



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 23, 2023 – 05:11 AM EDT

PDB ID : 3D6A
Title : Crystal structure of the 2H-phosphatase domain of Sts-2 in complex with tungstate.
Authors : Chen, Y.; Carpino, N.; Nassar, N.
Deposited on : 2008-05-19
Resolution : 2.25 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 : 4.02b-467
Xtriage (Phenix) : 1.13
EDS : 2.35
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) : 2.35

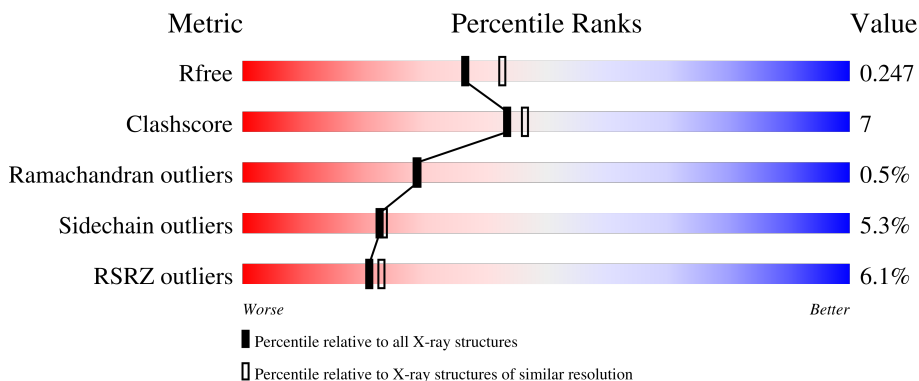
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.25 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	1377 (2.26-2.26)
Clashscore	141614	1487 (2.26-2.26)
Ramachandran outliers	138981	1449 (2.26-2.26)
Sidechain outliers	138945	1450 (2.26-2.26)
RSRZ outliers	127900	1356 (2.26-2.26)

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	273	 4% 83% 13% ..
1	B	273	 7% 77% 17% ..
1	C	273	 9% 79% 16% ..
1	D	273	 4% 73% 22% ..

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 8605 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 Sts-2 protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	266	2108	1333	374	386	15	0	0	0
1	B	264	2096	1327	372	382	15	0	0	0
1	C	265	2102	1330	373	384	15	0	0	0
1	D	266	2108	1333	374	386	15	0	0	0

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	350	ALA	-	expression tag	UNP Q8BX41
A	351	MET	-	expression tag	UNP Q8BX41
A	352	GLY	-	expression tag	UNP Q8BX41
A	353	SER	-	expression tag	UNP Q8BX41
A	364	ILE	VAL	conflict	UNP Q8BX41
B	350	ALA	-	expression tag	UNP Q8BX41
B	351	MET	-	expression tag	UNP Q8BX41
B	352	GLY	-	expression tag	UNP Q8BX41
B	353	SER	-	expression tag	UNP Q8BX41
B	364	ILE	VAL	conflict	UNP Q8BX41
C	350	ALA	-	expression tag	UNP Q8BX41
C	351	MET	-	expression tag	UNP Q8BX41
C	352	GLY	-	expression tag	UNP Q8BX41
C	353	SER	-	expression tag	UNP Q8BX41
C	364	ILE	VAL	conflict	UNP Q8BX41
D	350	ALA	-	expression tag	UNP Q8BX41
D	351	MET	-	expression tag	UNP Q8BX41
D	352	GLY	-	expression tag	UNP Q8BX41
D	353	SER	-	expression tag	UNP Q8BX41
D	364	ILE	VAL	conflict	UNP Q8BX41

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

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	4	Total Mg 4 4	0	0
2	B	1	Total Mg 1 1	0	0
2	C	2	Total Mg 2 2	0	0
2	D	2	Total Mg 2 2	0	0

- Molecule 3 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total Na 1 1	0	0
3	B	1	Total Na 1 1	0	0
3	C	1	Total Na 1 1	0	0
3	D	1	Total Na 1 1	0	0

