



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 14, 2017 – 03:42 pm GMT

PDB ID : 5F72
Title : De novo design and crystallographic validation of antibodies targeting a pre-selected epitope
Authors : Liu, X.; Taylor, R.D.; Griffin, L.; Coker, S.; Adams, R.; Ceska, T.; Shi, J.; Lawson, A.D.G.; Baker, T.
Deposited on : 2015-12-07
Resolution : 1.85 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

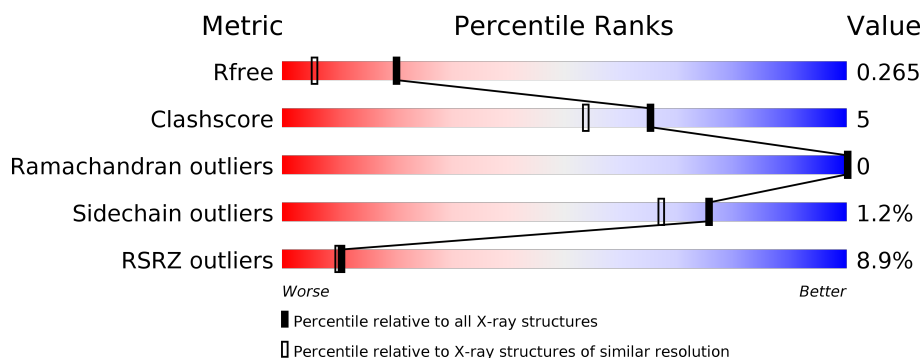
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.85 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	1923 (1.86-1.86)
Clashscore	112137	2083 (1.86-1.86)
Ramachandran outliers	110173	2060 (1.86-1.86)
Sidechain outliers	110143	2060 (1.86-1.86)
RSRZ outliers	101464	1932 (1.86-1.86)

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	C	296	<div> <div>16%</div> <div> <div></div> <div>79%</div> <div>15%</div> <div>• •</div> </div> </div>
1	K	296	<div> <div>6%</div> <div> <div></div> <div>81%</div> <div>14%</div> <div>• •</div> </div> </div>
2	S	257	<div> <div>6%</div> <div> <div></div> <div>77%</div> <div>11%</div> <div>• 12%</div> </div> </div>
2	T	257	<div> <div>4%</div> <div> <div></div> <div>84%</div> <div>• • 11%</div> </div> </div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 8333 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 Kelch-like ECH-associated protein 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	K	285	Total	C	N	O	S	0	0	0
			2190	1361	394	420	15			
1	C	285	Total	C	N	O	S	0	0	0
			2190	1361	394	420	15			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
K	316	GLY	-	expression tag	UNP Q14145
K	317	SER	-	expression tag	UNP Q14145
K	318	MET	-	expression tag	UNP Q14145
K	319	GLY	-	expression tag	UNP Q14145
K	320	HIS	-	expression tag	UNP Q14145
K	354	ASP	ARG	conflict	UNP Q14145
C	316	GLY	-	expression tag	UNP Q14145
C	317	SER	-	expression tag	UNP Q14145
C	318	MET	-	expression tag	UNP Q14145
C	319	GLY	-	expression tag	UNP Q14145
C	320	HIS	-	expression tag	UNP Q14145
C	354	ASP	ARG	conflict	UNP Q14145

- Molecule 2 is a protein called Single chain Fv from a Fab.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	T	229	Total	C	N	O	S	0	0	0
			1707	1069	288	342	8			
2	S	226	Total	C	N	O	S	0	0	0
			1682	1054	281	339	8			

