



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 14, 2017 – 12:01 pm GMT

PDB ID : 3ZUV
Title : Crystal structure of a designed selected Ankyrin Repeat protein in complex with the phosphorylated MAP kinase ERK2
Authors : Kummer, L.; Mittl, P.R.; Pluckthun, A.
Deposited on : 2011-07-20
Resolution : 2.72 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
Mogul : 1.7.2 (RC1), CSD as538be (2017)
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

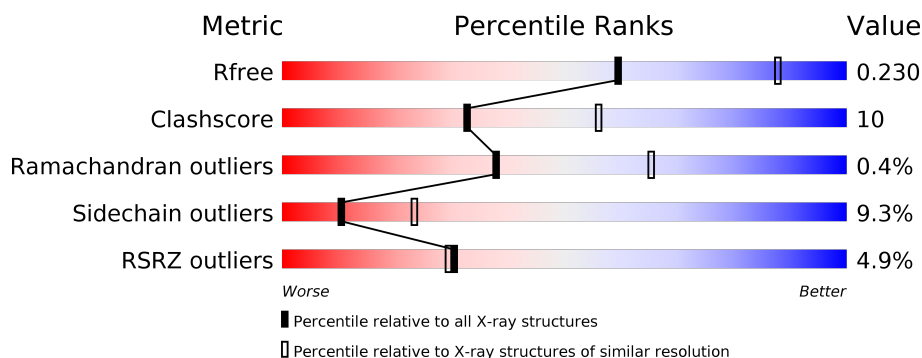
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.72 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	2649 (2.74-2.70)
Clashscore	112137	2993 (2.74-2.70)
Ramachandran outliers	110173	2946 (2.74-2.70)
Sidechain outliers	110143	2947 (2.74-2.70)
RSRZ outliers	101464	2665 (2.74-2.70)

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	364	<div> <div style="width: 76%; background-color: green;"></div> <div style="width: 19%; background-color: yellow;"></div> <div style="width: 5%; background-color: orange;"></div> <div style="width: 0%; background-color: red;"></div> <div style="width: 0%; background-color: grey;"></div> </div>
1	C	364	<div> <div style="width: 3%; background-color: red;"></div> <div style="width: 73%; background-color: green;"></div> <div style="width: 22%; background-color: yellow;"></div> <div style="width: 2%; background-color: orange;"></div> <div style="width: 0%; background-color: grey;"></div> </div>
2	B	136	<div> <div style="width: 71%; background-color: green;"></div> <div style="width: 14%; background-color: yellow;"></div> <div style="width: 10%; background-color: grey;"></div> <div style="width: 0%; background-color: orange;"></div> <div style="width: 0%; background-color: red;"></div> </div>
2	D	136	<div> <div style="width: 26%; background-color: red;"></div> <div style="width: 64%; background-color: green;"></div> <div style="width: 22%; background-color: yellow;"></div> <div style="width: 2%; background-color: orange;"></div> <div style="width: 10%; background-color: grey;"></div> </div>

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 8003 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 MITOGEN-ACTIVATED PROTEIN KINASE 1.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	359	Total	C	N	O	P	S	0	3	0
			2953	1886	510	539	2	16			
1	C	359	Total	C	N	O	P	S	0	6	0
			2979	1900	515	546	2	16			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-5	HIS	-	EXPRESSION TAG	UNP P63086
A	-4	HIS	-	EXPRESSION TAG	UNP P63086
A	-3	HIS	-	EXPRESSION TAG	UNP P63086
A	-2	HIS	-	EXPRESSION TAG	UNP P63086
A	-1	HIS	-	EXPRESSION TAG	UNP P63086
A	0	HIS	-	EXPRESSION TAG	UNP P63086
A	1	ALA	-	EXPRESSION TAG	UNP P63086
A	2	MET	-	EXPRESSION TAG	UNP P63086
C	-5	HIS	-	EXPRESSION TAG	UNP P63086
C	-4	HIS	-	EXPRESSION TAG	UNP P63086
C	-3	HIS	-	EXPRESSION TAG	UNP P63086
C	-2	HIS	-	EXPRESSION TAG	UNP P63086
C	-1	HIS	-	EXPRESSION TAG	UNP P63086
C	0	HIS	-	EXPRESSION TAG	UNP P63086
C	1	ALA	-	EXPRESSION TAG	UNP P63086
C	2	MET	-	EXPRESSION TAG	UNP P63086

- Molecule 2 is a protein called DESIGNED ANKYRIN REPEAT PROTEIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	122	Total	C	N	O	S	0	2	0
			939	587	161	190	1			
2	D	122	Total	C	N	O	S	0	0	0
			919	575	158	185	1			

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	O	S	0	0
			5	4	1		
3	C	1	Total	O	S	0	0
			5	4	1		


- Molecule 4 is water.

