



Full wwPDB X-ray Structure Validation Report ⓘ

May 14, 2020 – 11:09 am BST

PDB ID : 3UY8
Title : Designed protein KE59 R5_11/5F
Authors : Khersonsky, O.; Kiss, G.; Roethlisberger, D.; Dym, O.; Albeck, S.; Houk, K.N.; Baker, D.; Tawfik, D.S.; Israel Structural Proteomics Center (ISPC)
Deposited on : 2011-12-06
Resolution : 2.41 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 ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
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

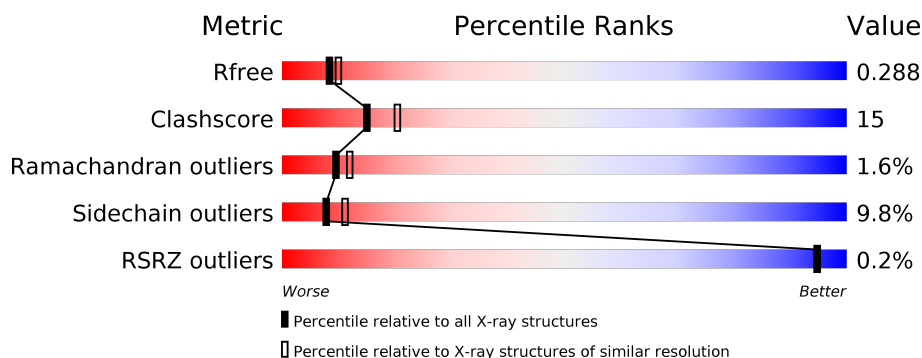
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.41 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	4647 (2.44-2.40)
Clashscore	141614	5161 (2.44-2.40)
Ramachandran outliers	138981	5073 (2.44-2.40)
Sidechain outliers	138945	5074 (2.44-2.40)
RSRZ outliers	127900	4543 (2.44-2.40)

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 $\leq 5\%$. 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	247	
1	B	247	

2 Entry composition [i](#)

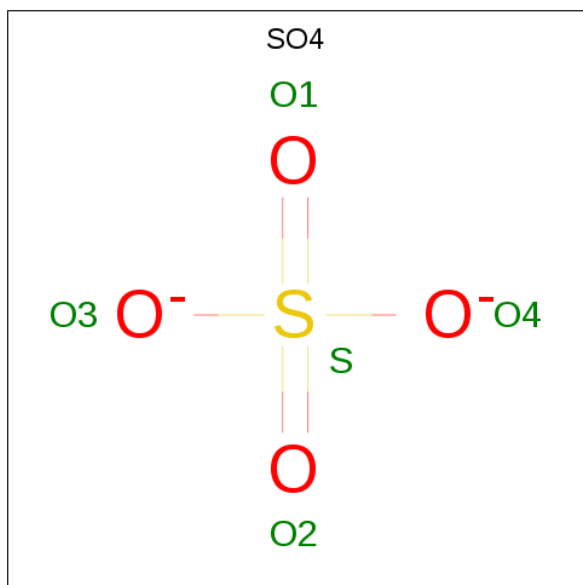
There are 3 unique types of molecules in this entry. The entry contains 3947 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Kemp eliminase KE59 R5_11/5F.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	246	Total	C	N	O	S	0	0	0
			1970	1261	335	369	5			
1	B	247	Total	C	N	O	S	0	0	0
			1962	1251	335	371	5			

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		

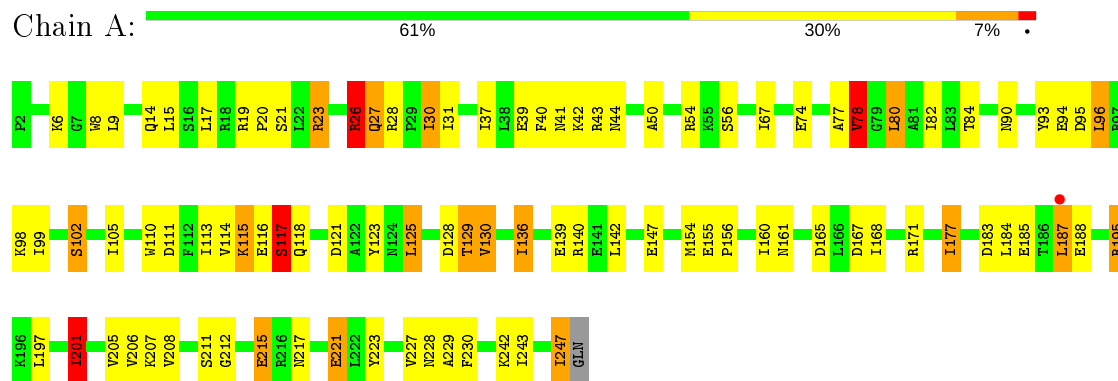
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total 1	O 1	0	0
3	B	4	Total 4	O 4	0	0