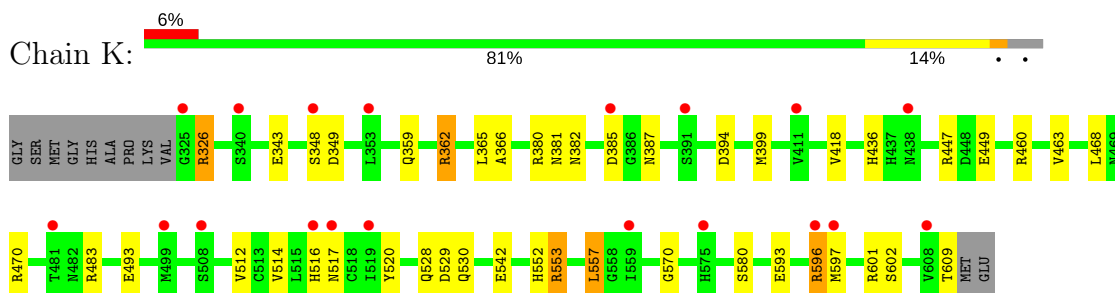
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	K	181	Total 181	O 181	0	0
3	C	155	Total 155	O 155	0	0
3	T	136	Total 136	O 136	0	0
3	S	92	Total 92	O 92	0	0

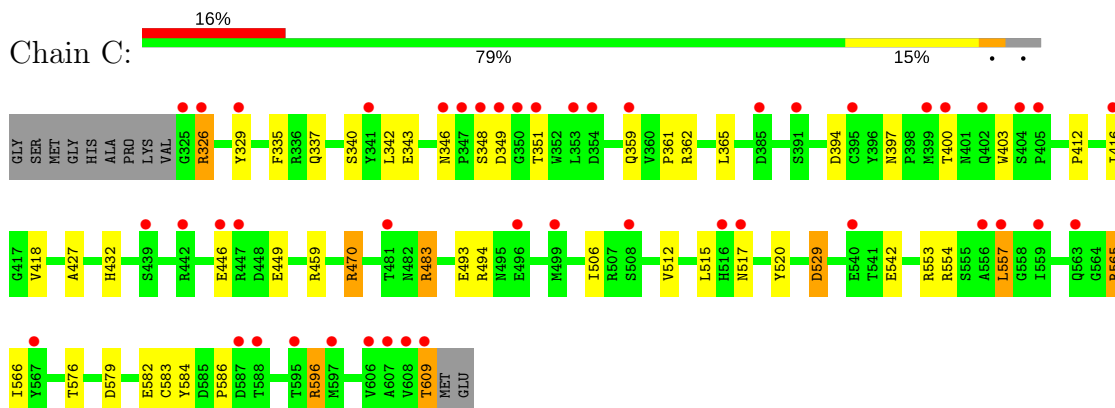
3 Residue-property plots [i](#)

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.

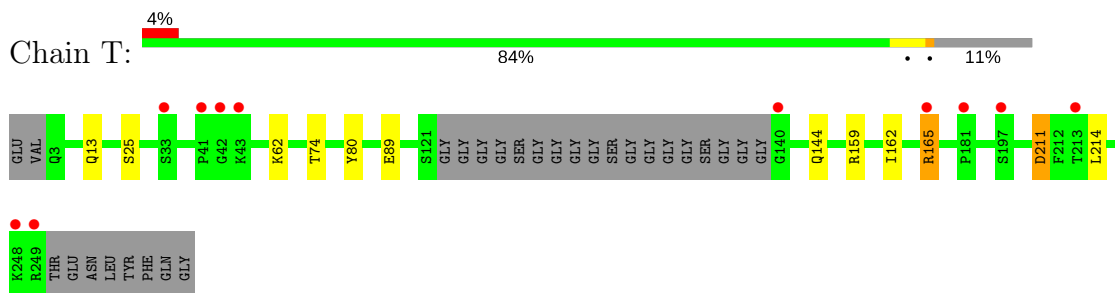
- Molecule 1: Kelch-like ECH-associated protein 1



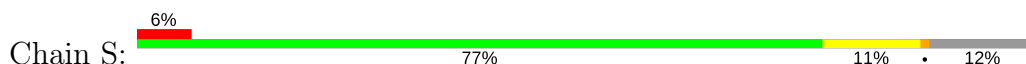
- Molecule 1: Kelch-like ECH-associated protein 1