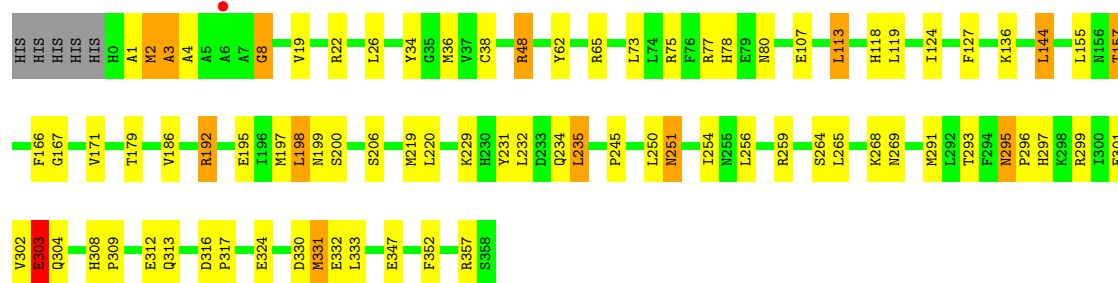
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	119	Total	O	0	0
			119	119		
4	B	12	Total	O	0	0
			12	12		
4	C	69	Total	O	0	0
			69	69		
4	D	3	Total	O	0	0
			3	3		

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.

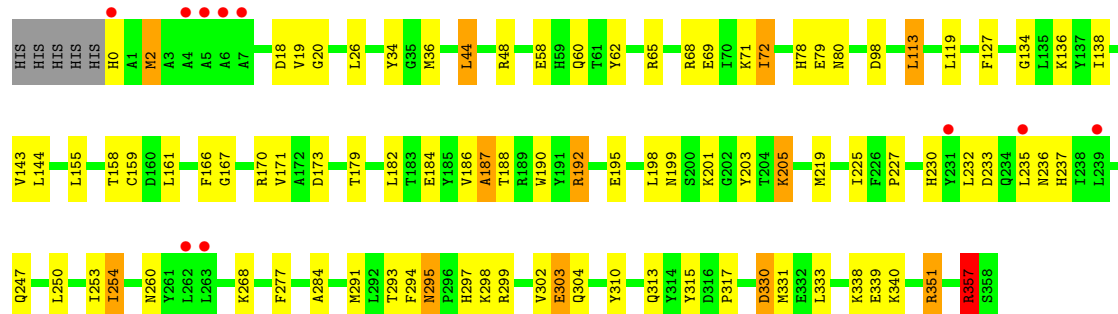
• Molecule 1: MITOGEN-ACTIVATED PROTEIN KINASE 1

Chain A: 



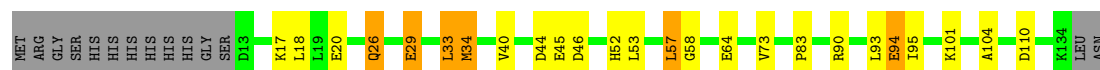
• Molecule 1: MITOGEN-ACTIVATED PROTEIN KINASE 1

Chain C: 



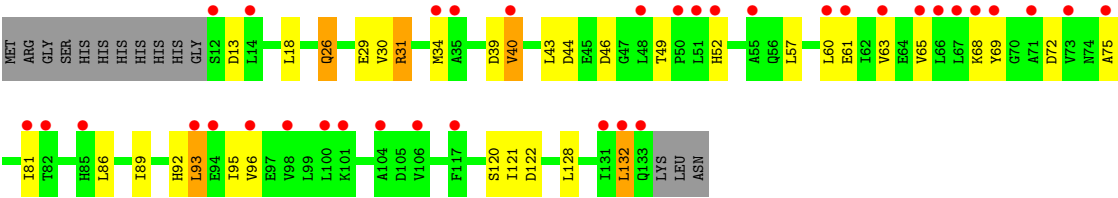
• Molecule 2: DESIGNED ANKYRIN REPEAT PROTEIN

