



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 02:46 PM UTC

PDB ID : 8B46 / pdb_00008b46
Title : Crystal structure of the SUN1-KASH6 9:9 complex
Authors : Gurusaran, M.; Erlandsen, B.S.; Davies, O.R.
Deposited on : 2022-09-19
Resolution : 1.67 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:

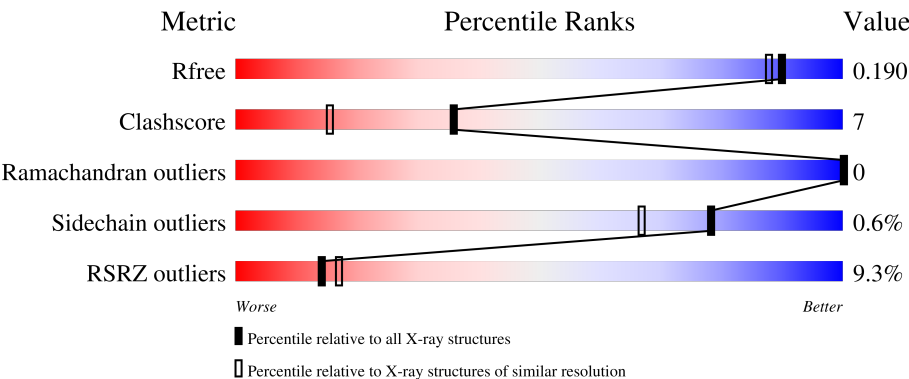
MolProbity	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

1 Overall quality at a glance i

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

The reported resolution of this entry is 1.67 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	1054 (1.68-1.68)
Clashscore	190562	1078 (1.68-1.68)
Ramachandran outliers	187476	1068 (1.68-1.68)
Sidechain outliers	187428	1067 (1.68-1.68)
RSRZ outliers	180081	1055 (1.68-1.68)

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	203	5% 82% 13% .
1	B	203	7% 85% 11% .
1	C	203	7% 84% 11% .
2	D	44	11% 48% 11% 41%
2	E	44	27% 30% 70%

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Mol	Chain	Length	Quality of chain
2	F	44	5% • 5% 93%

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 criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	CL	A	901	-	-	X	-

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 5547 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 SUN domain-containing protein 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	194	Total	C	N	O	S	0	0	0
			1537	985	253	291	8			
1	B	194	Total	C	N	O	S	0	0	0
			1537	985	253	291	8			
1	C	194	Total	C	N	O	S	0	0	0
			1537	985	253	291	8			

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	610	GLY	-	expression tag	UNP O94901
A	611	SER	-	expression tag	UNP O94901
A	612	GLY	-	expression tag	UNP O94901
A	613	GLY	-	expression tag	UNP O94901
A	614	SER	-	expression tag	UNP O94901
A	615	GLY	-	expression tag	UNP O94901
B	610	GLY	-	expression tag	UNP O94901
B	611	SER	-	expression tag	UNP O94901
B	612	GLY	-	expression tag	UNP O94901
B	613	GLY	-	expression tag	UNP O94901
B	614	SER	-	expression tag	UNP O94901
B	615	GLY	-	expression tag	UNP O94901
C	610	GLY	-	expression tag	UNP O94901
C	611	SER	-	expression tag	UNP O94901
C	612	GLY	-	expression tag	UNP O94901
C	613	GLY	-	expression tag	UNP O94901
C	614	SER	-	expression tag	UNP O94901
C	615	GLY	-	expression tag	UNP O94901

- Molecule 2 is a protein called Inositol 1,4,5-triphosphate receptor associated 2.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	D	26	Total	C	N	O	0	0	0
			222	143	40	39			
2	E	13	Total	C	N	O	0	0	0
			106	68	22	16			
2	F	3	Total	C	N	O	0	0	0
			22	15	3	4			

There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	512	GLY	-	expression tag	UNP Q12912
D	513	SER	-	expression tag	UNP Q12912
D	514	MET	-	expression tag	UNP Q12912
E	512	GLY	-	expression tag	UNP Q12912
E	513	SER	-	expression tag	UNP Q12912
E	514	MET	-	expression tag	UNP Q12912
F	512	GLY	-	expression tag	UNP Q12912
F	513	SER	-	expression tag	UNP Q12912
F	514	MET	-	expression tag	UNP Q12912

- Molecule 3 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Cl	0	0
			1	1		

- Molecule 4 is POTASSIUM ION (CCD ID: K) (formula: K).