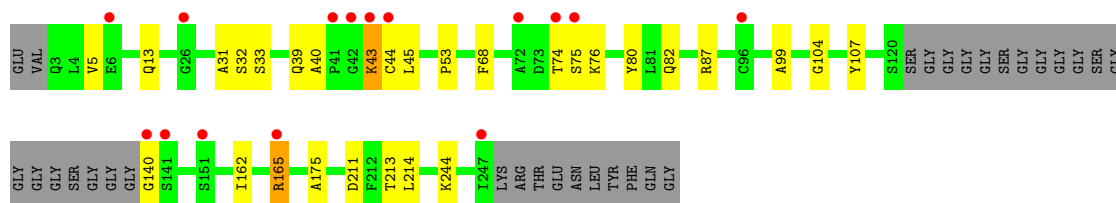


- Molecule 2: Single chain Fv from a Fab



- Molecule 2: Single chain Fv from a Fab





4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	70.50Å 69.81Å 99.56Å 90.00° 92.23° 90.00°	Depositor
Resolution (Å)	29.69 – 1.85 29.69 – 1.85	Depositor EDS
% Data completeness (in resolution range)	99.2 (29.69-1.85) 99.2 (29.69-1.85)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.05 (at 1.85Å)	Xtriage
Refinement program	REFMAC 5.8.0103	Depositor
R, R_{free}	0.223 , 0.265 0.223 , 0.265	Depositor DCC
R_{free} test set	4108 reflections (5.28%)	DCC
Wilson B-factor (Å ²)	21.8	Xtriage
Anisotropy	0.037	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 45.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.011 for k,h,-l 0.013 for -k,-h,-l 0.025 for h,-k,-l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	8333	wwPDB-VP
Average B, all atoms (Å ²)	25.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.72% 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

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	C	1.30	15/2243 (0.7%)	1.16	21/3055 (0.7%)
1	K	1.28	14/2243 (0.6%)	1.14	17/3055 (0.6%)
2	S	1.10	6/1718 (0.3%)	1.01	5/2335 (0.2%)
2	T	1.14	6/1743 (0.3%)	0.95	2/2366 (0.1%)
All	All	1.22	41/7947 (0.5%)	1.08	45/10811 (0.4%)

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	K	0	1

All (41) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	326	ARG	NE-CZ	20.09	1.59	1.33
1	K	326	ARG	CZ-NH2	16.48	1.54	1.33
1	K	326	ARG	CZ-NH1	-13.90	1.15	1.33
1	C	326	ARG	CD-NE	12.94	1.68	1.46
1	C	517	ASN	CG-OD1	12.23	1.50	1.24
1	K	326	ARG	CD-NE	11.57	1.66	1.46
2	S	75	SER	CB-OG	11.41	1.57	1.42
1	K	528	GLN	CD-OE1	11.10	1.48	1.24
2	S	43	LYS	CD-CE	9.99	1.76	1.51
1	K	326	ARG	NE-CZ	9.59	1.45	1.33
2	T	165	ARG	CZ-NH1	9.37	1.45	1.33
1	C	565	ARG	CZ-NH1	9.11	1.44	1.33
1	K	385	ASP	CB-CG	8.54	1.69	1.51
1	C	359	GLN	CD-OE1	-7.96	1.06	1.24
2	S	80	TYR	CG-CD1	-7.73	1.29	1.39
1	C	446	GLU	CG-CD	7.56	1.63	1.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	582	GLU	CD-OE2	-7.55	1.17	1.25
2	T	89	GLU	CD-OE2	-7.18	1.17	1.25
2	S	76	LYS	CE-NZ	7.13	1.66	1.49
2	T	80	TYR	CE1-CZ	-6.70	1.29	1.38
1	C	446	GLU	CB-CG	6.68	1.64	1.52
1	C	542	GLU	CD-OE2	-6.58	1.18	1.25
1	C	609	THR	CB-OG1	-6.50	1.30	1.43
1	C	553	ARG	NE-CZ	6.40	1.41	1.33
2	S	165	ARG	CD-NE	-6.30	1.35	1.46
1	K	528	GLN	CG-CD	6.24	1.65	1.51
1	K	493	GLU	CD-OE2	-6.05	1.19	1.25
1	K	542	GLU	CD-OE1	-5.94	1.19	1.25
2	S	140	GLY	C-O	-5.88	1.14	1.23
1	K	343	GLU	CD-OE2	-5.86	1.19	1.25
2	T	144	GLN	CD-NE2	5.64	1.47	1.32
1	C	343	GLU	CD-OE1	-5.43	1.19	1.25
1	C	517	ASN	CG-ND2	-5.41	1.19	1.32
2	T	80	TYR	CG-CD1	-5.32	1.32	1.39
2	T	165	ARG	CD-NE	5.26	1.55	1.46
1	K	542	GLU	CD-OE2	-5.19	1.20	1.25
1	K	399	MET	CB-CG	5.16	1.67	1.51
1	K	449	GLU	CD-OE2	-5.15	1.20	1.25
1	K	602	SER	CB-OG	-5.14	1.35	1.42
1	C	609	THR	CA-C	5.07	1.66	1.52
1	C	470	ARG	CZ-NH1	-5.04	1.26	1.33