Chain B: 



• Molecule 2: DESIGNED ANKYRIN REPEAT PROTEIN

Chain D: 



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	113.67Å 150.45Å 104.97Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	77.12 – 2.72 77.12 – 2.72	Depositor EDS
% Data completeness (in resolution range)	100.0 (77.12-2.72) 98.1 (77.12-2.72)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.43 (at 2.73Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.176 , 0.230 0.176 , 0.230	Depositor DCC
R_{free} test set	2411 reflections (5.26%)	DCC
Wilson B-factor (Å ²)	56.4	Xtriage
Anisotropy	0.048	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 48.0	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	0.95	EDS
Total number of atoms	8003	wwPDB-VP
Average B, all atoms (Å ²)	60.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.81% 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: TPO, SO4, PTR

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	1.03	5/2995 (0.2%)	1.01	7/4054 (0.2%)
1	C	0.93	4/3021 (0.1%)	0.97	5/4089 (0.1%)
2	B	0.90	1/949 (0.1%)	0.94	2/1284 (0.2%)
2	D	0.68	0/929	0.79	0/1258
All	All	0.94	10/7894 (0.1%)	0.96	14/10685 (0.1%)

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	A	0	2
1	C	0	1
All	All	0	3

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	347	GLU	CG-CD	8.00	1.64	1.51
1	A	303	GLU	CB-CG	7.09	1.65	1.52
1	A	303	GLU	CG-CD	6.46	1.61	1.51
1	C	303	GLU	CG-CD	5.81	1.60	1.51
2	B	20	GLU	CG-CD	5.61	1.60	1.51
1	A	38	CYS	CB-SG	-5.47	1.72	1.81
1	C	303	GLU	CB-CG	5.44	1.62	1.52
1	C	330	ASP	CB-CG	5.43	1.63	1.51
1	A	352	PHE	CE2-CZ	5.32	1.47	1.37
1	C	143	VAL	CB-CG2	-5.27	1.41	1.52

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	192	ARG	NE-CZ-NH2	-10.66	114.97	120.30
1	A	357	ARG	NE-CZ-NH2	-9.13	115.74	120.30
1	C	357	ARG	NE-CZ-NH2	-8.72	115.94	120.30
1	C	351	ARG	NE-CZ-NH1	8.11	124.36	120.30
1	A	357	ARG	NE-CZ-NH1	7.84	124.22	120.30
2	B	57	LEU	CA-CB-CG	-7.48	98.10	115.30
1	A	192	ARG	NE-CZ-NH1	7.17	123.89	120.30
2	B	90	ARG	NE-CZ-NH1	6.61	123.60	120.30
1	A	22	ARG	NE-CZ-NH2	-6.19	117.20	120.30
1	C	26	LEU	CA-CB-CG	6.11	129.35	115.30
1	C	192	ARG	NE-CZ-NH2	-5.83	117.38	120.30
1	A	144	LEU	CB-CG-CD1	-5.60	101.48	111.00
1	C	192	ARG	NE-CZ-NH1	5.39	122.99	120.30
1	A	48	ARG	NE-CZ-NH1	5.28	122.94	120.30

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	19	VAL	Peptide
1	A	8	GLY	Peptide
1	C	253	ILE	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	A	2953	0	2936	61	0
1	C	2979	0	2953	62	0
2	B	939	0	925	16	0
2	D	919	0	909	19	0
3	A	5	0	0	1	0
3	C	5	0	0	1	0
4	A	119	0	0	9	0
4	B	12	0	0	0	0
4	C	69	0	0	2	0
4	D	3	0	0	0	0
All	All	8003	0	7723	154	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 10.