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

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	189	Total	O	0	0
			189	189		
5	B	168	Total	O	0	0
			168	168		

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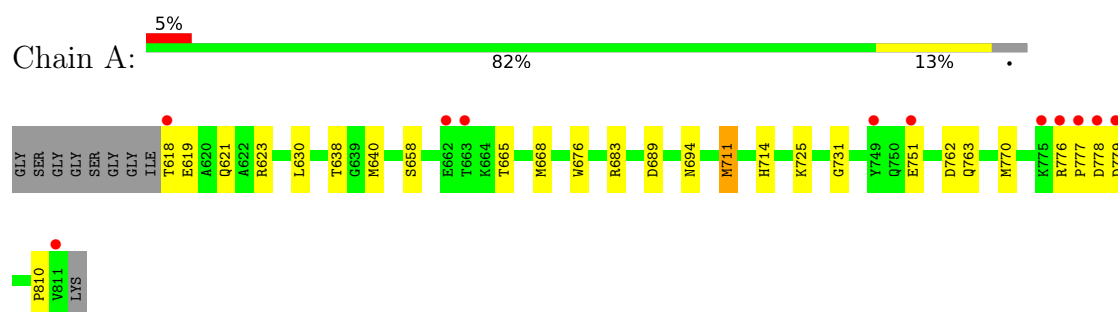
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	C	211	Total 211	O 211	0	0
5	D	12	Total 12	O 12	0	0
5	E	1	Total 1	O 1	0	0
5	F	1	Total 1	O 1	0	0

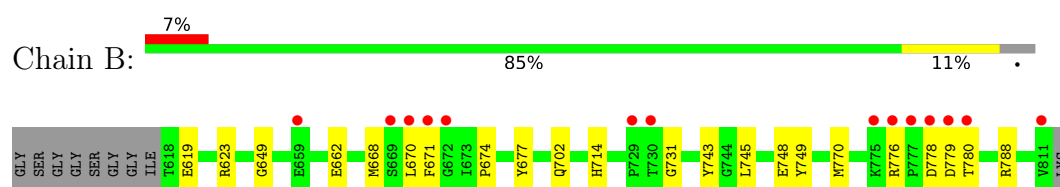
3 Residue-property plots [i](#)

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.

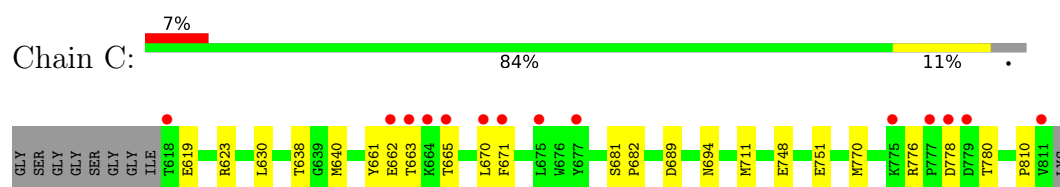
- Molecule 1: SUN domain-containing protein 1



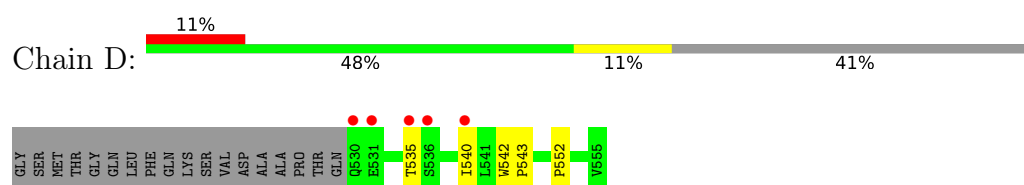
- Molecule 1: SUN domain-containing protein 1



