



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 01:10 PM UTC

PDB ID : 5KDD / pdb_00005kdd
Title : Apo-structure of humanised RadA-mutant humRadA22
Authors : Fischer, G.; Marsh, M.; Moschetti, T.; Sharpe, T.; Scott, D.; Morgan, M.; Ng, H.; Skidmore, J.; Venkitaraman, A.; Abell, C.; Blundell, T.L.; Hyvonen, M.
Deposited on : 2016-06-08
Resolution : 1.99 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
Mogul : 2022.3.0, CSD as543be (2022)
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

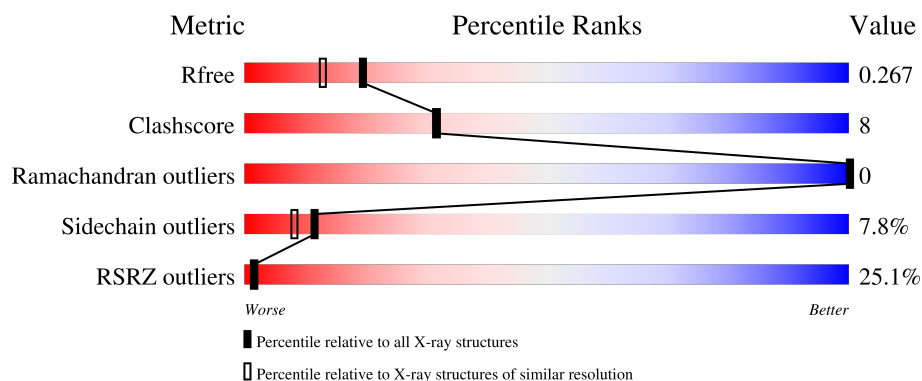
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.99 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	10052 (2.00-2.00)
Clashscore	190562	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)
RSRZ outliers	180081	10067 (2.00-2.00)

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	231	23% 68% 23% 6%
1	B	231	24% 73% 19% 6%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 3687 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 DNA repair and recombination protein RadA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	217	Total	C	N	O	S	0	2	0
			1711	1072	308	324	7			
1	B	218	Total	C	N	O	S	0	2	0
			1717	1076	309	325	7			

There are 78 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	107	MET	-	initiating methionine	UNP O74036
A	168	ALA	VAL	engineered mutation	UNP O74036
A	169	MET	ILE	engineered mutation	UNP O74036
A	170	TYR	TRP	engineered mutation	UNP O74036
A	182	LEU	ILE	engineered mutation	UNP O74036
A	198	ASP	LYS	engineered mutation	UNP O74036
A	199	ASN	HIS	engineered mutation	UNP O74036
A	200	VAL	ILE	engineered mutation	UNP O74036
A	201	ALA	TYR	engineered mutation	UNP O74036
A	202	TYR	VAL	engineered mutation	UNP O74036
A	213	GLN	LEU	engineered mutation	UNP O74036
A	215	LEU	VAL	engineered mutation	UNP O74036
A	216	TYR	GLN	engineered mutation	UNP O74036
A	219	SER	GLU	engineered mutation	UNP O74036
A	220	ALA	ASP	engineered mutation	UNP O74036
A	221	MET	LYS	engineered mutation	UNP O74036
A	222	MET	ILE	engineered mutation	UNP O74036
A	223	VAL	LYS	engineered mutation	UNP O74036
A	225	SER	LEU	engineered mutation	UNP O74036
A	232	TYR	VAL	engineered mutation	UNP O74036
A	263	ARG	LYS	engineered mutation	UNP O74036
A	264	PHE	HIS	engineered mutation	UNP O74036
A	266	ARG	ALA	engineered mutation	UNP O74036
A	267	MET	ASP	engineered mutation	UNP O74036
A	274	GLU	LEU	engineered mutation	UNP O74036