All (154) 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:107:GLU:OE2	1:A:157:THR:HG23	1.28	1.23
1:A:107:GLU:OE2	1:A:157:THR:CG2	2.05	1.03
1:C:313[B]:GLN:HE21	1:C:313[B]:GLN:H	1.08	0.98
1:A:78:HIS:HD2	1:A:80:ASN:H	1.09	0.95
1:C:313[B]:GLN:H	1:C:313[B]:GLN:NE2	1.62	0.95
1:A:113:LEU:HD13	1:A:119:LEU:HD21	1.52	0.92
1:C:78:HIS:HD2	1:C:80:ASN:H	1.04	0.92
1:A:78:HIS:CD2	1:A:80:ASN:H	1.92	0.88
1:A:251[B]:ASN:HA	1:A:259[B]:ARG:CZ	2.08	0.83
1:A:197:MET:HE1	1:A:234:GLN:HB3	1.61	0.83
1:C:144:LEU:HD22	1:C:205:LYS:HA	1.64	0.79
1:A:197:MET:CE	1:A:234:GLN:HB3	2.14	0.78
1:C:199:ASN:HD21	1:C:254:ILE:H	1.30	0.78
1:C:68:ARG:O	1:C:72:ILE:HG13	1.85	0.77
2:D:26:GLN:HB3	2:D:29:GLU:HB3	1.67	0.77
1:C:158:THR:O	1:C:159:CYS:HB2	1.86	0.76
2:D:93:LEU:O	2:D:96:VAL:HG22	1.85	0.76
1:C:313[B]:GLN:HE21	1:C:313[B]:GLN:N	1.82	0.75
1:C:340:LYS:HE2	4:C:2061:HOH:O	1.85	0.75
1:C:78:HIS:CD2	1:C:80:ASN:H	1.96	0.75
1:A:331:MET:HE3	4:A:2111:HOH:O	1.86	0.74
2:B:94[A]:GLU:CD	2:B:94[A]:GLU:H	1.92	0.72
1:C:295:ASN:HD22	1:C:297:HIS:H	1.35	0.72
2:B:53:LEU:O	2:B:57:LEU:HD12	1.90	0.72
1:C:295:ASN:ND2	1:C:297:HIS:H	1.91	0.69
1:A:291:MET:O	1:A:299:ARG:HD2	1.93	0.69
1:A:124:ILE:HD13	1:A:220:LEU:HD23	1.75	0.68
1:C:113:LEU:HD13	1:C:119:LEU:HD21	1.74	0.68
1:C:127:PHE:HD2	1:C:219:MET:CE	2.07	0.68
1:A:1:ALA:HA	4:A:2001:HOH:O	1.93	0.67
1:C:315:TYR:CZ	1:C:317:PRO:HG3	2.32	0.65
2:D:128:LEU:O	2:D:132:LEU:HD22	1.97	0.65
1:C:291:MET:O	1:C:299:ARG:HD2	1.97	0.64
1:A:199:ASN:HD21	1:A:254:ILE:H	1.46	0.64
1:C:161:LEU:C	1:C:161:LEU:HD23	2.19	0.63
1:C:184:GLU:OE1	2:D:122:ASP:HB3	1.99	0.63
1:A:295:ASN:ND2	1:A:297:HIS:H	1.97	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:251[A]:ASN:HD21	1:A:259[A]:ARG:HH21	1.48	0.61
1:A:2:MET:O	1:A:4:ALA:N	2.34	0.61
1:A:118[A]:HIS:HD2	4:A:2050:HOH:O	1.83	0.60
1:A:113:LEU:HD13	1:A:119:LEU:CD2	2.28	0.60
1:C:284:ALA:HB2	1:C:310:TYR:CE1	2.36	0.60
1:C:79:GLU:HG3	4:C:2024:HOH:O	2.02	0.60
1:C:186:VAL:O	1:C:192:ARG:HD3	2.02	0.59
1:A:295:ASN:HD22	1:A:296:PRO:HD2	1.67	0.59
1:A:295:ASN:C	1:A:295:ASN:HD22	2.06	0.59
2:B:26:GLN:HG2	2:B:29:GLU:HB2	1.84	0.59
1:C:65:ARG:HG2	1:C:167:GLY:O	2.04	0.58
1:A:245:PRO:HG2	1:A:250:LEU:HD13	1.84	0.58
1:A:48:ARG:NH1	3:A:1359:SO4:O3	2.33	0.57
2:D:92:HIS:HB3	2:D:95:ILE:HD13	1.85	0.56
1:A:293:THR:O	1:A:299:ARG:NH1	2.36	0.56
1:A:1:ALA:O	1:A:3:ALA:N	2.38	0.56
2:B:26:GLN:HG2	2:B:29:GLU:OE1	2.06	0.56
1:A:127:PHE:HD2	1:A:219:MET:CE	2.19	0.55
1:C:127:PHE:HD2	1:C:219:MET:HE3	1.69	0.55
1:C:48:ARG:NH1	3:C:1359:SO4:O1	2.38	0.55
1:A:251[B]:ASN:HA	1:A:259[B]:ARG:NH2	2.21	0.55
1:A:295:ASN:HD22	1:A:296:PRO:CD	2.20	0.54
1:A:301:GLU:H	1:A:304:GLN:NE2	2.05	0.54
1:A:118[A]:HIS:CD2	4:A:2050:HOH:O	2.59	0.54
1:C:182:LEU:HB3	1:C:203:TYR:CZ	2.43	0.54
1:C:295:ASN:HD22	1:C:297:HIS:N	2.03	0.53
2:D:31:ARG:HB3	2:D:31:ARG:HH11	1.73	0.53
2:D:120:SER:HB3	2:D:128:LEU:HD23	1.91	0.53
1:C:170:ARG:HG2	1:C:171:VAL:N	2.23	0.53
2:D:44:ASP:C	2:D:46:ASP:H	2.11	0.53
1:C:69:GLU:HG3	1:C:166:PHE:HB2	1.89	0.52
1:C:134:GLY:O	1:C:138:ILE:HG13	2.10	0.51
2:D:92:HIS:O	2:D:96:VAL:HG13	2.10	0.51
4:A:2064:HOH:O	1:C:357:ARG:HD3	2.10	0.51
1:C:195:GLU:CD	1:C:299:ARG:HH22	2.15	0.50
1:C:127:PHE:CD2	1:C:219:MET:HE3	2.46	0.50
2:B:34:MET:HE1	2:B:40:VAL:CG1	2.42	0.50
1:A:269:ASN:OD1	4:A:2094:HOH:O	2.20	0.49
2:D:34:MET:HB3	2:D:69:TYR:CE2	2.47	0.49
2:B:58:GLY:HA2	2:B:95:ILE:HD12	1.94	0.49
1:C:68:ARG:O	1:C:72:ILE:CG1	2.58	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:293:THR:O	1:C:299:ARG:HD3	2.12	0.49
