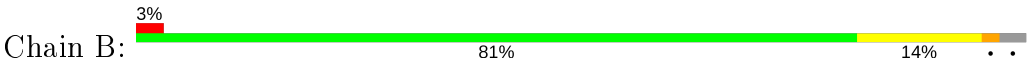
Chain A:

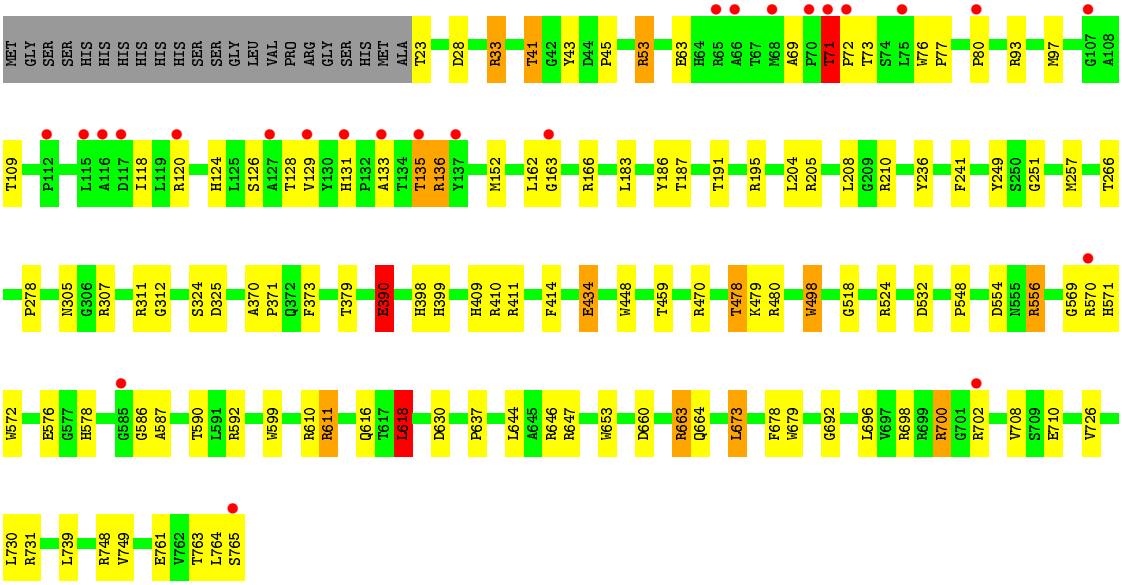




- Molecule 1: PUTATIVE SECRETED LYASE

Chain B:





4 Data and refinement statistics (i)

Property	Value	Source
Space group	H 3	Depositor
Cell constants a, b, c, α, β, γ	317.10Å 317.10Å 82.98Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	158.55 – 2.30 56.11 – 2.30	Depositor EDS
% Data completeness (in resolution range)	99.9 (158.55-2.30) 99.9 (56.11-2.30)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.79 (at 2.29Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.194 , 0.228 0.195 , 0.226	Depositor DCC
R_{free} test set	6932 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å^2)	23.2	Xtriage
Anisotropy	0.054	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.35 , 40.5	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Estimated twinning fraction	0.021 for h,-h-k,-l	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	12283	wwPDB-VP
Average B, all atoms (Å^2)	24.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.87% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MG

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	1.14	5/5874 (0.1%)	0.96	10/8026 (0.1%)
1	B	1.16	7/5877 (0.1%)	1.04	21/8032 (0.3%)
All	All	1.15	12/11751 (0.1%)	1.00	31/16058 (0.2%)