- Molecule 1: SUN domain-containing protein 1

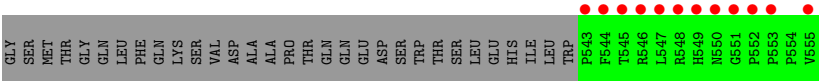


- Molecule 2: Inositol 1,4,5-triphosphate receptor associated 2

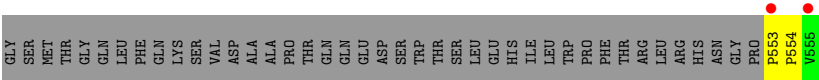


- Molecule 2: Inositol 1,4,5-triphosphate receptor associated 2





● Molecule 2: Inositol 1,4,5-triphosphate receptor associated 2



4 Data and refinement statistics

Property	Value	Source
Space group	P 63	Depositor
Cell constants a, b, c, α , β , γ	134.09Å 134.09Å 106.59Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	43.89 – 1.67 43.89 – 1.67	Depositor EDS
% Data completeness (in resolution range)	55.7 (43.89-1.67) 56.2 (43.89-1.67)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.89 (at 1.66Å)	Xtriage
Refinement program	PHENIX 1.20.1_4487	Depositor
R, R_{free}	0.166 , 0.190 0.166 , 0.190	Depositor DCC
R_{free} test set	3446 reflections (2.71%)	wwPDB-VP
Wilson B-factor (Å ²)	25.3	Xtriage
Anisotropy	0.024	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 51.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.030 for h,-h-k,-l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	5547	wwPDB-VP
Average B, all atoms (Å ²)	40.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.21% 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 [i](#)

5.1 Standard geometry [i](#)

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

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	0.58	0/1578	0.75	0/2142
1	B	0.57	0/1578	0.71	0/2142
1	C	0.66	0/1578	0.79	0/2142
2	D	0.56	0/232	0.75	0/318
2	E	0.41	0/111	0.56	0/150
2	F	0.49	0/23	0.86	0/30
All	All	0.60	0/5100	0.75	0/6924

There are no bond length outliers.

There are no bond angle outliers.