1:A:251[B]:ASN:HA	1:A:259[B]:ARG:NH1	2.29	0.48
1:C:186:VAL:O	1:C:192:ARG:CD	2.62	0.48
1:A:195:GLU:OE2	1:A:299:ARG:NH2	2.46	0.48
1:C:199:ASN:ND2	1:C:254:ILE:H	2.07	0.48
1:C:44:LEU:HD12	1:C:44:LEU:O	2.14	0.48
2:D:120:SER:CB	2:D:128:LEU:HD23	2.44	0.48
1:A:197:MET:CE	1:A:231:TYR:O	2.62	0.48
1:A:303:GLU:H	1:A:303:GLU:CD	2.18	0.48
1:C:190:TRP:CD1	1:C:227:PRO:HA	2.49	0.47
1:C:119:LEU:CD1	1:C:219:MET:HE2	2.43	0.47
1:C:199:ASN:HD21	1:C:254:ILE:N	2.04	0.47
1:A:229:LYS:NZ	2:B:46:ASP:OD2	2.34	0.47
1:A:295:ASN:HD22	1:A:296:PRO:N	2.13	0.47
1:A:73:LEU:HD21	1:A:166:PHE:CD1	2.50	0.47
1:A:232:LEU:HA	1:A:232:LEU:HD23	1.54	0.46
1:C:182:LEU:O	1:C:201:LYS:HG2	2.16	0.46
1:C:44:LEU:HD12	1:C:44:LEU:C	2.35	0.46
1:A:308:HIS:CG	1:A:309:PRO:HD2	2.50	0.46
1:C:195:GLU:OE2	1:C:299:ARG:NH2	2.49	0.46
1:C:36:MET:HE3	1:C:36:MET:HB3	1.74	0.46
2:D:49:THR:O	2:D:52:HIS:HB2	2.16	0.46
1:A:206:SER:HB2	4:A:2105:HOH:O	2.15	0.45
1:A:295:ASN:C	1:A:295:ASN:ND2	2.70	0.45
1:A:197:MET:HE3	1:A:234:GLN:HB3	1.94	0.45
1:A:198:LEU:HD13	1:A:235:LEU:HD21	1.97	0.45
1:A:78:HIS:HD2	1:A:80:ASN:N	1.93	0.45
1:C:187:ALA:O	1:C:188:THR:C	2.54	0.45
1:A:197:MET:HE3	1:A:231:TYR:HA	1.97	0.45
1:C:187:ALA:O	1:C:192:ARG:HD3	2.17	0.45
2:D:72:ASP:HB3	2:D:75:ALA:HB2	1.98	0.45
2:D:13:ASP:CG	2:D:13:ASP:O	2.55	0.45
1:C:158:THR:O	1:C:159:CYS:CB	2.61	0.45
1:A:295:ASN:ND2	1:A:296:PRO:HD2	2.32	0.44
1:A:231:TYR:OH	2:B:110:ASP:OD2	2.25	0.44
2:B:34:MET:HE1	2:B:40:VAL:HG12	2.00	0.44
1:A:171:VAL:HB	1:A:332:GLU:HG2	2.00	0.44
2:B:94[A]:GLU:N	2:B:94[A]:GLU:CD	2.67	0.44
1:A:36:MET:HB3	1:A:36:MET:HE3	1.81	0.43
1:A:127:PHE:HD2	1:A:219:MET:HE3	1.83	0.43
1:C:227:PRO:HD2	1:C:237:HIS:CE1	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:232:LEU:HD12	2:D:81:ILE:HD11	2.00	0.43
1:C:338:LYS:HG3	1:C:339:GLU:OE2	2.18	0.43
1:C:127:PHE:HB2	1:C:219:MET:HE1	2.01	0.43
1:C:295:ASN:ND2	1:C:298:LYS:H	2.17	0.43
1:C:2:MET:HE2	1:C:2:MET:HB2	1.63	0.43
1:A:34:TYR:CE1	1:A:62:TYR:CD1	3.07	0.42
1:A:127:PHE:HB2	1:A:219:MET:HE1	2.00	0.42
1:C:144:LEU:HD22	1:C:205:LYS:CA	2.42	0.42
1:A:136:LYS:HA	1:A:302:VAL:HG11	2.00	0.42
1:C:136:LYS:HA	1:C:302:VAL:HG11	2.00	0.42
2:D:86:LEU:O	2:D:89:ILE:HG22	2.20	0.42
1:C:260:ASN:HD22	1:C:260:ASN:HA	1.68	0.42
1:C:34:TYR:CE1	1:C:62:TYR:CD1	3.07	0.42
2:B:34:MET:CE	2:B:40:VAL:CG1	2.97	0.42
2:D:40:VAL:HG21	2:D:69:TYR:O	2.20	0.42
2:B:52:HIS:CE1	2:B:83:PRO:HD3	2.55	0.42
1:C:294:PHE:C	1:C:294:PHE:CD1	2.92	0.42
1:A:206:SER:CB	4:A:2105:HOH:O	2.68	0.41
2:D:31:ARG:NH1	2:D:31:ARG:HB3	2.34	0.41
1:C:19:VAL:O	1:C:20:GLY:O	2.38	0.41
1:A:197:MET:HG2	4:A:2076:HOH:O	2.20	0.41
2:B:18:LEU:HA	2:B:33:LEU:HD23	2.03	0.41
1:C:173:ASP:OD1	1:C:173:ASP:C	2.58	0.41
1:A:127:PHE:CD2	1:A:219:MET:HE3	2.56	0.41
1:C:225:ILE:HD12	1:C:277:PHE:HZ	1.86	0.41
1:A:124:ILE:HA	1:A:219:MET:HE1	2.01	0.41
2:B:34:MET:CE	2:B:40:VAL:HG13	2.50	0.41
2:B:73:VAL:HG22	2:B:104:ALA:HB2	2.03	0.41
1:A:197:MET:HE1	1:A:231:TYR:O	2.21	0.41
2:B:52:HIS:NE2	2:B:83:PRO:HD3	2.35	0.41
2:D:18:LEU:CD1	2:D:30:VAL:HG13	2.50	0.41
1:A:65:ARG:HG2	1:A:167:GLY:O	2.21	0.40
1:C:233:ASP:O	1:C:236:ASN:HB3	2.21	0.40
1:A:186:VAL:O	1:A:192:ARG:HD3	2.22	0.40
1:A:316:ASP:HA	1:A:317:PRO:HD2	1.90	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	358/364 (98%)	338 (94%)	17 (5%)	3 (1%)	22	48
1	C	361/364 (99%)	331 (92%)	29 (8%)	1 (0%)	44	72
2	B	122/136 (90%)	116 (95%)	6 (5%)	0	100	100
2	D	120/136 (88%)	110 (92%)	10 (8%)	0	100	100
All	All	961/1000 (96%)	895 (93%)	62 (6%)	4 (0%)	38	65