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	1	1

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	547	VAL	CB-CG1	6.42	1.66	1.52
1	A	759	GLU	CG-CD	5.88	1.60	1.51
1	B	434	GLU	CB-CG	5.85	1.63	1.52
1	B	390	GLU	CG-CD	5.84	1.60	1.51
1	A	56	GLU	CG-CD	5.66	1.60	1.51
1	B	236	TYR	CG-CD1	5.64	1.46	1.39
1	A	583	VAL	CB-CG1	-5.58	1.41	1.52
1	B	726	VAL	CB-CG2	-5.56	1.41	1.52
1	A	468	TRP	CE3-CZ3	5.48	1.47	1.38
1	B	576	GLU	CG-CD	5.47	1.60	1.51
1	B	710	GLU	CG-CD	5.26	1.59	1.51
1	B	698	ARG	CZ-NH1	5.09	1.39	1.33

All (31) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	71	THR	C-N-CD	-22.63	70.81	120.60
1	B	195	ARG	NE-CZ-NH2	-9.72	115.44	120.30
1	A	354	ARG	NE-CZ-NH2	-9.12	115.74	120.30
1	B	325	ASP	CB-CG-OD1	8.45	125.90	118.30
1	B	660	ASP	CB-CG-OD1	7.90	125.41	118.30
1	B	646	ARG	NE-CZ-NH2	-7.83	116.38	120.30
1	B	618	LEU	CA-CB-CG	7.70	133.01	115.30
1	A	718	LEU	CB-CG-CD1	-7.45	98.33	111.00
1	B	480	ARG	NE-CZ-NH1	6.88	123.74	120.30
1	B	611	ARG	NE-CZ-NH1	6.18	123.39	120.30
1	B	470	ARG	NE-CZ-NH1	6.08	123.34	120.30
1	B	532	ASP	CB-CG-OD1	5.85	123.56	118.30
1	B	673	LEU	CB-CG-CD2	-5.74	101.24	111.00
1	B	311	ARG	NE-CZ-NH1	5.72	123.16	120.30
1	A	263	ARG	NE-CZ-NH1	5.68	123.14	120.30
1	A	454	ARG	NE-CZ-NH2	5.58	123.09	120.30
1	B	610	ARG	NE-CZ-NH2	-5.54	117.53	120.30
1	B	195	ARG	NE-CZ-NH1	5.51	123.05	120.30
1	B	480	ARG	NE-CZ-NH2	-5.46	117.57	120.30
1	B	696	LEU	CA-CB-CG	5.39	127.69	115.30
1	B	663	ARG	NE-CZ-NH1	5.36	122.98	120.30
1	A	129	VAL	CB-CA-C	-5.28	101.37	111.40
1	A	589	ARG	CG-CD-NE	-5.22	100.83	111.80
1	A	484	ARG	NE-CZ-NH2	-5.17	117.71	120.30
1	A	162	LEU	CA-CB-CG	5.15	127.14	115.30
1	B	28	ASP	CB-CG-OD1	5.10	122.89	118.30
1	B	210	ARG	NE-CZ-NH2	-5.09	117.76	120.30
1	A	197	ASP	CB-CG-OD1	5.08	122.87	118.30
1	A	31	ARG	NE-CZ-NH2	5.04	122.82	120.30
1	B	630	ASP	CB-CG-OD1	5.04	122.83	118.30
1	B	33	ARG	CG-CD-NE	-5.01	101.28	111.80

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	A	571[B]	HIS	CA

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	764	LEU	Peptide

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	5719	0	5531	61	0
1	B	5722	0	5540	75	0
2	B	1	0	0	0	0
3	A	419	0	0	10	0
3	B	422	0	0	5	0
All	All	12283	0	11071	136	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 6.