- Molecule 4 is TUNGSTEN ION (three-letter code: W) (formula: W).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total W 1 1	0	0
4	B	1	Total W 1 1	0	0
4	C	1	Total W 1 1	0	0
4	D	1	Total W 1 1	0	0

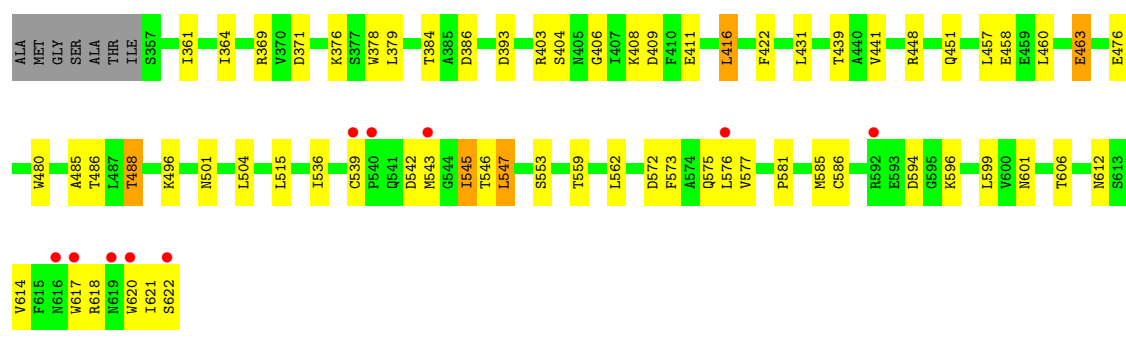
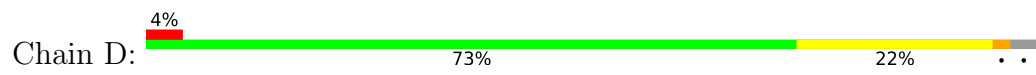
- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	60	Total O 60 60	0	0
5	B	36	Total O 36 36	0	0
5	C	38	Total O 38 38	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	D	40	Total	O	0	0
			40	40		



4 Data and refinement statistics i

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	78.20Å 116.67Å 121.47Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.95 – 2.25 47.97 – 2.25	Depositor EDS
% Data completeness (in resolution range)	99.2 (47.95-2.25) 99.2 (47.97-2.25)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.13 (at 2.24Å)	Xtrriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.208 , 0.257 0.201 , 0.247	Depositor DCC
R_{free} test set	2704 reflections (5.08%)	wwPDB-VP
Wilson B-factor (Å ²)	39.5	Xtrriage
Anisotropy	0.294	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 45.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	0.002 for -h,l,k	Xtrriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	8605	wwPDB-VP
Average B, all atoms (Å ²)	40.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 22.38 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 5.7652e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: NA, W, 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	0.55	1/2156 (0.0%)	0.62	0/2921
1	B	0.47	0/2144	0.60	1/2905 (0.0%)
1	C	0.50	0/2150	0.60	0/2913
1	D	0.49	0/2156	0.60	0/2921
All	All	0.50	1/8606 (0.0%)	0.61	1/11660 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	586	CYS	CB-SG	-9.01	1.67	1.82

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	460	LEU	CA-CB-CG	5.11	127.05	115.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2108	0	2107	27	0
1	B	2096	0	2097	36	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	2102	0	2102	26	0
1	D	2108	0	2107	47	0
2	A	4	0	0	0	0
2	B	1	0	0	0	0
2	C	2	0	0	0	0
2	D	2	0	0	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
4	C	1	0	0	0	0
4	D	1	0	0	0	0
5	A	60	0	0	2	0
5	B	36	0	0	2	0
5	C	38	0	0	1	0
5	D	40	0	0	2	0
All	All	8605	0	8413	113	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 7.

