



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 14, 2017 – 03:57 pm GMT

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

<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
Xtriage (Phenix)	:	1.9-1692
EDS	:	trunk28620
Percentile statistics	:	20161228.v01 (using entries in the PDB archive December 28th 2016)
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)	:	recalc28949

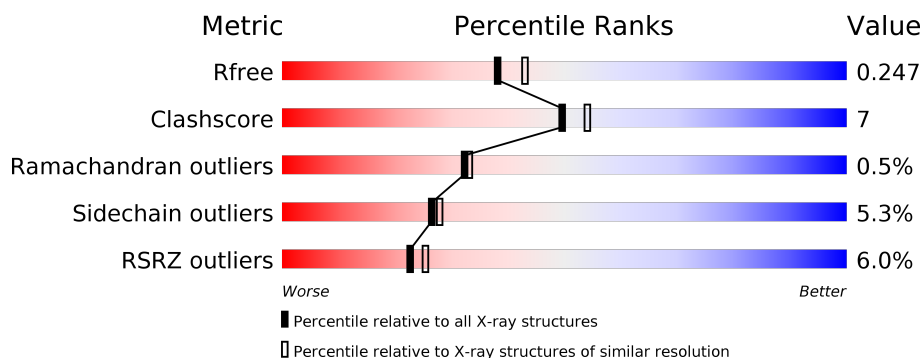
1 Overall quality at a glance

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}	100719	1062 (2.26-2.26)
Clashscore	112137	1178 (2.26-2.26)
Ramachandran outliers	110173	1145 (2.26-2.26)
Sidechain outliers	110143	1146 (2.26-2.26)
RSRZ outliers	101464	1066 (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 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	273	<div> <div>4%</div> <div> <div></div> <div>83%</div> <div>13%</div> <div>••</div> </div> </div>
1	B	273	<div> <div>7%</div> <div> <div></div> <div>77%</div> <div>17%</div> <div>••</div> </div> </div>
1	C	273	<div> <div>9%</div> <div> <div></div> <div>79%</div> <div>16%</div> <div>••</div> </div> </div>
1	D	273	<div> <div>4%</div> <div> <div></div> <div>73%</div> <div>22%</div> <div>••</div> </div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	MG	C	8	-	-	-	X

2 Entry composition

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
1	A	266	Total	C	N	O	S	0	0	0
			2108	1333	374	386	15			
1	B	264	Total	C	N	O	S	0	0	0
			2096	1327	372	382	15			
1	C	265	Total	C	N	O	S	0	0	0
			2102	1330	373	384	15			
1	D	266	Total	C	N	O	S	0	0	0
			2108	1333	374	386	15			

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	B	1	Total	Mg	0	0
			1	1		
2	A	4	Total	Mg	0	0
			4	4		
2	D	2	Total	Mg	0	0
			2	2		
2	C	2	Total	Mg	0	0
			2	2		

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

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

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

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

- Molecule 5 is water.

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

Continued on next page...

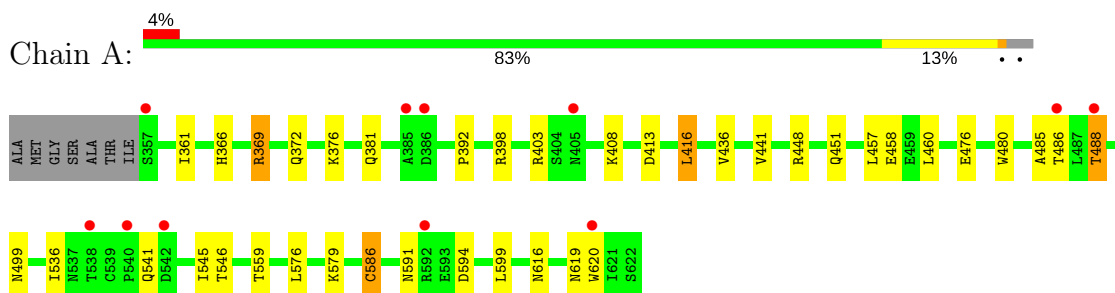
Continued from previous page...