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	2	MET
1	A	8	GLY
1	A	3	ALA
1	C	187	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	320/322 (99%)	295 (92%)	25 (8%)	15	33
1	C	323/322 (100%)	295 (91%)	28 (9%)	12	27
2	B	97/107 (91%)	85 (88%)	12 (12%)	5	12
2	D	95/107 (89%)	81 (85%)	14 (15%)	3	8
All	All	835/858 (97%)	756 (90%)	79 (10%)	10	22

All (79) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	26	LEU
1	A	75	ARG
1	A	77	ARG
1	A	113	LEU
1	A	144	LEU
1	A	155	LEU
1	A	157	THR
1	A	179	THR
1	A	198	LEU
1	A	200	SER
1	A	235	LEU
1	A	251[A]	ASN
1	A	251[B]	ASN
1	A	256	LEU
1	A	264	SER
1	A	265	LEU
1	A	268	LYS
1	A	295	ASN
1	A	303	GLU
1	A	312	GLU
1	A	313	GLN
1	A	324	GLU
1	A	330	ASP
1	A	331	MET
1	A	333	LEU
2	B	17	LYS
2	B	26	GLN
2	B	29	GLU
2	B	33	LEU
2	B	34	MET
2	B	44	ASP
2	B	45	GLU
2	B	64	GLU
2	B	93	LEU
2	B	94[A]	GLU
2	B	94[B]	GLU
2	B	101	LYS
1	C	0	HIS
1	C	2	MET
1	C	18	ASP
1	C	44	LEU
1	C	58	GLU