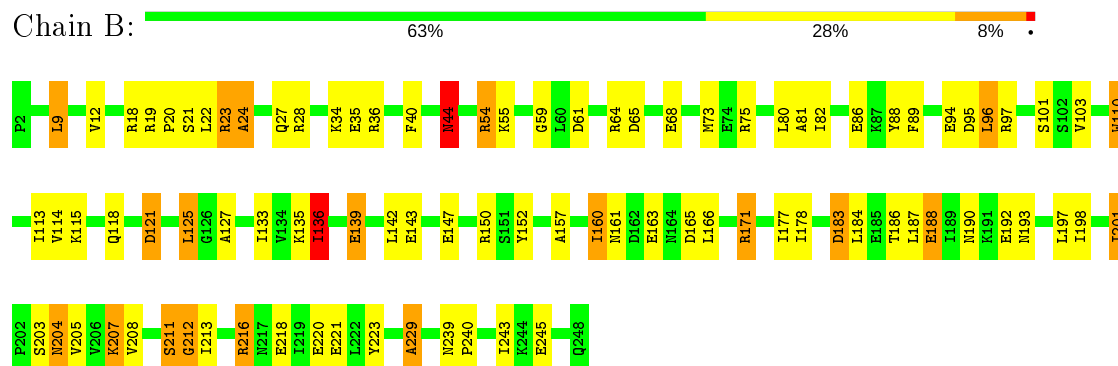
3 Residue-property plots

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: Kemp eliminase KE59 R5_11/5F



- Molecule 1: Kemp eliminase KE59 R5_11/5F



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	87.96 Å 102.73 Å 66.30 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	43.98 – 2.41 40.60 – 2.41	Depositor EDS
% Data completeness (in resolution range)	98.2 (43.98-2.41) 98.2 (40.60-2.41)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	0.06	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.07 (at 2.42 Å)	Xtriage
Refinement program	REFMAC 5.5.0088	Depositor
R, R_{free}	0.215 , 0.299 0.217 , 0.288	Depositor DCC
R_{free} test set	1201 reflections (5.11%)	wwPDB-VP
Wilson B-factor (Å ²)	46.0	Xtriage
Anisotropy	0.167	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 27.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	3947	wwPDB-VP
Average B, all atoms (Å ²)	44.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.79% 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

Bond lengths and bond angles in the following residue types are not validated in this section: SO4

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	1.74	20/2000 (1.0%)	1.27	7/2696 (0.3%)
1	B	1.70	26/1992 (1.3%)	1.37	23/2690 (0.9%)
All	All	1.72	46/3992 (1.2%)	1.32	30/5386 (0.6%)