All (113) 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:599:LEU:HD11	1:C:621:ILE:HG22	1.33	1.06
1:A:369:ARG:HG3	1:A:372:GLN:HG3	1.54	0.87
1:A:599:LEU:HD11	1:C:621:ILE:CG2	2.05	0.87
1:A:376:LYS:NZ	1:D:476:GLU:OE2	2.07	0.86
1:D:441:VAL:HG11	1:D:457:LEU:HD11	1.63	0.81
1:B:520:SER:H	1:B:523:GLN:HE21	1.28	0.80
1:B:369:ARG:HG3	1:B:372:GLN:HG3	1.67	0.76
1:D:384:THR:HG22	1:D:386:ASP:H	1.50	0.75
1:C:425:ARG:NH1	1:C:458:GLU:OE1	2.18	0.74
1:A:616:ASN:HD22	1:A:619:ASN:H	1.37	0.71
1:B:579:LYS:HE2	1:D:620:TRP:CG	2.27	0.70
1:C:491:THR:OG1	1:C:494:GLU:HG3	1.92	0.69
1:D:458:GLU:HA	1:D:463:GLU:CG	2.22	0.69
1:A:599:LEU:CD1	1:C:621:ILE:HG22	2.20	0.68
1:A:476:GLU:OE2	1:D:376:LYS:NZ	2.21	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:376:LYS:HD2	1:D:480:TRP:HB3	1.77	0.66
1:C:614:VAL:HG11	1:D:620:TRP:HZ3	1.60	0.66
1:B:379:LEU:HD12	1:B:411:GLU:HG3	1.76	0.65
1:B:441:VAL:HG21	1:B:457:LEU:HD21	1.77	0.65
1:D:403:ARG:NH2	1:D:488:THR:O	2.29	0.65
1:A:369:ARG:HD2	1:A:448:ARG:HD2	1.79	0.64
1:D:458:GLU:HA	1:D:463:GLU:HG3	1.81	0.62
1:B:563:LEU:HD11	1:B:599:LEU:HD22	1.81	0.62
1:B:586:CYS:SG	1:B:599:LEU:HD11	2.39	0.61
1:B:454:LYS:O	1:B:458:GLU:HG3	2.00	0.61
1:C:436:VAL:HB	1:C:545:ILE:HD12	1.82	0.61
1:A:579:LYS:NZ	1:D:614:VAL:HG21	2.15	0.60
1:A:403:ARG:NH2	1:A:488:THR:O	2.32	0.60
1:B:576:LEU:HD23	1:D:620:TRP:CD1	2.37	0.59
1:A:485:ALA:O	1:A:488:THR:HG22	2.02	0.59
1:B:621:ILE:HG22	1:D:599:LEU:HD11	1.84	0.59
1:C:416:LEU:HD22	1:C:451:GLN:HB3	1.84	0.58
1:C:536:ILE:HG13	1:C:562:LEU:HD21	1.85	0.58
1:D:485:ALA:O	1:D:488:THR:HG22	2.04	0.57
1:B:579:LYS:O	1:B:579:LYS:HD3	2.04	0.57
1:A:366:HIS:NE2	5:A:625:HOH:O	2.33	0.57
1:D:408:LYS:O	1:D:411:GLU:HG2	2.05	0.56
1:A:576:LEU:HD11	1:C:620:TRP:O	2.06	0.56
1:D:458:GLU:HG2	1:D:463:GLU:HG2	1.89	0.55
1:B:412:ASN:HB3	1:B:487:LEU:HG	1.89	0.55
1:B:426:LEU:HD23	1:B:607:LEU:HD13	1.89	0.54
1:D:620:TRP:N	1:D:621:ILE:HA	2.23	0.54
1:B:520:SER:H	1:B:523:GLN:NE2	2.01	0.54
1:A:441:VAL:HG21	1:A:457:LEU:HD21	1.89	0.54
1:B:579:LYS:O	1:B:579:LYS:CD	2.57	0.53
1:B:576:LEU:HA	1:D:620:TRP:HE1	1.72	0.52
1:D:575:GLN:NE2	5:D:645:HOH:O	2.42	0.52
1:A:416:LEU:HD22	1:A:451:GLN:HB3	1.91	0.52
1:D:620:TRP:CG	1:D:620:TRP:O	2.63	0.52
1:B:391:ARG:HD2	1:B:398:ARG:HA	1.91	0.51
1:C:559:THR:HG21	1:C:586:CYS:SG	2.51	0.51
1:D:496:LYS:HD3	1:D:504:LEU:HD21	1.91	0.51
1:C:553:SER:HB2	1:C:573:PHE:HZ	1.76	0.50
1:A:579:LYS:HZ1	1:D:614:VAL:HG21	1.76	0.50
1:D:553:SER:HB2	1:D:573:PHE:HZ	1.77	0.50
1:D:369:ARG:HD2	1:D:448:ARG:HD2	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:359:ARG:HH21	1:C:539:CYS:HB3	1.76	0.49
1:A:369:ARG:HD2	1:A:448:ARG:CD	2.41	0.49
1:D:458:GLU:HA	1:D:463:GLU:HG2	1.92	0.49