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

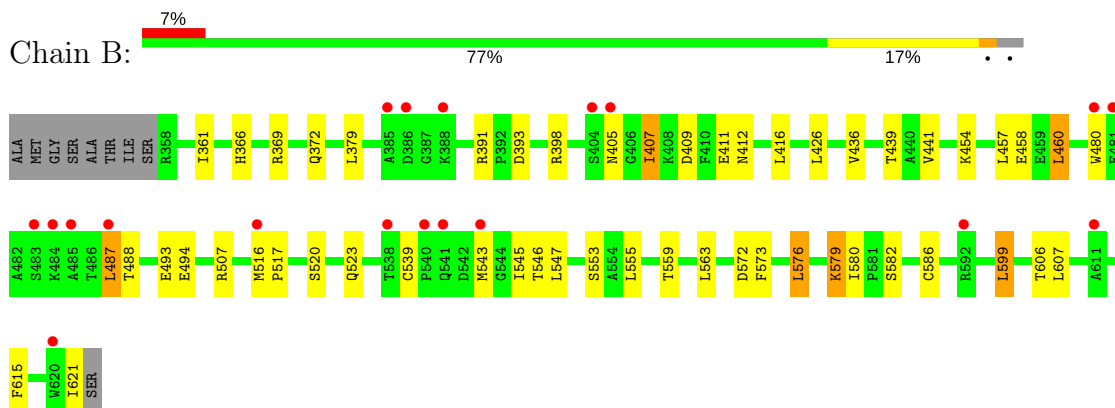
3 Residue-property plots [i](#)

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.

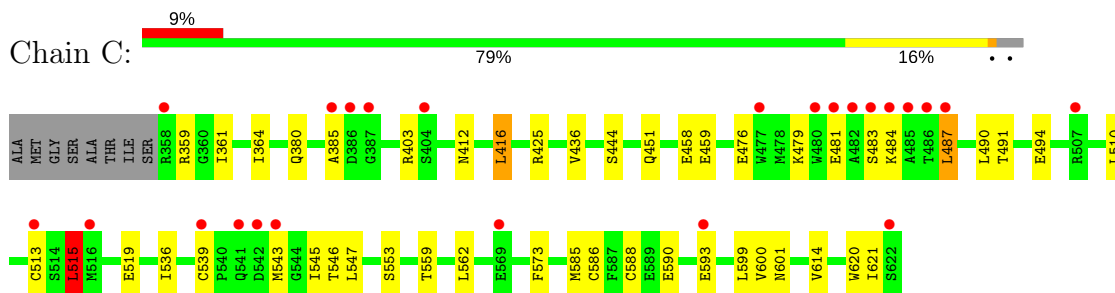
- Molecule 1: Sts-2 protein



- Molecule 1: Sts-2 protein

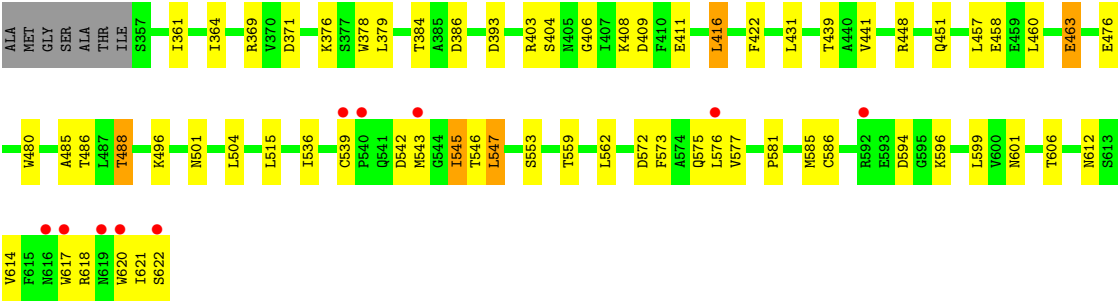


- Molecule 1: Sts-2 protein



- Molecule 1: Sts-2 protein





4 Data and refinement statistics

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)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.208 , 0.257 0.201 , 0.247	Depositor DCC
R_{free} test set	2694 reflections (5.35%)	DCC
Wilson B-factor (Å ²)	39.5	Xtriage
Anisotropy	0.294	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 45.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.002 for -h,l,k	Xtriage
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

Xtriage'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, MG, W

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

Continued on next page...