All (45) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	553	ARG	NE-CZ-NH2	9.75	125.17	120.30
1	K	385	ASP	CB-CG-OD1	-9.54	109.72	118.30
1	C	596	ARG	NE-CZ-NH2	-9.00	115.80	120.30
1	K	362	ARG	NE-CZ-NH1	-8.96	115.82	120.30
1	K	385	ASP	CB-CG-OD2	8.92	126.33	118.30
1	C	470	ARG	NE-CZ-NH1	8.81	124.70	120.30
1	K	542	GLU	OE1-CD-OE2	-8.46	113.15	123.30
2	S	13	GLN	CG-CD-NE2	7.85	135.55	116.70
1	K	326	ARG	NE-CZ-NH2	-7.77	116.41	120.30
1	C	609	THR	CA-CB-CG2	7.71	123.20	112.40
1	C	542	GLU	OE1-CD-OE2	-7.22	114.64	123.30
1	C	326	ARG	CD-NE-CZ	7.01	133.42	123.60
2	S	165	ARG	NE-CZ-NH2	-6.96	116.82	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	K	362	ARG	NE-CZ-NH2	6.90	123.75	120.30
1	K	326	ARG	CD-NE-CZ	6.82	133.15	123.60
1	C	449	GLU	OE1-CD-OE2	-6.78	115.17	123.30
1	K	596	ARG	CB-CG-CD	6.69	129.00	111.60
1	C	609	THR	CB-CA-C	-6.57	93.87	111.60
1	C	554	ARG	NE-CZ-NH1	6.56	123.58	120.30
1	K	343	GLU	OE1-CD-OE2	-6.50	115.50	123.30
1	C	553	ARG	NE-CZ-NH1	-6.47	117.06	120.30
2	S	165	ARG	NE-CZ-NH1	6.38	123.49	120.30
1	C	343	GLU	OE1-CD-OE2	-6.26	115.79	123.30
1	K	326	ARG	NE-CZ-NH1	-6.01	117.29	120.30
1	C	418	VAL	CG1-CB-CG2	-5.98	101.33	110.90
1	C	554	ARG	NE-CZ-NH2	-5.96	117.32	120.30
1	K	326	ARG	NH1-CZ-NH2	5.82	125.81	119.40
1	C	459	ARG	NE-CZ-NH2	5.75	123.18	120.30
1	C	326	ARG	NE-CZ-NH1	-5.75	117.43	120.30
1	K	399	MET	CG-SD-CE	-5.69	91.10	100.20
1	C	446	GLU	OE1-CD-OE2	-5.65	116.52	123.30
1	K	553	ARG	NE-CZ-NH2	5.58	123.09	120.30
1	K	483	ARG	NE-CZ-NH1	5.49	123.04	120.30
1	K	601	ARG	NE-CZ-NH2	-5.47	117.56	120.30
1	K	449	GLU	OE1-CD-OE2	-5.45	116.76	123.30
1	C	553	ARG	CG-CD-NE	-5.43	100.39	111.80
2	T	13	GLN	CG-CD-OE1	5.42	132.44	121.60
2	S	76	LYS	CD-CE-NZ	-5.41	99.26	111.70
1	C	582	GLU	OE1-CD-OE2	-5.39	116.84	123.30
1	C	579	ASP	CB-CG-OD2	-5.33	113.50	118.30
1	C	494	ARG	NE-CZ-NH2	5.32	122.96	120.30
1	K	349	ASP	CB-CG-OD1	5.20	122.98	118.30
1	C	359	GLN	OE1-CD-NE2	-5.12	110.12	121.90
2	S	43	LYS	CB-CA-C	-5.04	100.32	110.40
2	T	211	ASP	CB-CG-OD1	5.01	122.81	118.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	K	529	ASP	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	C	2190	0	2075	28	0
1	K	2190	0	2075	22	0
2	S	1682	0	1617	17	0
2	T	1707	0	1648	6	0
3	C	155	0	0	3	0
3	K	181	0	0	2	0
3	S	92	0	0	2	0
3	T	136	0	0	3	0
All	All	8333	0	7415	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 5.