1:C:403:ARG:HG2	1:C:490:LEU:HD21	1.95	0.49
1:C:476:GLU:HB2	5:C:71:HOH:O	2.12	0.49
1:B:599:LEU:CD2	1:D:622:SER:HB2	2.43	0.49
1:C:412:ASN:HB3	1:C:487:LEU:HG	1.95	0.49
1:B:553:SER:HB2	1:B:573:PHE:HZ	1.77	0.48
1:D:545:ILE:HD11	1:D:547:LEU:CD1	2.43	0.48
1:D:536:ILE:HG21	1:D:562:LEU:HD11	1.94	0.48
1:B:493:GLU:HG2	1:B:494:GLU:N	2.29	0.48
1:B:582:SER:H	1:D:612:ASN:HD21	1.60	0.47
1:B:615:PHE:HB2	1:D:581:PRO:HG3	1.96	0.47
1:A:381:GLN:O	1:A:392:PRO:HG3	2.14	0.47
1:D:416:LEU:HD22	1:D:451:GLN:HB3	1.97	0.47
1:A:559:THR:HG21	1:A:586:CYS:SG	2.54	0.47
1:A:403:ARG:HH22	1:A:413:ASP:CB	2.27	0.47
1:D:618:ARG:O	1:D:621:ILE:HG13	2.15	0.46
1:B:366:HIS:NE2	5:B:626:HOH:O	2.35	0.46
1:C:479:LYS:HB2	1:C:519:GLU:O	2.16	0.46
1:D:559:THR:HG21	1:D:586:CYS:SG	2.56	0.46
1:B:409:ASP:HB2	5:B:655:HOH:O	2.15	0.46
1:B:579:LYS:CD	1:B:579:LYS:C	2.83	0.46
1:C:588:CYS:SG	1:C:599:LEU:HD12	2.56	0.46
1:B:436:VAL:HB	1:B:545:ILE:HD12	1.98	0.45
1:B:599:LEU:HD23	1:D:622:SER:HB2	1.99	0.45
1:B:393:ASP:OD2	1:D:606:THR:HG23	2.16	0.45
1:B:580:ILE:HD11	1:D:617:TRP:CZ3	2.52	0.45
1:B:361:ILE:HD13	1:B:546:THR:HB	1.98	0.44
1:D:572:ASP:O	1:D:576:LEU:HD13	2.17	0.44
1:A:480:TRP:HB3	1:D:376:LYS:HD2	1.99	0.44
1:D:486:THR:HG21	1:D:515:LEU:HB2	1.99	0.44
1:C:483:SER:OG	1:C:484:LYS:N	2.49	0.43
1:C:510:LEU:HD23	1:C:515:LEU:HD22	1.98	0.43
1:D:361:ILE:HD13	1:D:546:THR:HB	1.99	0.43
1:A:436:VAL:HB	1:A:545:ILE:HD12	2.00	0.43
1:D:501:ASN:HB3	5:D:659:HOH:O	2.18	0.43
1:A:591:ASN:HB3	1:A:594:ASP:OD1	2.19	0.43
1:A:361:ILE:HD13	1:A:546:THR:HB	2.00	0.42
1:B:606:THR:HG23	1:D:393:ASP:OD2	2.20	0.42
1:C:361:ILE:HD13	1:C:546:THR:HB	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:404:SER:C	1:D:406:GLY:H	2.22	0.42
1:B:572:ASP:O	1:B:576:LEU:HD12	2.20	0.42
1:D:371:ASP:HB3	1:D:378:TRP:CD1	2.55	0.42
1:B:559:THR:HG21	1:B:586:CYS:SG	2.60	0.41
1:C:481:GLU:OE1	1:C:483:SER:HB3	2.20	0.41
1:A:536:ILE:HD13	1:A:536:ILE:HA	1.86	0.41
1:C:586:CYS:SG	1:C:599:LEU:HD11	2.60	0.41
1:C:600:VAL:CG1	1:C:601:ASN:N	2.83	0.41
1:B:582:SER:N	1:D:612:ASN:HD21	2.18	0.41
1:C:364:ILE:HG12	1:C:585:MET:HG2	2.02	0.41
1:D:364:ILE:HG12	1:D:585:MET:HG2	2.02	0.41
1:A:458:GLU:OE1	5:A:669:HOH:O	2.21	0.40
1:D:594:ASP:OD1	1:D:596:LYS:HG2	2.22	0.40
1:B:555:LEU:HD22	1:B:580:ILE:HD13	2.03	0.40
1:C:425:ARG:NH2	1:C:459:GLU:OE2	2.55	0.40
1:B:516:MET:HA	1:B:517:PRO:HD2	1.99	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	264/273 (97%)	255 (97%)	9 (3%)	0	100	100
1	B	262/273 (96%)	256 (98%)	4 (2%)	2 (1%)	19	17
1	C	263/273 (96%)	248 (94%)	12 (5%)	3 (1%)	14	10
1	D	264/273 (97%)	257 (97%)	7 (3%)	0	100	100
All	All	1053/1092 (96%)	1016 (96%)	32 (3%)	5 (0%)	29	29