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	B	0	1

All (46) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	221	GLU	CG-CD	9.77	1.66	1.51
1	A	223	TYR	CD1-CE1	9.30	1.53	1.39
1	A	116	GLU	C-O	7.67	1.38	1.23
1	B	86	GLU	CG-CD	7.48	1.63	1.51
1	B	211	SER	C-O	6.87	1.36	1.23
1	B	89	PHE	CE2-CZ	6.80	1.50	1.37
1	B	218	GLU	CG-CD	6.66	1.61	1.51
1	A	206	VAL	CB-CG2	6.37	1.66	1.52
1	B	139	GLU	CG-CD	6.32	1.61	1.51
1	B	147	GLU	CG-CD	6.31	1.61	1.51
1	A	115	LYS	CD-CE	6.30	1.67	1.51
1	B	143	GLU	CG-CD	6.28	1.61	1.51
1	B	143	GLU	CD-OE2	6.24	1.32	1.25
1	B	54	ARG	CD-NE	-6.06	1.36	1.46
1	A	8	TRP	CB-CG	-6.05	1.39	1.50
1	A	117	SER	C-O	5.98	1.34	1.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	147	GLU	CG-CD	5.86	1.60	1.51
1	B	223	TYR	CD2-CE2	5.85	1.48	1.39
1	A	215	GLU	CB-CG	5.84	1.63	1.52
1	A	78	VAL	CB-CG2	-5.73	1.40	1.52
1	B	229	ALA	CA-CB	5.67	1.64	1.52
1	B	55	LYS	CD-CE	5.65	1.65	1.51
1	A	230	PHE	CD2-CE2	5.63	1.50	1.39
1	A	130	VAL	CB-CG2	5.62	1.64	1.52
1	B	110	TRP	CB-CG	-5.62	1.40	1.50
1	A	77	ALA	N-CA	-5.62	1.35	1.46
1	B	54	ARG	CG-CD	5.61	1.66	1.51
1	B	88	TYR	CD1-CE1	5.61	1.47	1.39
1	A	90	ASN	CB-CG	5.44	1.63	1.51
1	B	88	TYR	CE1-CZ	5.42	1.45	1.38
1	B	94	GLU	CG-CD	5.42	1.60	1.51
1	B	152	TYR	CE1-CZ	-5.39	1.31	1.38
1	A	155	GLU	CD-OE2	5.37	1.31	1.25
1	B	40	PHE	CE2-CZ	5.36	1.47	1.37
1	B	35	GLU	CB-CG	5.32	1.62	1.52
1	B	139	GLU	CB-CG	5.32	1.62	1.52
1	A	227	VAL	CB-CG1	5.29	1.64	1.52
1	B	245	GLU	CG-CD	5.27	1.59	1.51
1	B	64	ARG	CZ-NH1	5.24	1.39	1.33
1	A	129	THR	CA-CB	5.18	1.66	1.53
1	B	163	GLU	CD-OE1	5.15	1.31	1.25
1	A	129	THR	CB-CG2	-5.09	1.35	1.52
1	A	37	ILE	CA-CB	5.09	1.66	1.54
1	A	93	TYR	C-O	5.07	1.32	1.23
1	B	133	ILE	C-O	5.02	1.32	1.23
1	B	88	TYR	CG-CD2	5.01	1.45	1.39

All (30) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	28	ARG	NE-CZ-NH2	14.38	127.49	120.30
1	B	171	ARG	NE-CZ-NH2	8.69	124.64	120.30
1	B	171	ARG	NE-CZ-NH1	-8.64	115.98	120.30
1	B	54	ARG	NE-CZ-NH2	-8.56	116.02	120.30
1	B	188	GLU	N-CA-C	6.82	129.41	111.00
1	B	187	LEU	CA-CB-CG	6.49	130.23	115.30
1	B	28	ARG	NE-CZ-NH1	-6.44	117.08	120.30
1	A	80	LEU	CB-CG-CD2	-6.36	100.18	111.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	97	ARG	NE-CZ-NH1	5.93	123.27	120.30
1	B	218	GLU	OE1-CD-OE2	-5.82	116.31	123.30
1	B	36	ARG	NE-CZ-NH2	-5.78	117.41	120.30
1	A	15	LEU	CA-CB-CG	5.77	128.57	115.30
1	A	177	ILE	CG1-CB-CG2	-5.62	99.02	111.40
1	B	150	ARG	NE-CZ-NH1	-5.61	117.50	120.30
1	B	44	ASN	N-CA-C	5.59	126.10	111.00
1	B	187	LEU	C-N-CA	5.56	135.61	121.70
1	A	201	ILE	CB-CG1-CD1	-5.51	98.47	113.90
1	B	115	LYS	CD-CE-NZ	-5.46	99.13	111.70
1	A	187	LEU	CA-CB-CG	5.46	127.85	115.30
1	B	204	ASN	N-CA-C	5.34	125.42	111.00
1	B	136	ILE	CA-CB-CG2	5.30	121.50	110.90
1	B	61	ASP	CB-CG-OD2	5.21	122.99	118.30
1	B	80	LEU	CB-CG-CD1	-5.17	102.22	111.00
1	A	23	ARG	NE-CZ-NH2	5.16	122.88	120.30
1	B	59	GLY	N-CA-C	5.16	125.99	113.10
1	B	18	ARG	NE-CZ-NH1	5.08	122.84	120.30
1	B	121	ASP	CB-CG-OD1	5.08	122.87	118.30
1	B	103	VAL	CB-CA-C	-5.06	101.79	111.40
1	A	26	ARG	NE-CZ-NH2	-5.01	117.79	120.30
1	B	101	SER	CB-CA-C	-5.01	100.58	110.10

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	203	SER	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	1970	0	2027	69	0
1	B	1962	0	1991	53	0
2	A	5	0	0	0	0
2	B	5	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	1	0	0	0	0
3	B	4	0	0	0	0
All	All	3947	0	4018	120	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 15.