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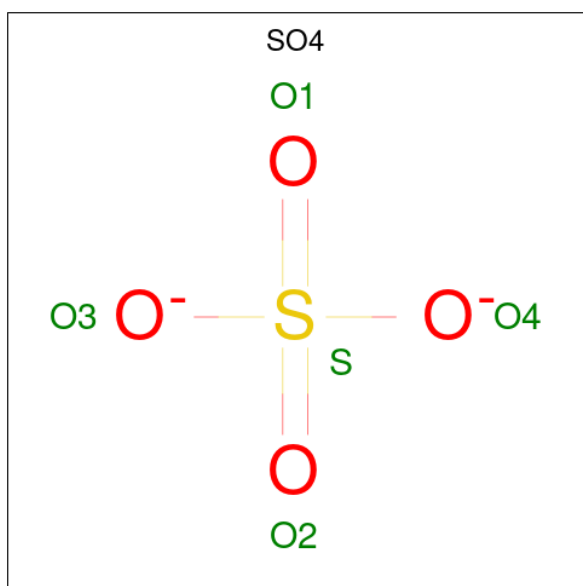
Chain	Residue	Modelled	Actual	Comment	Reference
A	275	PHE	TYR	engineered mutation	UNP O74036
A	?	-	ARG	deletion	UNP O74036
A	?	-	PRO	deletion	UNP O74036
A	?	-	ASP	deletion	UNP O74036
A	?	-	ALA	deletion	UNP O74036
A	?	-	PHE	deletion	UNP O74036
A	?	-	PHE	deletion	UNP O74036
A	?	-	GLY	deletion	UNP O74036
A	?	-	ASP	deletion	UNP O74036
A	?	-	PRO	deletion	UNP O74036
A	?	-	THR	deletion	UNP O74036
A	?	-	ARG	deletion	UNP O74036
A	?	-	PRO	deletion	UNP O74036
A	300	ASN	ILE	engineered mutation	UNP O74036
B	107	MET	-	initiating methionine	UNP O74036
B	168	ALA	VAL	engineered mutation	UNP O74036
B	169	MET	ILE	engineered mutation	UNP O74036
B	170	TYR	TRP	engineered mutation	UNP O74036
B	182	LEU	ILE	engineered mutation	UNP O74036
B	198	ASP	LYS	engineered mutation	UNP O74036
B	199	ASN	HIS	engineered mutation	UNP O74036
B	200	VAL	ILE	engineered mutation	UNP O74036
B	201	ALA	TYR	engineered mutation	UNP O74036
B	202	TYR	VAL	engineered mutation	UNP O74036
B	213	GLN	LEU	engineered mutation	UNP O74036
B	215	LEU	VAL	engineered mutation	UNP O74036
B	216	TYR	GLN	engineered mutation	UNP O74036
B	219	SER	GLU	engineered mutation	UNP O74036
B	220	ALA	ASP	engineered mutation	UNP O74036
B	221	MET	LYS	engineered mutation	UNP O74036
B	222	MET	ILE	engineered mutation	UNP O74036
B	223	VAL	LYS	engineered mutation	UNP O74036
B	225	SER	LEU	engineered mutation	UNP O74036
B	232	TYR	VAL	engineered mutation	UNP O74036
B	263	ARG	LYS	engineered mutation	UNP O74036
B	264	PHE	HIS	engineered mutation	UNP O74036
B	266	ARG	ALA	engineered mutation	UNP O74036
B	267	MET	ASP	engineered mutation	UNP O74036
B	274	GLU	LEU	engineered mutation	UNP O74036
B	275	PHE	TYR	engineered mutation	UNP O74036
B	?	-	ARG	deletion	UNP O74036
B	?	-	PRO	deletion	UNP O74036

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Chain	Residue	Modelled	Actual	Comment	Reference
B	?	-	ASP	deletion	UNP O74036
B	?	-	ALA	deletion	UNP O74036
B	?	-	PHE	deletion	UNP O74036
B	?	-	PHE	deletion	UNP O74036
B	?	-	GLY	deletion	UNP O74036
B	?	-	ASP	deletion	UNP O74036
B	?	-	PRO	deletion	UNP O74036
B	?	-	THR	deletion	UNP O74036
B	?	-	ARG	deletion	UNP O74036
B	?	-	PRO	deletion	UNP O74036
B	300	ASN	ILE	engineered mutation	UNP O74036