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)
2:S:43:LYS:CD	2:S:43:LYS:CE	1.76	1.55
1:C:326:ARG:NE	1:C:326:ARG:CD	1.68	1.51
1:K:359:GLN:HG3	3:K:863:HOH:O	1.62	0.99
1:C:609:THR:HG23	1:C:609:THR:O	1.67	0.93
1:C:609:THR:O	1:C:609:THR:CG2	2.29	0.78
1:C:326:ARG:HD3	1:C:609:THR:C	2.11	0.70
2:S:165:ARG:HG2	2:S:211:ASP:OD1	1.89	0.70
2:S:43:LYS:CE	2:S:43:LYS:CG	2.71	0.69
1:K:326:ARG:HD2	1:K:609:THR:C	2.14	0.68
1:C:329:TYR:HE1	1:C:609:THR:HG22	1.57	0.68
1:K:530:GLN:NE2	2:S:53:PRO:O	2.28	0.66
1:C:329:TYR:CE1	1:C:609:THR:HG22	2.31	0.66
2:S:40:ALA:HB3	2:S:43:LYS:HG3	1.82	0.61
3:C:748:HOH:O	2:T:74:THR:HG21	2.01	0.60
1:K:380:ARG:HD2	1:K:387:ASN:HD22	1.67	0.60
2:T:62:LYS:HD3	3:T:421:HOH:O	2.02	0.59
2:T:62:LYS:HD2	3:T:399:HOH:O	2.03	0.58
1:C:365:LEU:H	1:C:365:LEU:HD23	1.68	0.57
1:K:596:ARG:HH21	1:K:596:ARG:HG3	1.70	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:529:ASP:HB3	3:C:716:HOH:O	2.04	0.56
1:C:566:ILE:HB	1:C:584:TYR:HB3	1.87	0.55
2:S:5:VAL:HG23	2:S:5:VAL:O	2.08	0.53
1:C:576:THR:HB	3:C:812:HOH:O	2.08	0.53
1:C:397:ASN:CG	1:C:400:THR:HG22	2.30	0.53
1:C:470:ARG:NH2	1:C:493:GLU:OE1	2.41	0.52
2:T:162:ILE:HD11	2:T:214:LEU:HD23	1.91	0.52
1:K:570:GLY:HA3	1:K:597:MET:HE1	1.93	0.51
2:T:165:ARG:HG3	2:T:211:ASP:OD1	2.10	0.51
2:S:244:LYS:HE3	3:S:380:HOH:O	2.10	0.51
1:K:365:LEU:HD23	1:K:365:LEU:H	1.76	0.50
2:S:107:TYR:CD1	2:S:175:ALA:HB2	2.45	0.50
1:K:470:ARG:HD3	3:K:817:HOH:O	2.11	0.50
1:K:382:ASN:HA	1:K:387:ASN:HB3	1.93	0.49
1:C:515:LEU:HD21	1:C:586:PRO:HG3	1.94	0.49
1:K:436:HIS:CE1	2:S:104:GLY:HA2	2.48	0.49
1:K:552:HIS:NE2	1:K:593:GLU:OE2	2.46	0.47
1:K:362:ARG:NH1	1:K:394:ASP:OD2	2.47	0.47
1:K:447:ARG:HB3	1:K:447:ARG:HE	1.33	0.47
1:C:565:ARG:HD3	1:C:583:CYS:SG	2.55	0.46
2:T:159:ARG:HG2	3:T:415:HOH:O	2.15	0.46
1:K:596:ARG:NH2	1:K:596:ARG:HG3	2.30	0.45