All (120) 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:B:177:ILE:CD1	1:B:177:ILE:CG1	1.82	1.57
1:A:21:SER:HB2	1:A:121:ASP:OD1	1.39	1.18
1:A:26:ARG:CA	1:A:27:GLN:HB2	1.70	1.18
1:A:26:ARG:HA	1:A:27:GLN:CB	1.77	1.14
1:A:195:ARG:HG3	1:A:195:ARG:HH21	1.21	1.00
1:B:23:ARG:HG2	1:B:23:ARG:O	1.64	0.98
1:B:23:ARG:HA	1:B:24:ALA:HB3	1.46	0.93
1:A:21:SER:CB	1:A:121:ASP:OD1	2.18	0.91
1:B:81:ALA:C	1:B:82:ILE:HD13	1.94	0.88
1:A:201:ILE:HD11	1:A:207:LYS:HD3	1.53	0.87
1:A:26:ARG:HA	1:A:27:GLN:HB2	0.90	0.85
1:A:95:ASP:O	1:A:99:ILE:HG13	1.79	0.82
1:A:9:LEU:HD12	1:A:185:GLU:HG3	1.64	0.80
1:A:201:ILE:HD11	1:A:207:LYS:CD	2.10	0.79
1:A:187:LEU:N	1:A:188:GLU:HB2	1.98	0.79
1:A:201:ILE:CD1	1:A:207:LYS:HD3	2.12	0.79
1:A:44:ASN:HD21	1:B:27:GLN:H	1.30	0.78
1:B:23:ARG:CA	1:B:24:ALA:HB3	2.13	0.78
1:A:44:ASN:ND2	1:B:27:GLN:H	1.84	0.76
1:B:198:ILE:O	1:B:198:ILE:HG22	1.86	0.75
1:B:9:LEU:HD21	1:B:136:ILE:HD11	1.67	0.74
1:B:198:ILE:O	1:B:198:ILE:CG2	2.36	0.73
1:A:195:ARG:HH21	1:A:195:ARG:CG	2.00	0.72
1:B:208:VAL:HG22	1:B:229:ALA:HB3	1.71	0.72
1:B:22:LEU:CD1	1:B:125:LEU:HD11	2.22	0.68
1:B:23:ARG:CA	1:B:24:ALA:CB	2.71	0.68
1:A:54:ARG:NH2	1:A:95:ASP:OD2	2.26	0.67
1:A:195:ARG:HG3	1:A:195:ARG:NH2	2.02	0.67
1:B:201:ILE:HD11	1:B:205:VAL:HB	1.76	0.66
1:B:114:VAL:H	1:B:118:GLN:NE2	1.93	0.66
1:A:115:LYS:HG2	1:A:118:GLN:HE21	1.61	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:114:VAL:H	1:A:118:GLN:NE2	1.95	0.64
1:A:96:LEU:HD13	1:A:125:LEU:HB3	1.80	0.64
1:A:139:GLU:HG3	1:A:168:ILE:HG23	1.80	0.64
1:A:115:LYS:HE3	1:A:117:SER:OG	1.97	0.63
1:A:19:ARG:HD2	1:A:20:PRO:HD2	1.81	0.62
1:B:114:VAL:HG22	1:B:118:GLN:HE22	1.65	0.61
1:A:82:ILE:HD12	1:A:99:ILE:HD12	1.83	0.61
1:B:139:GLU:OE1	1:B:171:ARG:NH1	2.32	0.61
1:A:114:VAL:HG22	1:A:118:GLN:HE22	1.65	0.60
1:A:177:ILE:HD12	1:A:205:VAL:HG11	1.84	0.60
1:A:19:ARG:O	1:A:115:LYS:NZ	2.27	0.60
1:B:81:ALA:O	1:B:82:ILE:HD13	2.01	0.60
1:B:22:LEU:HD13	1:B:125:LEU:HD11	1.83	0.59
1:B:23:ARG:O	1:B:23:ARG:CG	2.42	0.57
1:A:39:GLU:O	1:A:43:ARG:HG3	2.04	0.56
1:A:67:ILE:HD11	1:A:98:LYS:HB3	1.88	0.56
1:A:26:ARG:HD3	1:A:123:TYR:CZ	2.40	0.56
1:A:98:LYS:O	1:A:102:SER:OG	2.23	0.55
1:B:201:ILE:HD12	1:B:207:LYS:CG	2.37	0.55
1:B:9:LEU:CD2	1:B:136:ILE:HD11	2.38	0.54
1:A:114:VAL:CG2	1:A:118:GLN:HE22	2.21	0.54
1:B:190:ASN:HD21	1:B:192:GLU:HG2	1.73	0.54
1:B:21:SER:OG	1:B:121:ASP:OD1	2.19	0.54
1:B:135:LYS:NZ	1:B:165:ASP:OD1	2.41	0.53
1:A:201:ILE:HD11	1:A:207:LYS:HZ2	1.71	0.53
1:A:201:ILE:HD11	1:A:207:LYS:CG	2.37	0.53
1:B:160:ILE:HB	1:B:165:ASP:HB2	1.90	0.53
1:A:201:ILE:O	1:A:201:ILE:HD13	2.09	0.53
1:A:217:ASN:O	1:A:221:GLU:HG3	2.10	0.52
1:A:40:PHE:CD2	1:A:78:VAL:HG23	2.43	0.52
1:B:211:SER:OG	1:B:212:GLY:N	2.41	0.52