- Molecule 2 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



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

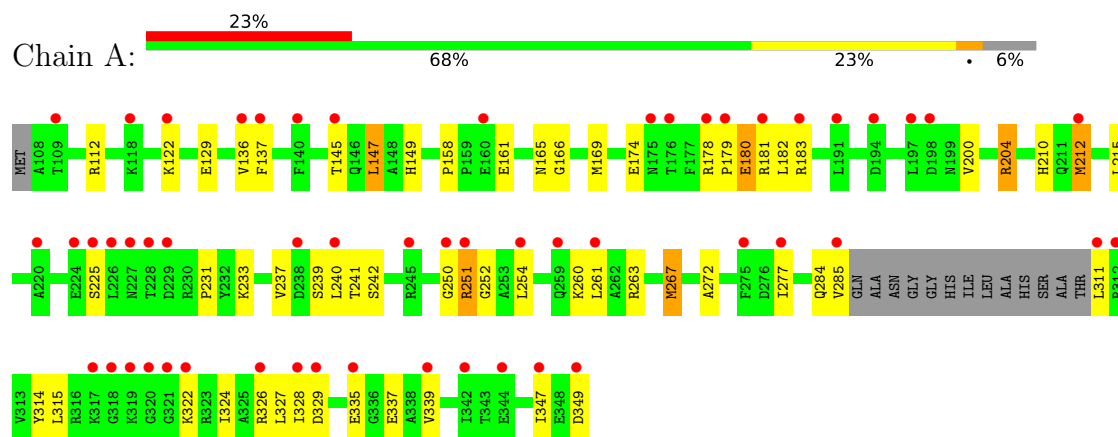
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	129	Total 129	O 129	0	0
3	B	110	Total 110	O 110	0	0

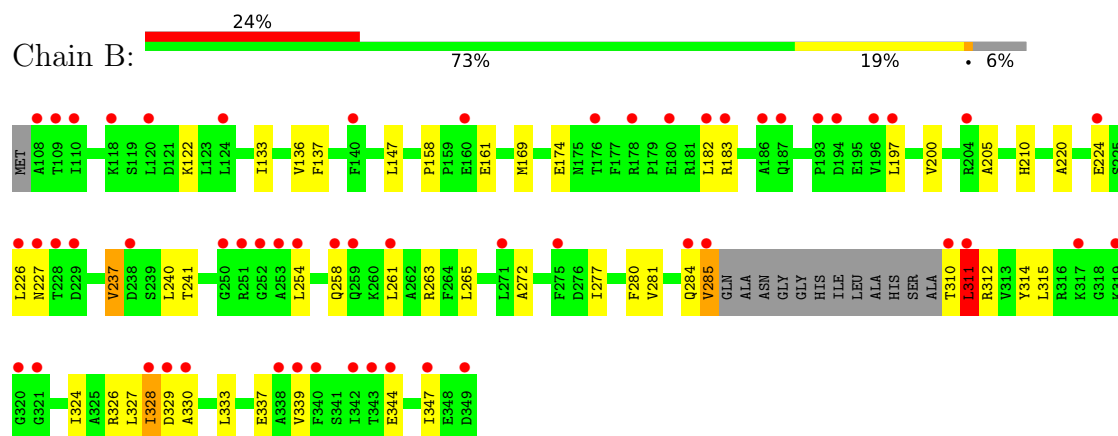
3 Residue-property plots [i](#)

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: DNA repair and recombination protein RadA



- Molecule 1: DNA repair and recombination protein RadA



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	37.85Å 42.58Å 86.44Å 78.66° 85.49° 63.63°	Depositor
Resolution (Å)	84.75 – 1.99 84.75 – 1.99	Depositor EDS
% Data completeness (in resolution range)	95.0 (84.75-1.99) 95.1 (84.75-1.99)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	0.18	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.25 (at 1.98Å)	Xtriage
Refinement program	BUSTER 2.11.4	Depositor
R, R_{free}	0.229 , 0.250 0.246 , 0.267	Depositor DCC
R_{free} test set	1566 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å ²)	17.5	Xtriage
Anisotropy	0.594	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 42.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	0.018 for -h,-k,-k+1	Xtriage
F_o, F_c correlation	0.88	EDS
Total number of atoms	3687	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 8.49% 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	0.90	0/1736	1.30	7/2335 (0.3%)
1	B	0.91	0/1742	1.27	4/2345 (0.2%)
All	All	0.91	0/3478	1.28	11/4680 (0.2%)

There are no bond length outliers.