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Mol	Chain	Res	Type
1	C	60	GLN
1	C	71	LYS
1	C	72	ILE
1	C	98	ASP
1	C	113	LEU
1	C	155	LEU
1	C	179	THR
1	C	198	LEU
1	C	205	LYS
1	C	230	HIS
1	C	235	LEU
1	C	247	GLN
1	C	250	LEU
1	C	254	ILE
1	C	268	LYS
1	C	295	ASN
1	C	303	GLU
1	C	304	GLN
1	C	330	ASP
1	C	331	MET
1	C	333	LEU
1	C	351	ARG
1	C	357	ARG
2	D	26	GLN
2	D	31	ARG
2	D	39	ASP
2	D	40	VAL
2	D	43	LEU
2	D	57	LEU
2	D	60	LEU
2	D	61	GLU
2	D	63	VAL
2	D	65	VAL
2	D	68	LYS
2	D	93	LEU
2	D	121	ILE
2	D	132	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (15) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	78	HIS

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Mol	Chain	Res	Type
1	A	121	ASN
1	A	199	ASN
1	A	295	ASN
1	A	304	GLN
2	B	123	ASN
1	C	15	GLN
1	C	78	HIS
1	C	199	ASN
1	C	251	ASN
1	C	260	ASN
1	C	269	ASN
1	C	295	ASN
2	D	78	ASN
2	D	123	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