All (136) 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:152:MET:CE	1:A:208:LEU:HD12	1.62	1.30
1:A:152:MET:HE3	1:A:208:LEU:HD12	1.24	1.10
1:B:152:MET:HE3	1:B:208:LEU:HD12	1.33	1.06
1:B:390:GLU:HA	1:B:390:GLU:OE1	1.54	1.01
1:A:24:ALA:HB3	3:A:2001:HOH:O	1.58	1.01
1:A:700:ARG:HH11	1:A:700:ARG:HG2	1.23	0.98
1:B:53[B]:ARG:NH2	1:B:370:ALA:O	1.98	0.96
1:A:571[B]:HIS:CD2	1:A:571[B]:HIS:N	2.27	0.95
1:A:556[B]:ARG:HE	1:A:578:HIS:HD2	1.18	0.91
1:A:152:MET:HE3	1:A:208:LEU:CD1	2.02	0.89
1:B:556[B]:ARG:HE	1:B:578:HIS:HD2	1.20	0.88
1:A:570:ARG:CA	1:A:571[B]:HIS:N	2.40	0.84
1:B:152:MET:CE	1:B:208:LEU:HD12	2.06	0.84
1:B:592:ARG:HH21	1:B:616:GLN:HE21	1.26	0.83
1:B:478:THR:HB	1:B:548:PRO:O	1.79	0.82
1:A:152:MET:CE	1:A:208:LEU:CD1	2.54	0.80
1:A:570:ARG:CA	1:A:571[A]:HIS:N	2.45	0.79
1:A:569:GLY:HA3	1:A:572:TRP:CE2	2.18	0.77
1:A:556[A]:ARG:HD3	1:A:578:HIS:HD2	1.49	0.77
1:A:556[A]:ARG:HD3	1:A:578:HIS:CD2	2.21	0.76
1:B:478:THR:HG23	3:B:2032:HOH:O	1.88	0.74
1:A:152:MET:HE1	1:A:208:LEU:HD12	1.70	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:556[B]:ARG:HE	1:A:578:HIS:CD2	2.07	0.71
1:B:478:THR:CG2	3:B:2032:HOH:O	2.37	0.71
1:B:586:GLY:HA2	3:B:2287:HOH:O	1.91	0.71
1:A:705:THR:HG23	3:A:2378:HOH:O	1.91	0.70
1:A:700:ARG:HG2	1:A:700:ARG:NH1	2.02	0.67
1:B:163:GLY:H	1:B:166:ARG:HH11	1.42	0.67
1:A:700:ARG:HH11	1:A:700:ARG:CG	2.03	0.65
1:A:132:PRO:HA	1:A:176:HIS:CD2	2.32	0.65
1:B:570:ARG:O	1:B:571:HIS:HB2	1.96	0.64
1:B:590:THR:HG22	1:B:618:LEU:HD13	1.80	0.63
1:B:312:GLY:HA3	1:B:599:TRP:CD2	2.33	0.62
1:B:556[B]:ARG:HE	1:B:578:HIS:CD2	2.10	0.62
1:B:390:GLU:OE1	1:B:390:GLU:CA	2.42	0.61
1:B:700:ARG:HH11	1:B:700:ARG:HG2	1.65	0.61
1:A:399:HIS:HD2	3:A:2102:HOH:O	1.83	0.60
1:A:312:GLY:HA3	1:A:599:TRP:CD2	2.37	0.60
1:B:556[A]:ARG:CD	1:B:578:HIS:HD2	2.15	0.57
1:A:556[A]:ARG:HH11	1:A:578:HIS:HD2	1.53	0.57
1:B:128:THR:O	1:B:131:HIS:HE1	1.88	0.57
1:A:382:HIS:HD2	3:A:2155:HOH:O	1.88	0.55
1:A:152:MET:HE2	1:A:204:LEU:HB3	1.89	0.55
1:B:592:ARG:HE	1:B:616:GLN:NE2	2.04	0.55
1:A:569:GLY:HA3	1:A:572:TRP:CZ2	2.42	0.55