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	284	GLN	CA-C-N	7.78	135.71	121.70
1	A	284	GLN	C-N-CA	7.78	135.71	121.70
1	A	239	SER	CA-C-N	7.05	130.04	120.38
1	A	239	SER	C-N-CA	7.05	130.04	120.38
1	B	226	LEU	N-CA-C	6.04	117.86	111.28
1	A	250	GLY	CA-C-N	6.04	133.07	121.54
1	A	250	GLY	C-N-CA	6.04	133.07	121.54
1	B	227	ASN	CA-CB-CG	5.82	118.42	112.60
1	A	237	VAL	N-CA-CB	5.53	118.94	112.35
1	B	237	VAL	N-CA-CB	5.33	118.60	112.15
1	B	311	LEU	CD1-CG-CD2	5.18	122.19	110.80

There are no chirality outliers.

There are no planarity outliers.

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	A	1711	0	1719	31	0
1	B	1717	0	1726	26	0
2	A	10	0	0	0	0
2	B	10	0	0	0	0
3	A	129	0	0	4	0
3	B	110	0	0	6	0
All	All	3687	0	3445	56	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 8.

All (56) 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:242:SER:HB3	3:A:579:HOH:O	1.65	0.95
1:B:241:THR:HG22	1:B:261:LEU:HD11	1.51	0.91
1:B:169[A]:MET:HE1	3:B:503:HOH:O	1.71	0.90
1:A:166:GLY:HA3	1:A:233:LYS:HD2	1.53	0.88
1:A:165:ASN:HB3	3:A:501:HOH:O	1.78	0.84
1:A:241:THR:HG22	1:A:261:LEU:HD11	1.59	0.83
1:A:322:LYS:HE2	3:A:569:HOH:O	1.91	0.69
1:B:133:ILE:HB	1:B:310:THR:HG22	1.75	0.68
1:B:133:ILE:HB	1:B:310:THR:CG2	2.25	0.67
1:A:215:LEU:HB3	1:A:267:MET:HE3	1.76	0.66
1:B:328:ILE:HG13	3:B:531:HOH:O	1.96	0.66
1:A:147:LEU:HD22	1:A:347:ILE:HG13	1.79	0.64
1:B:136:VAL:HG22	1:B:315:LEU:HG	1.83	0.60
1:A:149:HIS:CE1	1:A:178:ARG:H	2.22	0.58
1:A:136:VAL:HG22	1:A:315:LEU:HG	1.83	0.57
1:A:311:LEU:HD11	1:A:327:LEU:HD11	1.86	0.57
1:B:311:LEU:HD21	1:B:327:LEU:HD11	1.87	0.56
1:A:166:GLY:CA	1:A:233:LYS:HD2	2.30	0.56
1:B:285:VAL:HG22	3:B:584:HOH:O	2.08	0.54
1:A:251:ARG:HD3	1:A:252:GLY:H	1.72	0.54
1:A:212[A]:MET:HE2	1:A:263:ARG:HG2	1.90	0.53
1:A:215:LEU:CB	1:A:267:MET:HE3	2.38	0.53
1:A:326:ARG:HD3	1:A:337:GLU:OE2	2.11	0.51
1:A:179:PRO:O	1:A:183:ARG:HG3	2.11	0.50
1:B:136:VAL:CG2	1:B:315:LEU:HG	2.41	0.50
1:A:145:THR:HB	3:A:538:HOH:O	2.11	0.50
1:A:324:ILE:HG12	1:A:339:VAL:HG22	1.94	0.50
1:A:136:VAL:CG2	1:A:315:LEU:HG	2.43	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:147:LEU:HD12	1:B:347:ILE:HG13	1.94	0.48
1:A:231:PRO:HD2	1:A:233:LYS:HE3	1.95	0.48
1:B:326:ARG:HD3	1:B:337:GLU:OE2	2.13	0.48
1:B:147:LEU:HD23	1:B:280:PHE:HZ	1.79	0.48
1:B:312:ARG:HD2	3:B:561:HOH:O	2.13	0.47
1:A:272:ALA:HA	1:A:277:ILE:HG13	1.95	0.47
1:A:158:PRO:HD2	1:A:161:GLU:HB2	1.96	0.47
1:A:178:ARG:HB3	1:A:180:GLU:OE2	2.15	0.46
1:A:112:ARG:NH1	1:A:129:GLU:HG3	2.30	0.46
1:B:258:GLN:HG2	3:B:598:HOH:O	2.15	0.46
1:A:241:THR:HG22	1:A:261:LEU:CD1	2.40	0.45
1:B:158:PRO:HD2	1:B:161:GLU:HB2	1.97	0.45
1:B:182:LEU:HD21	1:B:200:VAL:HG21	1.99	0.44
1:B:205:ALA:HA	1:B:210:HIS:HD2	1.82	0.44
1:A:182:LEU:HD21	1:A:200:VAL:HG21	1.98	0.44
1:B:324:ILE:HG12	1:B:339:VAL:HG22	1.98	0.44
1:A:137:PHE:CZ	1:A:314:TYR:HB2	2.53	0.44
1:A:212[B]:MET:HE1	1:A:260:LYS:HD2	2.00	0.44
1:B:137:PHE:CZ	1:B:314:TYR:HB2	2.53	0.43
1:A:263:ARG:HH21	1:B:263:ARG:NH1	2.17	0.43
1:B:220:ALA:O	1:B:224:GLU:HG3	2.19	0.43
1:A:251:ARG:HD3	1:A:251:ARG:N	2.33	0.42
1:B:183:ARG:HD2	1:B:197:LEU:HD11	2.00	0.42
1:B:284:GLN:HB3	3:B:555:HOH:O	2.19	0.42
1:B:237:VAL:HB	1:B:281:VAL:HG12	2.03	0.41
1:B:272:ALA:HA	1:B:277:ILE:HG13	2.01	0.41
1:B:330:ALA:CB	1:B:333:LEU:HB2	2.52	0.40
1:A:204:ARG:O	1:A:210:HIS:HE1	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	215/231 (93%)	214 (100%)	1 (0%)	0	100	100
1	B	216/231 (94%)	215 (100%)	1 (0%)	0	100	100
All	All	431/462 (93%)	429 (100%)	2 (0%)	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	181/188 (96%)	162 (90%)	19 (10%)	6	4
1	B	182/188 (97%)	172 (94%)	10 (6%)	19	17
All	All	363/376 (96%)	334 (92%)	29 (8%)	11	8