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	543	MET
1	C	515	LEU
1	B	405	ASN
1	B	407	ILE
1	C	385	ALA

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	233/237 (98%)	223 (96%)	10 (4%)	29	33
1	B	231/237 (98%)	217 (94%)	14 (6%)	18	18
1	C	232/237 (98%)	223 (96%)	9 (4%)	32	38
1	D	233/237 (98%)	217 (93%)	16 (7%)	15	14
All	All	929/948 (98%)	880 (95%)	49 (5%)	22	23

All (49) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	369	ARG
1	A	398	ARG
1	A	408	LYS
1	A	416	LEU
1	A	460	LEU
1	A	486	THR
1	A	488	THR
1	A	499	ASN
1	A	541	GLN
1	A	620	TRP
1	B	407	ILE
1	B	416	LEU
1	B	439	THR
1	B	460	LEU
1	B	480	TRP
1	B	487	LEU
1	B	488	THR

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Mol	Chain	Res	Type
1	B	507	ARG
1	B	539	CYS
1	B	543	MET
1	B	547	LEU
1	B	576	LEU
1	B	579	LYS
1	B	599	LEU
1	C	380	GLN
1	C	416	LEU
1	C	444	SER
1	C	487	LEU
1	C	513	CYS
1	C	515	LEU
1	C	547	LEU
1	C	590	GLU
1	C	593	GLU
1	D	379	LEU
1	D	409	ASP
1	D	416	LEU
1	D	422	PHE
1	D	431	LEU
1	D	439	THR
1	D	460	LEU
1	D	463	GLU
1	D	488	THR
1	D	539	CYS
1	D	542	ASP
1	D	543	MET
1	D	545	ILE
1	D	547	LEU
1	D	577	VAL
1	D	601	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	612	ASN
1	A	616	ASN
1	B	523	GLN
1	D	575	GLN
1	D	612	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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 17 ligands modelled in this entry, 17 are 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 [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	266/273 (97%)	0.19	11 (4%) 37 40	20, 34, 55, 63	0
1	B	264/273 (96%)	0.39	19 (7%) 15 16	25, 43, 58, 66	0
1	C	265/273 (97%)	0.48	25 (9%) 8 9	21, 41, 66, 74	0
1	D	266/273 (97%)	0.24	10 (3%) 40 43	24, 39, 58, 70	0
All	All	1061/1092 (97%)	0.33	65 (6%) 21 23	20, 39, 59, 74	0