Continued from previous page...

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

Continued on next page...

Continued from previous page...

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:CD	1:B:579:LYS:O	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:O	1:D:620:TRP:CG	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

Continued on next page...

Continued from previous page...

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:C:412:ASN:HB3	1:C:487:LEU:HG	1.95	0.49
1:B:599:LEU:CD2	1:D:622:SER:HB2	2.43	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

Continued on next page...

Continued from previous page...

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 ⓘ

5.3.1 Protein backbone ⓘ

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%)	22	20
1	C	263/273 (96%)	248 (94%)	12 (5%)	3 (1%)	17	12
1	D	264/273 (97%)	257 (97%)	7 (3%)	0	100	100
All	All	1053/1092 (96%)	1016 (96%)	32 (3%)	5 (0%)	32	33

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 ⓘ

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%)	33	39
1	B	231/237 (98%)	217 (94%)	14 (6%)	22	21
1	C	232/237 (98%)	223 (96%)	9 (4%)	37	45
1	D	233/237 (98%)	217 (93%)	16 (7%)	18	17
All	All	929/948 (98%)	880 (95%)	49 (5%)	26	28

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

Continued on next page...

Continued from previous page...

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

Some 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 carbohydrates 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%) 38 41	20, 34, 55, 63	0
1	B	264/273 (96%)	0.39	19 (7%) 16 18	25, 43, 58, 66	0
1	C	265/273 (97%)	0.48	24 (9%) 10 11	21, 41, 66, 74	0
1	D	266/273 (97%)	0.24	10 (3%) 41 44	24, 39, 58, 70	0
All	All	1061/1092 (97%)	0.33	64 (6%) 23 25	20, 39, 59, 74	0

All (64) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	480	TRP	8.6
1	B	620	TRP	7.8
1	C	482	ALA	7.0
1	B	386	ASP	6.4
1	A	620	TRP	6.0
1	B	485	ALA	5.9
1	A	488	THR	5.7
1	D	620	TRP	5.2
1	C	485	ALA	5.2
1	B	543	MET	4.7
1	C	481	GLU	4.3
1	B	483	SER	4.2
1	A	357	SER	4.1
1	B	480	TRP	4.0
1	C	543	MET	4.0
1	B	385	ALA	4.0
1	C	483	SER	3.7
1	C	487	LEU	3.7
1	D	540	PRO	3.7
1	C	484	LYS	3.7
1	B	481	GLU	3.6

Continued on next page...

Continued from previous page...

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

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
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 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å ²)	Q<0.9
2	MG	C	8	1/1	0.80	0.44	4.66	64,64,64,64	0
2	MG	D	1	1/1	0.91	0.28	0.81	29,29,29,29	0
2	MG	A	7	1/1	0.95	0.28	0.06	31,31,31,31	0
4	W	C	12	1/1	1.00	0.11	-0.33	32,32,32,32	0
4	W	B	7	1/1	1.00	0.11	-0.91	34,34,34,34	0
4	W	D	17	1/1	1.00	0.10	-1.76	30,30,30,30	0
4	W	A	624	1/1	1.00	0.11	-2.05	28,28,28,28	0
2	MG	A	2	1/1	0.89	0.28	-	54,54,54,54	0
3	NA	B	1	1/1	0.88	0.10	-	48,48,48,48	0
3	NA	D	623	1/1	0.98	0.29	-	38,38,38,38	0
2	MG	D	4	1/1	0.98	0.25	-	44,44,44,44	0
2	MG	A	3	1/1	0.96	0.18	-	44,44,44,44	0
2	MG	A	5	1/1	0.87	0.31	-	44,44,44,44	0
3	NA	A	623	1/1	0.99	0.19	-	36,36,36,36	0
2	MG	B	9	1/1	0.82	0.34	-	62,62,62,62	0
2	MG	C	6	1/1	0.73	0.30	-	58,58,58,58	0
3	NA	C	3	1/1	0.96	0.07	-	38,38,38,38	0

6.5 Other polymers [i](#)

There are no such residues in this entry.