1:K:381:ASN:O	1:K:387:ASN:HA	2.17	0.45
2:S:43:LYS:HB3	2:S:44:CYS:H	1.55	0.45
2:S:33:SER:HB2	2:S:99:ALA:HB3	1.98	0.45
1:C:416:ILE:HD11	1:C:427:ALA:HB1	1.98	0.45
2:S:213:THR:HG23	3:S:378:HOH:O	2.16	0.44
1:K:366:ALA:HB3	1:K:418:VAL:HG13	1.99	0.44
2:S:39:GLN:HB2	2:S:45:LEU:HD23	1.99	0.44
1:C:329:TYR:HE1	1:C:609:THR:CG2	2.26	0.43
1:C:346:ASN:OD1	1:C:348:SER:HB3	2.18	0.43
1:K:516:HIS:O	1:K:517:ASN:CB	2.66	0.43
2:S:162:ILE:HG21	2:S:162:ILE:HD13	1.69	0.43
1:C:397:ASN:HB3	1:C:400:THR:CG2	2.49	0.43
1:C:512:VAL:HA	1:C:520:TYR:O	2.18	0.43
1:K:512:VAL:HA	1:K:520:TYR:O	2.19	0.43
2:S:162:ILE:HD12	2:S:214:LEU:HD23	2.01	0.43
1:C:483:ARG:HB3	1:C:506:ILE:CG2	2.48	0.43
2:S:31:ALA:O	2:S:32:SER:HB3	2.20	0.42
1:C:335:PHE:C	1:C:337:GLN:H	2.24	0.41
1:C:342:LEU:HD22	1:C:403:TRP:CZ2	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:468:LEU:HD13	1:K:514:VAL:HG21	2.01	0.41
1:K:557:LEU:HD23	1:K:557:LEU:H	1.86	0.41
1:C:596:ARG:HG2	1:C:596:ARG:NH2	2.36	0.41
1:C:362:ARG:NH1	1:C:394:ASP:OD2	2.54	0.41
1:K:460:ARG:HB3	1:K:463:VAL:HB	2.02	0.41
1:C:349:ASP:OD1	1:C:351:THR:OG1	2.27	0.41
1:C:340:SER:OG	1:C:361:PRO:HG3	2.21	0.40
1:K:570:GLY:CA	1:K:597:MET:HE1	2.51	0.40
1:C:412:PRO:HG2	1:C:432:HIS:CD2	2.56	0.40
1:C:557:LEU:HD23	1:C:557:LEU:H	1.86	0.40
2:S:68:PHE:HA	2:S:82:GLN:O	2.21	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	C	283/296 (96%)	273 (96%)	10 (4%)	0	100	100
1	K	283/296 (96%)	276 (98%)	7 (2%)	0	100	100
2	S	222/257 (86%)	214 (96%)	8 (4%)	0	100	100
2	T	225/257 (88%)	220 (98%)	5 (2%)	0	100	100
All	All	1013/1106 (92%)	983 (97%)	30 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	C	231/239 (97%)	228 (99%)	3 (1%)	73	63
1	K	231/239 (97%)	227 (98%)	4 (2%)	66	52
2	S	182/197 (92%)	180 (99%)	2 (1%)	78	70
2	T	185/197 (94%)	184 (100%)	1 (0%)	91	89
All	All	829/872 (95%)	819 (99%)	10 (1%)	75	67