1:B:186:TYR:CE1	1:B:191:THR:HA	2.42	0.55
1:B:730:LEU:HD21	1:B:763:THR:CG2	2.37	0.55
1:B:572:TRP:CE3	1:B:644:LEU:HD23	2.42	0.54
1:A:65:ARG:HD2	1:A:117:ASP:OD2	2.08	0.54
1:A:697:VAL:HG22	1:A:706:LEU:HG	1.88	0.54
1:B:647:ARG:HD2	1:B:653:TRP:CE2	2.43	0.54
1:B:76:TRP:CD1	1:B:93:ARG:NH1	2.76	0.54
1:B:448:TRP:CE3	1:B:637:PRO:HB3	2.43	0.54
1:B:324:SER:HB2	1:B:459:THR:HG23	1.90	0.53
1:B:592:ARG:HH21	1:B:616:GLN:NE2	2.01	0.53
1:A:574:HIS:CD2	1:A:641:ARG:HA	2.44	0.53
1:B:312:GLY:HA3	1:B:599:TRP:CE2	2.44	0.52
1:B:556[A]:ARG:HD3	1:B:578:HIS:HD2	1.73	0.52
1:B:664:GLN:NE2	1:B:679:TRP:HE1	2.08	0.52
1:A:158:LEU:O	1:A:162:LEU:HD22	2.09	0.52
1:A:398:HIS:HD2	1:A:409:HIS:ND1	2.07	0.52
1:B:590:THR:HG22	1:B:618:LEU:CD1	2.39	0.52
1:A:572:TRP:CE3	1:A:644:LEU:HD23	2.45	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:390:GLU:HA	1:A:390:GLU:OE1	2.09	0.51
1:B:33:ARG:NH1	1:B:266:THR:O	2.39	0.51
1:B:479:LYS:HE2	1:B:518:GLY:O	2.10	0.51
1:B:399:HIS:HD2	3:B:2099:HOH:O	1.92	0.51
1:B:152:MET:HE2	1:B:204:LEU:C	2.30	0.51
1:B:71:THR:O	1:B:124:HIS:CE1	2.63	0.51
1:A:54:LEU:HD13	1:A:104:GLU:O	2.11	0.51
1:B:739:LEU:HD11	1:B:748:ARG:HB2	1.93	0.50
1:B:569:GLY:HA3	1:B:572:TRP:CE2	2.45	0.50
1:B:673:LEU:C	1:B:673:LEU:HD23	2.31	0.50
1:B:731:ARG:NH2	1:B:761:GLU:OE1	2.45	0.49
1:A:324:SER:HB2	1:A:459:THR:HG23	1.95	0.49
1:B:556[A]:ARG:HD3	1:B:578:HIS:CD2	2.47	0.49
1:B:586:GLY:O	1:B:587:ALA:HB3	2.12	0.48
1:B:611:ARG:NH1	3:B:2320:HOH:O	2.38	0.48
1:A:454:ARG:NH1	3:A:2199:HOH:O	2.17	0.48
1:A:448:TRP:CE3	1:A:637:PRO:HB3	2.49	0.48
1:B:556[A]:ARG:HD2	1:B:578:HIS:HD2	1.78	0.48
1:B:128:THR:O	1:B:131:HIS:CE1	2.66	0.48
1:A:320:HIS:HE1	3:A:2306:HOH:O	1.97	0.47
1:B:664:GLN:HE21	1:B:679:TRP:HE1	1.63	0.47
1:B:708:VAL:HG11	1:B:749:VAL:HG21	1.95	0.47
1:B:241:PHE:CZ	1:B:257[B]:MET:HG3	2.50	0.47
1:B:69:ALA:O	1:B:71:THR:HG23	2.14	0.47
1:A:647:ARG:HD2	1:A:653:TRP:CE2	2.50	0.47
1:A:71:THR:O	1:A:73:THR:N	2.48	0.47
1:A:312:GLY:HA3	1:A:599:TRP:CE2	2.49	0.47
1:A:461:TRP:CE2	1:A:611:ARG:HG3	2.51	0.46
1:B:43:TYR:O	1:B:45:PRO:HD3	2.16	0.46
1:A:200:ARG:O	1:A:204:LEU:HD23	2.15	0.46