All (65) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	480	TRP	8.7
1	B	620	TRP	7.8
1	C	482	ALA	6.9
1	B	386	ASP	6.3
1	B	485	ALA	6.0
1	A	620	TRP	5.8
1	A	488	THR	5.8
1	C	485	ALA	5.2
1	D	620	TRP	5.2
1	B	543	MET	4.7
1	B	483	SER	4.3
1	C	481	GLU	4.3
1	A	357	SER	4.2
1	C	543	MET	4.2
1	B	480	TRP	4.0
1	B	385	ALA	4.0
1	C	487	LEU	3.7
1	D	540	PRO	3.7
1	C	484	LYS	3.7
1	C	483	SER	3.6
1	C	386	ASP	3.6

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Mol	Chain	Res	Type	RSRZ
1	B	481	GLU	3.6
1	D	616	ASN	3.5
1	C	486	THR	3.5
1	B	404	SER	3.5
1	B	516	MET	3.4
1	A	405	ASN	3.3
1	A	538	THR	3.2
1	C	539	CYS	3.2
1	D	539	CYS	3.2
1	C	593	GLU	3.1
1	A	542	ASP	3.0
1	B	484	LYS	3.0
1	B	487	LEU	2.9
1	D	592	ARG	2.9
1	A	592	ARG	2.9
1	B	541	GLN	2.9
1	B	538	THR	2.8
1	C	542	ASP	2.8
1	C	516	MET	2.8
1	A	486	THR	2.7
1	C	569	GLU	2.7
1	C	404	SER	2.7
1	B	388	LYS	2.7
1	D	622	SER	2.6
1	C	541	GLN	2.6
1	D	543	MET	2.6
1	A	540	PRO	2.5
1	A	386	ASP	2.4
1	B	592	ARG	2.4
1	B	540	PRO	2.4
1	C	385	ALA	2.4
1	D	576	LEU	2.3
1	C	358	ARG	2.3
1	A	385	ALA	2.3
1	C	387	GLY	2.3
1	B	405	ASN	2.2
1	D	619	ASN	2.2
1	B	611	ALA	2.2
1	C	622	SER	2.1
1	D	617	TRP	2.1
1	C	513	CYS	2.1
1	C	507	ARG	2.0

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Mol	Chain	Res	Type	RSRZ
1	C	540	PRO	2.0
1	C	477	TRP	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 monosaccharides 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, 95th 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	C	6	1/1	0.73	0.30	58,58,58,58	0
2	MG	C	8	1/1	0.80	0.44	64,64,64,64	0
2	MG	B	9	1/1	0.82	0.34	62,62,62,62	0
2	MG	A	5	1/1	0.88	0.31	44,44,44,44	0
2	MG	A	2	1/1	0.89	0.28	54,54,54,54	0
3	NA	B	1	1/1	0.89	0.10	48,48,48,48	0
2	MG	D	1	1/1	0.91	0.28	29,29,29,29	0
2	MG	A	7	1/1	0.95	0.28	31,31,31,31	0
2	MG	A	3	1/1	0.96	0.18	44,44,44,44	0
3	NA	C	3	1/1	0.96	0.07	38,38,38,38	0
2	MG	D	4	1/1	0.98	0.26	44,44,44,44	0
3	NA	D	623	1/1	0.98	0.29	38,38,38,38	0
3	NA	A	623	1/1	0.99	0.19	36,36,36,36	0
4	W	A	624	1/1	1.00	0.11	28,28,28,28	0
4	W	B	7	1/1	1.00	0.11	34,34,34,34	0
4	W	C	12	1/1	1.00	0.11	32,32,32,32	0
4	W	D	17	1/1	1.00	0.10	30,30,30,30	0

6.5 Other polymers [i](#)

There are no such residues in this entry.