All (29) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	122	LYS
1	A	147	LEU
1	A	169	MET
1	A	174	GLU
1	A	180	GLU
1	A	181	ARG
1	A	204	ARG
1	A	212[A]	MET
1	A	212[B]	MET
1	A	225	SER
1	A	240	LEU
1	A	251	ARG
1	A	254	LEU
1	A	267	MET
1	A	285	VAL
1	A	328	ILE
1	A	329	ASP
1	A	335	GLU

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Mol	Chain	Res	Type
1	A	349	ASP
1	B	122	LYS
1	B	174	GLU
1	B	240	LEU
1	B	254	LEU
1	B	265	LEU
1	B	285	VAL
1	B	311	LEU
1	B	328	ILE
1	B	329	ASP
1	B	344	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	149	HIS
1	A	165	ASN
1	A	187	GLN
1	A	188	ASN
1	A	273	ASN
1	A	284	GLN
1	B	131	GLN
1	B	165	ASN
1	B	175	ASN
1	B	187	GLN
1	B	210	HIS
1	B	259	GLN
1	B	273	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 ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

4 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	401	-	4,4,4	0.35	0	6,6,6	0.51	0
2	SO4	B	402	-	4,4,4	0.28	0	6,6,6	0.27	0
2	SO4	A	401	-	4,4,4	0.45	0	6,6,6	0.61	0
2	SO4	A	402	-	4,4,4	0.40	0	6,6,6	0.22	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

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	217/231 (93%)	1.52	54 (24%)	2 1	7, 22, 43, 57	2 (0%)
1	B	218/231 (94%)	1.54	55 (25%)	1 1	7, 23, 41, 65	2 (0%)
All	All	435/462 (94%)	1.53	109 (25%)	1 1	7, 22, 41, 65	4 (0%)