1:A:556[A]:ARG:CD	1:A:578:HIS:HD2	2.20	0.46
1:A:328:HIS:HE1	3:A:2116:HOH:O	1.97	0.46
1:A:404:MET:O	1:A:406:ARG:HG2	2.16	0.46
1:A:409:HIS:CE1	1:A:529:PHE:HB3	2.51	0.46
1:B:126:SER:O	1:B:131:HIS:HB3	2.16	0.46
1:A:744[B]:ARG:NH1	3:A:2405:HOH:O	2.26	0.45
1:A:556[A]:ARG:HH11	1:A:578:HIS:CD2	2.33	0.45
1:B:556[A]:ARG:CD	1:B:578:HIS:CD2	2.98	0.45
1:B:307:ARG:NE	1:B:434:GLU:OE1	2.48	0.44
1:B:135:THR:O	1:B:136:ARG:O	2.36	0.44
1:B:251:GLY:HA3	1:B:305:ASN:OD1	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:251:GLY:HA3	1:A:305:ASN:OD1	2.18	0.44
1:B:41:THR:O	1:B:379:THR:HG21	2.17	0.44
1:B:498:TRP:HE3	1:B:498:TRP:C	2.22	0.44
1:A:235:LEU:HD12	1:A:240:SER:O	2.18	0.43
1:A:211:ALA:HA	1:A:212:PRO:HD2	1.78	0.43
1:A:382:HIS:CD2	3:A:2155:HOH:O	2.69	0.43
1:A:498:TRP:CH2	1:A:711:PRO:HG2	2.54	0.43
1:A:556[B]:ARG:NE	1:A:578:HIS:HD2	2.00	0.43
1:B:398:HIS:HD2	1:B:409:HIS:ND1	2.17	0.42
1:A:277:ASP:HA	1:A:278:PRO:HD2	1.86	0.42
1:B:524:ARG:HD2	1:B:679:TRP:CD2	2.54	0.42
1:B:764:LEU:HD23	1:B:764:LEU:HA	1.81	0.42
1:B:76:TRP:HA	1:B:77:PRO:HD2	1.75	0.42
1:B:370:ALA:HA	1:B:371:PRO:HD3	1.83	0.42
1:B:73:THR:O	1:B:80:PRO:HA	2.19	0.42
1:B:93:ARG:O	1:B:97:MET:HG3	2.20	0.41
1:A:180:ASP:OD1	1:A:214:LYS:NZ	2.38	0.41
1:B:556[B]:ARG:NE	1:B:578:HIS:HD2	2.01	0.41
1:B:370:ALA:HB3	1:B:373:PHE:CD2	2.55	0.41
1:B:678:PHE:O	1:B:692:GLY:HA2	2.20	0.41
1:B:730:LEU:HD21	1:B:763:THR:HG23	2.02	0.41
1:A:524:ARG:NH1	3:A:2258:HOH:O	2.42	0.41
1:B:131:HIS:CD2	1:B:133:ALA:HB3	2.55	0.41
1:B:700:ARG:HG2	1:B:700:ARG:NH1	2.34	0.41
1:A:131:HIS:CE1	1:A:133:ALA:HB3	2.56	0.41
1:A:678:PHE:O	1:A:692:GLY:HA2	2.21	0.41
1:B:414:PHE:CB	1:B:637:PRO:HB2	2.51	0.41
1:A:80:PRO:O	1:A:86:GLY:HA3	2.21	0.40
1:B:131:HIS:NE2	1:B:133:ALA:HB3	2.37	0.40
1:B:410:ARG:O	1:B:411:ARG:HD2	2.21	0.40
1:B:97:MET:HE2	1:B:118:ILE:HG13	2.02	0.40
1:A:226:PHE:N	1:A:227:PRO:HD3	2.35	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	742/765 (97%)	712 (96%)	28 (4%)	2 (0%)	41 50
1	B	745/765 (97%)	703 (94%)	39 (5%)	3 (0%)	34 42
All	All	1487/1530 (97%)	1415 (95%)	67 (4%)	5 (0%)	41 50