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	K	348	SER
1	K	553	ARG
1	K	557	LEU
1	K	580	SER
1	C	483	ARG
1	C	529	ASP
1	C	557	LEU
2	T	25	SER
2	S	74	THR
2	S	87	ARG

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

Mol	Chain	Res	Type
1	K	387	ASN
2	S	35	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 [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	C	285/296 (96%)	0.93	46 (16%) 2 2	9, 25, 47, 67	23 (8%)
1	K	285/296 (96%)	0.40	19 (6%) 19 18	6, 21, 39, 67	19 (6%)
2	S	226/257 (87%)	0.30	15 (6%) 19 18	13, 26, 43, 64	2 (0%)
2	T	229/257 (89%)	0.03	11 (4%) 31 30	10, 19, 36, 61	3 (1%)
All	All	1025/1106 (92%)	0.44	91 (8%) 10 10	6, 23, 43, 67	47 (4%)

All (91) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	416	ILE	13.1
2	S	96	CYS	7.7
2	S	41	PRO	6.6
1	C	481	THR	6.3
2	T	213	THR	5.9
1	C	608	VAL	5.5
2	T	42	GLY	5.5
1	C	353	LEU	5.5
1	C	597	MET	5.3
1	K	391	SER	5.3
2	T	33	SER	5.2
1	C	395	CYS	4.6
1	C	609	THR	4.6
1	K	385	ASP	4.6
1	C	391	SER	4.6
1	K	517	ASN	4.5
1	C	349	ASP	4.4
1	K	325	GLY	4.3
1	C	588	THR	4.2
1	C	325	GLY	4.2
2	S	75	SER	4.2

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Mol	Chain	Res	Type	RSRZ
1	K	411	VAL	4.1
1	C	446	GLU	4.0
1	C	595	THR	3.9
1	K	481	THR	3.8
1	C	385	ASP	3.7
1	C	348	SER	3.7
1	C	351	THR	3.6
1	C	404	SER	3.6
2	T	43	LYS	3.6
1	C	517	ASN	3.5
1	K	499	MET	3.5
1	C	557	LEU	3.4
1	K	608	VAL	3.3
2	T	197	SER	3.3
2	S	6	GLU	3.3
1	C	359	GLN	3.3
1	K	353	LEU	3.2
1	C	326	ARG	3.2
2	T	41	PRO	3.2
1	C	556	ALA	3.1
1	K	508	SER	3.1
2	S	72	ALA	3.0
1	K	596	ARG	3.0
1	C	439	SER	2.9
2	S	43	LYS	2.9
1	C	354	ASP	2.9
1	C	402	GLN	2.9
1	C	516	HIS	2.8
1	C	559	ILE	2.8
1	C	508	SER	2.8
2	S	140	GLY	2.7
2	S	74	THR	2.7
2	S	42	GLY	2.7
1	C	346	ASN	2.6
1	K	575	HIS	2.6
1	K	516	HIS	2.6
1	C	563	GLN	2.6
1	C	567	TYR	2.5
1	C	405	PRO	2.5
1	C	399	MET	2.5
1	C	447	ARG	2.5
2	T	140	GLY	2.4

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Mol	Chain	Res	Type	RSRZ
1	C	329	TYR	2.4
1	C	587	ASP	2.3
2	S	26	GLY	2.3
2	S	141	SER	2.3
2	S	44	CYS	2.3
1	C	606	VAL	2.3
1	K	559	ILE	2.2
1	C	540	GLU	2.2
1	K	348	SER	2.2
1	C	350	GLY	2.2
2	S	151	SER	2.2
1	C	496	GLU	2.2
1	K	519	ILE	2.2
1	K	340	SER	2.2
1	C	341	TYR	2.2
2	S	165	ARG	2.2
1	C	347	PRO	2.1
1	K	597	MET	2.1
1	C	442	ARG	2.1
1	C	499	MET	2.1
1	C	607	ALA	2.1
2	S	247	ILE	2.1
2	T	248	LYS	2.1
2	T	165	ARG	2.0
1	K	438	ASN	2.0
2	T	249	ARG	2.0
2	T	181	PRO	2.0
1	C	400	THR	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.