All (109) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	140	PHE	5.8
1	B	328	ILE	5.6
1	B	349	ASP	5.3
1	A	227	ASN	5.1
1	B	319	LYS	4.7
1	A	212[A]	MET	4.7
1	B	252	GLY	4.5
1	A	285	VAL	4.5
1	A	228	THR	4.3
1	A	328	ILE	4.3
1	B	251	ARG	4.2
1	A	319	LYS	4.2
1	B	227	ASN	4.2
1	B	285	VAL	4.1
1	B	108	ALA	4.1
1	A	329	ASP	3.7
1	A	181	ARG	3.7
1	B	321	GLY	3.7
1	B	140	PHE	3.6
1	A	349	ASP	3.6
1	A	311	LEU	3.5
1	B	320	GLY	3.5
1	B	228	THR	3.4
1	B	118	LYS	3.4

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Mol	Chain	Res	Type	RSRZ
1	B	238	ASP	3.4
1	A	229	ASP	3.3
1	A	136	VAL	3.3
1	B	317	LYS	3.3
1	A	238	ASP	3.2
1	B	339	VAL	3.1
1	B	229	ASP	3.1
1	A	320	GLY	3.1
1	A	118	LYS	3.1
1	B	226	LEU	3.0
1	A	194	ASP	3.0
1	A	183	ARG	3.0
1	B	330	ALA	3.0
1	A	220	ALA	3.0
1	A	347	ILE	2.9
1	B	253	ALA	2.9
1	B	197	LEU	2.9
1	B	310	THR	2.9
1	A	191	LEU	2.9
1	A	245	ARG	2.8
1	B	180	GLU	2.8
1	A	240	LEU	2.8
1	A	254	LEU	2.8
1	A	176	THR	2.7
1	B	254	LEU	2.7
1	A	251	ARG	2.6
1	B	284	GLN	2.6
1	B	311	LEU	2.6
1	A	318	GLY	2.6
1	A	322	LYS	2.6
1	B	182	LEU	2.6
1	B	120	LEU	2.5
1	B	347	ILE	2.5
1	B	329	ASP	2.5
1	A	122	LYS	2.5
1	A	312	ARG	2.5
1	A	342	ILE	2.5
1	A	178	ARG	2.4
1	B	186	ALA	2.4
1	A	339	VAL	2.4
1	A	175	ASN	2.4
1	B	250	GLY	2.4

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Mol	Chain	Res	Type	RSRZ
1	B	204	ARG	2.4
1	A	197	LEU	2.4
1	A	317	LYS	2.4
1	B	194	ASP	2.4
1	A	225	SER	2.4
1	B	183	ARG	2.3
1	A	275	PHE	2.3
1	A	321	GLY	2.3
1	A	179	PRO	2.3
1	B	258	GLN	2.3
1	B	259	GLN	2.3
1	B	338	ALA	2.2
1	A	198	ASP	2.2
1	A	259	GLN	2.2
1	A	250	GLY	2.2
1	B	196	VAL	2.2
1	A	226	LEU	2.2
1	B	124	LEU	2.2
1	B	261	LEU	2.2
1	A	137	PHE	2.2
1	B	275	PHE	2.2
1	A	326	ARG	2.2
1	A	335	GLU	2.2
1	A	344	GLU	2.1
1	B	224	GLU	2.1
1	B	340	PHE	2.1
1	B	109	THR	2.1
1	B	343	THR	2.1
1	B	271	LEU	2.1
1	B	160	GLU	2.1
1	B	110	ILE	2.1
1	B	342	ILE	2.1
1	A	224	GLU	2.1
1	A	277	ILE	2.1
1	A	109	THR	2.1
1	A	145	THR	2.1
1	A	160	GLU	2.1
1	B	344	GLU	2.1
1	A	261	LEU	2.1
1	B	176	THR	2.0
1	B	187	GLN	2.0
1	B	193	PRO	2.0

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Mol	Chain	Res	Type	RSRZ
1	B	178	ARG	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 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
2	SO4	B	402	5/5	0.86	0.13	48,48,52,52	0
2	SO4	A	401	5/5	0.91	0.11	24,24,26,31	0
2	SO4	A	402	5/5	0.93	0.09	32,35,36,36	0
2	SO4	B	401	5/5	0.94	0.10	29,29,31,33	0

6.5 Other polymers [i](#)

There are no such residues in this entry.