1:B:183:ASP:OD1	1:B:186:THR:HG23	2.08	0.52
1:A:30:ILE:HD11	1:A:123:TYR:CE1	2.46	0.51
1:A:21:SER:HB3	1:A:121:ASP:OD2	2.10	0.51
1:A:9:LEU:HD22	1:A:136:ILE:HD11	1.93	0.51
1:A:154:MET:O	1:A:156:PRO:HD3	2.11	0.50
1:B:114:VAL:H	1:B:118:GLN:HE22	1.58	0.50
1:B:44:ASN:O	1:B:44:ASN:OD1	2.30	0.50
1:B:239:ASN:O	1:B:240:PRO:C	2.47	0.50
1:A:247:ILE:N	1:A:247:ILE:CD1	2.75	0.49
1:B:211:SER:C	1:B:213:ILE:H	2.15	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:82:ILE:HD13	1:B:82:ILE:N	2.28	0.49
1:A:96:LEU:HD13	1:A:125:LEU:CB	2.42	0.49
1:B:65:ASP:HB3	1:B:68:GLU:HG3	1.95	0.49
1:B:201:ILE:HD12	1:B:207:LYS:HG2	1.95	0.48
1:A:41:ASN:ND2	1:A:228:ASN:HD22	2.11	0.48
1:A:195:ARG:NH2	1:A:195:ARG:CG	2.67	0.47
1:A:201:ILE:HD13	1:A:201:ILE:C	2.35	0.47
1:A:50:ALA:O	1:A:80:LEU:HA	2.14	0.47
1:A:201:ILE:HD11	1:A:207:LYS:NZ	2.29	0.46
1:A:21:SER:CB	1:A:121:ASP:CG	2.83	0.46
1:B:9:LEU:HD23	1:B:9:LEU:O	2.15	0.46
1:A:31:ILE:O	1:A:128:ASP:HB3	2.15	0.45
1:A:115:LYS:HG2	1:A:118:GLN:NE2	2.29	0.45
1:B:201:ILE:HD11	1:B:205:VAL:CB	2.46	0.45
1:B:22:LEU:HD12	1:B:125:LEU:HD11	1.96	0.45
1:B:177:ILE:CD1	1:B:177:ILE:CB	2.81	0.45
1:A:84:THR:OG1	1:A:111:ASP:OD2	2.26	0.45
1:B:157:ALA:HB1	1:B:178:ILE:HG13	1.99	0.45
1:B:19:ARG:HA	1:B:20:PRO:HD3	1.73	0.45
1:A:208:VAL:HG22	1:A:229:ALA:HB3	1.98	0.44
1:A:247:ILE:N	1:A:247:ILE:HD13	2.33	0.44
1:A:160:ILE:HB	1:A:165:ASP:HB3	1.99	0.44
1:A:167:ASP:OD2	1:A:171:ARG:NH2	2.51	0.43
1:B:96:LEU:HD11	1:B:127:ALA:HB2	2.01	0.43
1:B:216:ARG:O	1:B:216:ARG:HG3	2.17	0.43
1:B:114:VAL:CG2	1:B:118:GLN:HE22	2.29	0.43
1:A:125:LEU:HD12	1:A:125:LEU:HA	1.85	0.43
1:B:201:ILE:HD11	1:B:205:VAL:CG1	2.48	0.43
1:A:113:ILE:HD12	1:A:130:VAL:HB	2.00	0.43
1:A:187:LEU:CA	1:A:188:GLU:HB2	2.50	0.42
1:B:9:LEU:HD11	1:B:184:LEU:HB3	2.02	0.42
1:B:23:ARG:N	1:B:24:ALA:CB	2.82	0.42
1:A:197:LEU:HA	1:A:197:LEU:HD23	1.63	0.42
1:A:41:ASN:HD21	1:A:228:ASN:HD22	1.67	0.42
1:A:183:ASP:HB3	1:A:187:LEU:H	1.85	0.42
1:B:54:ARG:NH2	1:B:95:ASP:OD2	2.40	0.42
1:A:211:SER:O	1:A:212:GLY:C	2.58	0.41
1:A:17:LEU:HD23	1:A:17:LEU:HA	1.85	0.41
1:A:94:GLU:O	1:A:98:LYS:HG3	2.21	0.41
1:B:197:LEU:HA	1:B:197:LEU:HD23	1.91	0.41
1:B:216:ARG:NH2	1:B:220:GLU:OE1	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:201:ILE:HD12	1:A:201:ILE:HG23	1.73	0.41
1:A:242:LYS:O	1:A:243:ILE:C	2.59	0.41
1:B:201:ILE:C	1:B:201:ILE:HD13	2.41	0.40
1:B:73:MET:SD	1:B:243:ILE:HD12	2.61	0.40
1:A:139:GLU:HG3	1:A:168:ILE:CG2	2.50	0.40
1:B:166:LEU:O	1:B:166:LEU:HD12	2.20	0.40
1:A:80:LEU:HD12	1:A:105:ILE:HD11	2.04	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	244/247 (99%)	227 (93%)	14 (6%)	3 (1%)	13	17
1	B	245/247 (99%)	230 (94%)	10 (4%)	5 (2%)	7	8
All	All	489/494 (99%)	457 (94%)	24 (5%)	8 (2%)	9	12