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	1537	0	1486	20	0
1	B	1537	0	1486	26	0
1	C	1537	0	1486	23	0
2	D	222	0	206	4	0
2	E	106	0	106	0	0
2	F	22	0	23	6	0
3	A	1	0	0	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	A	1	0	0	0	0
4	B	1	0	0	0	0
4	C	1	0	0	0	0
5	A	189	0	0	8	0
5	B	168	0	0	6	0
5	C	211	0	0	4	0
5	D	12	0	0	2	0
5	E	1	0	0	0	0
5	F	1	0	0	0	0
All	All	5547	0	4793	71	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 (71) 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:C:663:THR:HG21	2:F:554:PRO:HG3	1.46	0.97
1:B:788:ARG:NH1	5:B:1001:HOH:O	2.04	0.89
1:A:762:ASP:OD2	5:A:1001:HOH:O	1.97	0.81
1:C:751:GLU:OE2	5:C:1001:HOH:O	2.01	0.78
1:C:689:ASP:OD1	1:C:694:ASN:ND2	2.16	0.78
1:B:776:ARG:CZ	1:B:780:THR:H	1.96	0.77
3:A:901:CL:CL	5:A:1150:HOH:O	2.41	0.74
1:B:649:GLY:HA2	2:F:553:PRO:HG2	1.68	0.74
1:C:665:THR:HB	2:F:553:PRO:HG3	1.71	0.73
1:B:776:ARG:NH1	1:B:780:THR:H	1.89	0.71
3:A:901:CL:CL	5:A:1138:HOH:O	2.45	0.70
1:A:778:ASP:OD1	1:A:779:ASP:N	2.26	0.68
1:C:670:LEU:HD22	2:D:540:ILE:HD11	1.76	0.66
1:A:731:GLY:O	5:A:1002:HOH:O	2.14	0.66
1:B:731:GLY:O	5:B:1002:HOH:O	2.14	0.64
1:B:668:MET:HE1	1:C:671:PHE:CZ	2.32	0.64
1:C:665:THR:HG21	2:F:553:PRO:HA	1.79	0.64
1:B:776:ARG:HH22	1:B:780:THR:CB	2.10	0.64
1:B:776:ARG:NH2	1:B:780:THR:H	1.96	0.63
1:A:776:ARG:HG3	1:A:777:PRO:HD2	1.79	0.63
1:A:689:ASP:OD1	1:A:694:ASN:ND2	2.28	0.62
1:B:623:ARG:NH2	5:B:1004:HOH:O	2.34	0.60
1:C:711:MET:HE2	1:C:810:PRO:HB3	1.84	0.59
1:A:618:THR:HA	1:A:621:GLN:OE1	2.02	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:662:GLU:HG2	5:B:1061:HOH:O	2.02	0.59
1:B:623:ARG:NH2	5:B:1005:HOH:O	2.35	0.58
1:B:619:GLU:O	1:B:623:ARG:HG3	2.05	0.57
1:B:748:GLU:HG3	1:B:749:TYR:CD2	2.42	0.55
1:C:662:GLU:O	5:C:1003:HOH:O	2.18	0.55
1:C:780:THR:N	5:C:1004:HOH:O	2.20	0.54
1:B:778:ASP:OD1	1:B:779:ASP:N	2.41	0.54
1:C:776:ARG:HD2	1:C:778:ASP:OD1	2.07	0.53
1:A:725:LYS:NZ	1:A:763:GLN:O	2.37	0.53
1:C:638:THR:HB	1:C:640:MET:HE3	1.90	0.53
1:A:638:THR:HB	1:A:640:MET:HE2	1.89	0.53
1:A:711:MET:HE2	1:A:810:PRO:HB3	1.92	0.52
1:B:649:GLY:CA	2:F:553:PRO:HG2	2.39	0.51
1:C:663:THR:HG21	2:F:554:PRO:CG	2.29	0.50
1:C:640:MET:HE1	1:C:770:MET:HE1	1.93	0.50
1:B:714:HIS:NE2	1:B:779:ASP:HB2	2.27	0.50
1:B:702:GLN:HG3	5:B:1007:HOH:O	2.13	0.48
1:B:776:ARG:HH12	1:B:780:THR:HB	1.77	0.48
1:A:725:LYS:HD3	5:A:1002:HOH:O	2.12	0.48
1:B:743:TYR:CE1	1:B:788:ARG:HD2	2.49	0.48
1:C:681:SER:HB2	1:C:682:PRO:HD2	1.96	0.48
1:A:619:GLU:O	1:A:623:ARG:HG3	2.14	0.47
1:A:658:SER:HB3	5:A:1070:HOH:O	2.14	0.47
1:B:776:ARG:NH2	1:B:780:THR:N	2.62	0.47
1:B:668:MET:HE2	1:B:668:MET:HB3	1.79	0.47
1:A:640:MET:HE1	1:A:770:MET:SD	2.55	0.46
1:A:751:GLU:HG3	5:A:1148:HOH:O	2.15	0.46
1:C:640:MET:HE1	1:C:770:MET:SD	2.55	0.46
1:B:674:PRO:HB2	1:B:677:TYR:OH	2.16	0.45
1:B:776:ARG:HH21	1:B:778:ASP:HB3	1.80	0.45
1:B:748:GLU:H	1:B:748:GLU:HG2	1.54	0.44
1:A:714:HIS:ND1	1:A:779:ASP:HB3	2.33	0.44
1:C:619:GLU:O	1:C:623:ARG:HG3	2.18	0.44
1:C:662:GLU:O	1:C:662:GLU:HG3	2.17	0.44
1:C:748:GLU:HG2	5:C:1036:HOH:O	2.18	0.44
1:C:661:TYR:HD2	1:C:663:THR:CG2	2.31	0.43
1:C:630:LEU:HD23	1:C:630:LEU:HA	1.87	0.43
1:A:665:THR:HG21	5:D:606:HOH:O	2.18	0.43
1:A:683:ARG:HH11	2:D:535:THR:HG21	1.83	0.43
2:D:542:TRP:HB3	2:D:543:PRO:HD3	2.00	0.43
1:A:668:MET:HG3	1:A:676:TRP:CZ2	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:776:ARG:HB2	5:A:1061:HOH:O	2.20	0.41
1:B:670:LEU:HG	1:B:671:PHE:CD2	2.55	0.41
2:D:552:PRO:HB2	5:D:605:HOH:O	2.19	0.41
1:A:630:LEU:HD23	1:C:630:LEU:HD21	2.03	0.40
1:B:748:GLU:HG3	1:B:749:TYR:CE2	2.56	0.40
1:C:663:THR:O	1:C:665:THR:HG23	2.21	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	192/203 (95%)	186 (97%)	6 (3%)	0	100	100
1	B	192/203 (95%)	183 (95%)	9 (5%)	0	100	100
1	C	192/203 (95%)	186 (97%)	6 (3%)	0	100	100
2	D	24/44 (54%)	24 (100%)	0	0	100	100
2	E	11/44 (25%)	10 (91%)	1 (9%)	0	100	100
2	F	1/44 (2%)	1 (100%)	0	0	100	100
All	All	612/741 (83%)	590 (96%)	22 (4%)	0	100	100

There are no Ramachandran outliers to report.