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	136	ARG
1	A	72	PRO
1	B	71	THR
1	B	72	PRO
1	A	701	GLY

5.3.2 Protein sidechains (i)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	566/581 (97%)	545 (96%)	21 (4%)	34 48
1	B	567/581 (98%)	541 (95%)	26 (5%)	27 38
All	All	1133/1162 (98%)	1086 (96%)	47 (4%)	32 43

All (47) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	33	ARG
1	A	53	ARG
1	A	73	THR
1	A	119	LEU
1	A	129	VAL
1	A	135	THR
1	A	162	LEU

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Mol	Chain	Res	Type
1	A	205	ARG
1	A	249	TYR
1	A	282	LEU
1	A	498	TRP
1	A	554	ASP
1	A	556[A]	ARG
1	A	556[B]	ARG
1	A	583	VAL
1	A	663	ARG
1	A	700	ARG
1	A	703	THR
1	A	706	LEU
1	A	718	LEU
1	A	765	SER
1	B	23	THR
1	B	41	THR
1	B	53[A]	ARG
1	B	53[B]	ARG
1	B	63	GLU
1	B	109	THR
1	B	120	ARG
1	B	129	VAL
1	B	135	THR
1	B	162	LEU
1	B	183	LEU
1	B	187	THR
1	B	205	ARG
1	B	249	TYR
1	B	278	PRO
1	B	390	GLU
1	B	478	THR
1	B	498	TRP
1	B	554	ASP
1	B	556[A]	ARG
1	B	556[B]	ARG
1	B	618	LEU
1	B	663	ARG
1	B	700	ARG
1	B	702	ARG
1	B	765	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (18) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	64	HIS
1	A	243	GLN
1	A	289	HIS
1	A	320	HIS
1	A	328	HIS
1	A	382	HIS
1	A	398	HIS
1	A	399	HIS
1	A	578	HIS
1	B	79	HIS
1	B	131	HIS
1	B	243	GLN
1	B	328	HIS
1	B	398	HIS
1	B	399	HIS
1	B	578	HIS
1	B	616	GLN
1	B	664	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

Of 1 ligands modelled in this entry, 1 is monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95^{th} 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	742/765 (96%)	-0.26	10 (1%)	77	81	7, 21, 47, 57	1 (0%)
1	B	743/765 (97%)	-0.19	25 (3%)	45	52	8, 20, 59, 75	1 (0%)
All	All	1485/1530 (97%)	-0.23	35 (2%)	59	66	7, 21, 52, 75	2 (0%)

All (35) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	133	ALA	4.3
1	B	116	ALA	3.9
1	B	68	MET	3.4
1	A	765	SER	3.4
1	B	75	LEU	3.3
1	A	133	ALA	3.2
1	B	70	PRO	3.2
1	B	66	ALA	3.1
1	B	585	GLY	3.1
1	B	129	VAL	3.0
1	B	120	ARG	2.9
1	B	163	GLY	2.8
1	A	129	VAL	2.8
1	B	765	SER	2.7
1	B	107	GLY	2.7
1	B	112	PRO	2.7
1	A	134	THR	2.7
1	A	651	ARG	2.6
1	B	127	ALA	2.6
1	B	135	THR	2.5
1	A	135	THR	2.4
1	B	80	PRO	2.4
1	B	702	ARG	2.4
1	A	702	ARG	2.3

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Mol	Chain	Res	Type	RSRZ
1	B	72	PRO	2.3
1	B	71	THR	2.3
1	A	132	PRO	2.3
1	A	75	LEU	2.3
1	B	570	ARG	2.3
1	A	73	THR	2.2
1	B	115	LEU	2.2
1	B	117	ASP	2.2
1	B	137	TYR	2.2
1	B	131	HIS	2.1
1	B	65	ARG	2.1

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)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	MG	B	1766	1/1	0.96	0.10	30,30,30,30	0

6.5 Other polymers (i)

There are no such residues in this entry.