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	27	GLN
1	B	24	ALA
1	B	204	ASN
1	A	74	GLU
1	B	44	ASN
1	B	188	GLU
1	B	212	GLY
1	A	30	ILE

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	215/221 (97%)	192 (89%)	23 (11%)	6	8
1	B	213/221 (96%)	194 (91%)	19 (9%)	9	14
All	All	428/442 (97%)	386 (90%)	42 (10%)	8	11

All (42) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	6	LYS
1	A	14	GLN
1	A	23	ARG
1	A	26	ARG
1	A	28	ARG
1	A	42	LYS
1	A	56	SER
1	A	78	VAL
1	A	96	LEU
1	A	102	SER
1	A	110	TRP
1	A	117	SER
1	A	125	LEU
1	A	129	THR
1	A	136	ILE
1	A	140	ARG
1	A	142	LEU
1	A	161	ASN
1	A	184	LEU
1	A	195	ARG
1	A	201	ILE
1	A	215	GLU
1	A	247	ILE
1	B	9	LEU
1	B	12	VAL
1	B	23	ARG
1	B	34	LYS

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Mol	Chain	Res	Type
1	B	75	ARG
1	B	96	LEU
1	B	110	TRP
1	B	113	ILE
1	B	125	LEU
1	B	136	ILE
1	B	142	LEU
1	B	160	ILE
1	B	161	ASN
1	B	183	ASP
1	B	193	ASN
1	B	201	ILE
1	B	207	LYS
1	B	216	ARG
1	B	221	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	41	ASN
1	A	44	ASN
1	A	118	GLN
1	A	124	ASN
1	A	161	ASN
1	B	44	ASN
1	B	118	GLN
1	B	124	ASN
1	B	161	ASN
1	B	190	ASN

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](#)

2 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	SO4	B	1	-	4,4,4	0.40	0	6,6,6	0.60	0
2	SO4	A	249	-	4,4,4	0.16	0	6,6,6	0.65	0

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 [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	246/247 (99%)	-0.33	1 (0%) 92 91	22, 42, 66, 88	0
1	B	247/247 (100%)	-0.34	0 100 100	24, 41, 68, 87	0
All	All	493/494 (99%)	-0.33	1 (0%) 95 95	22, 41, 68, 88	0

All (1) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	187	LEU	2.2

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, 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	SO4	A	249	5/5	0.75	0.30	126,127,128,128	0
2	SO4	B	1	5/5	0.83	0.22	88,90,92,92	0

6.5 Other polymers ⓘ

There are no such residues in this entry.