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	166/170 (98%)	165 (99%)	1 (1%)	78	67
1	B	166/170 (98%)	164 (99%)	2 (1%)	63	43
1	C	166/170 (98%)	166 (100%)	0	100	100
2	D	25/39 (64%)	25 (100%)	0	100	100
2	E	12/39 (31%)	12 (100%)	0	100	100
2	F	3/39 (8%)	3 (100%)	0	100	100
All	All	538/627 (86%)	535 (99%)	3 (1%)	78	67

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	711	MET
1	B	745	LEU
1	B	770	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	C	783	GLN
2	D	539	HIS

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 oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 4 ligands modelled in this entry, 4 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

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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	194/203 (95%)	0.01	11 (5%) 29 38	20, 31, 72, 106	0
1	B	194/203 (95%)	0.11	14 (7%) 21 27	20, 35, 77, 119	0
1	C	194/203 (95%)	0.00	14 (7%) 21 27	18, 28, 73, 98	0
2	D	26/44 (59%)	1.01	5 (19%) 3 4	24, 49, 112, 120	0
2	E	13/44 (29%)	3.98	12 (92%) 0 0	50, 110, 134, 140	0
2	F	3/44 (6%)	3.55	2 (66%) 0 0	24, 24, 31, 37	3 (100%)
All	All	624/741 (84%)	0.18	58 (9%) 14 17	18, 33, 79, 140	3 (0%)

All (58) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	E	544	PHE	8.2
2	E	543	PRO	6.5
2	F	553	PRO	5.7
2	E	549	HIS	5.5
1	C	663	THR	5.4
1	C	665	THR	5.2
1	A	618	THR	5.1
2	E	547	LEU	5.1
1	C	618	THR	4.8
1	B	779	ASP	4.2
1	A	776	ARG	4.2
2	E	545	THR	4.1
1	B	777	PRO	4.0
1	A	662	GLU	3.9
1	A	751	GLU	3.8
2	D	540	ILE	3.7
1	B	659	GLU	3.7
2	E	548	ARG	3.7
2	E	552	PRO	3.7

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Mol	Chain	Res	Type	RSRZ
2	E	551	GLY	3.7
1	C	777	PRO	3.5
1	B	730	THR	3.4
2	D	531	GLU	3.3
2	E	550	ASN	3.2
1	A	811	VAL	3.2
2	F	555	VAL	3.2
1	C	670	LEU	3.1
1	C	662	GLU	3.1
1	B	780	THR	3.0
1	C	811	VAL	2.8
1	C	779	ASP	2.8
1	C	664	LYS	2.8
1	A	778	ASP	2.8
1	A	779	ASP	2.7
2	D	530	GLN	2.7
1	B	778	ASP	2.7
1	B	729	PRO	2.7
1	C	671	PHE	2.7
1	C	775	LYS	2.7
2	E	546	ARG	2.6
2	E	555	VAL	2.6
1	B	672	GLY	2.5
1	C	677	TYR	2.5
1	A	749	TYR	2.5
1	B	776	ARG	2.5
1	B	670	LEU	2.4
1	C	778	ASP	2.4
1	B	811	VAL	2.4
1	B	669	SER	2.3
1	A	777	PRO	2.3
2	E	553	PRO	2.3
1	B	671	PHE	2.3
1	A	775	LYS	2.3
2	D	535	THR	2.3
2	D	536	SER	2.3
1	B	775	LYS	2.3
1	C	675	LEU	2.2
1	A	663	THR	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 oligosaccharides 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($\text{\AA}^2$)	Q<0.9
3	CL	A	901	1/1	0.97	0.12	57,57,57,57	0
4	K	B	901	1/1	0.99	0.03	21,21,21,21	0
4	K	A	902	1/1	1.00	0.09	16,16,16,16	0
4	K	C	901	1/1	1.00	0.08	13,13,13,13	0

6.5 Other polymers [i](#)

There are no such residues in this entry.