4 non-standard protein/DNA/RNA residues 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	$\# Z > 2$
1	TPO	A	183	1	9,10,11	1.00	0	10,14,16	1.32	2 (20%)
1	PTR	A	185	1	15,16,17	1.95	2 (13%)	19,22,24	1.11	2 (10%)
1	TPO	C	183	1	9,10,11	0.87	0	10,14,16	1.33	1 (10%)
1	PTR	C	185	1	15,16,17	2.01	1 (6%)	19,22,24	1.19	2 (10%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means

no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	TPO	A	183	1	-	0/8/11/13	0/0/0/0
1	PTR	A	185	1	-	0/9/11/13	0/1/1/1
1	TPO	C	183	1	-	0/8/11/13	0/0/0/0
1	PTR	C	185	1	-	0/9/11/13	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	185	PTR	OH-CZ	-6.65	1.25	1.40
1	C	185	PTR	OH-CZ	-6.40	1.25	1.40
1	A	185	PTR	CE2-CZ	2.09	1.43	1.38

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	183	TPO	OG1-P-O1P	-2.31	100.19	109.26
1	C	185	PTR	O-C-CA	-2.28	118.72	125.02
1	A	183	TPO	O-C-CA	-2.15	120.13	125.15
1	A	183	TPO	OG1-P-O1P	-2.14	100.87	109.26
1	A	185	PTR	CB-CA-N	-2.07	104.40	112.54
1	A	185	PTR	CG-CB-CA	2.29	118.91	114.29
1	C	185	PTR	CG-CB-CA	3.02	120.39	114.29

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates

There are no carbohydrates in this entry.

5.6 Ligand geometry

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	$\# Z > 2$
3	SO4	A	1359	-	4,4,4	0.41	0	6,6,6	0.61	0
3	SO4	C	1359	-	4,4,4	0.24	0	6,6,6	0.57	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	SO4	A	1359	-	-	0/0/0/0	0/0/0/0
3	SO4	C	1359	-	-	0/0/0/0	0/0/0/0

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.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1359	SO4	1	0
3	C	1359	SO4	1	0

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 ⓘ

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	357/364 (98%)	-0.18	1 (0%) 93 94	27, 46, 75, 139	0
1	C	357/364 (98%)	0.02	10 (2%) 53 54	32, 55, 88, 139	0
2	B	122/136 (89%)	-0.18	0 100 100	39, 62, 83, 97	0
2	D	122/136 (89%)	1.47	36 (29%) 1 0	66, 98, 135, 152	0
All	All	958/1000 (95%)	0.10	47 (4%) 30 29	27, 56, 112, 152	0

All (47) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	7	ALA	5.6
2	D	63	VAL	4.3
2	D	12	SER	4.1
1	C	0	HIS	3.9
2	D	60	LEU	3.9
2	D	100	LEU	3.6
2	D	55	ALA	3.6
1	A	6	ALA	3.6
2	D	132	LEU	3.4
2	D	67	LEU	3.4
1	C	6	ALA	3.3
1	C	5	ALA	3.2
2	D	48	LEU	3.2
2	D	50	PRO	3.1
1	C	263	LEU	3.0
2	D	73	VAL	2.9
2	D	96	VAL	2.9
2	D	98	VAL	2.9
2	D	81	ILE	2.9
2	D	101	LYS	2.8
2	D	94	GLU	2.8

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Mol	Chain	Res	Type	RSRZ
2	D	40	VAL	2.7
2	D	68	LYS	2.6
1	C	239	LEU	2.5
2	D	34	MET	2.5
2	D	104	ALA	2.5
2	D	52	HIS	2.5
2	D	133	GLN	2.4
1	C	262	LEU	2.4
2	D	66	LEU	2.4
2	D	131	ILE	2.4
2	D	117	PHE	2.4
2	D	51	LEU	2.4
2	D	69	TYR	2.4
2	D	35	ALA	2.3
1	C	231	TYR	2.3
2	D	14	LEU	2.3
2	D	75	ALA	2.3
1	C	235	LEU	2.3
2	D	93	LEU	2.3
2	D	61	GLU	2.3
1	C	4	ALA	2.2
2	D	65	VAL	2.1
2	D	85	HIS	2.1
2	D	82	THR	2.1
2	D	71	ALA	2.1
2	D	106	VAL	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [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
1	PTR	A	185	16/17	0.99	0.17	-	34,39,43,44	0
1	TPO	C	183	11/12	0.99	0.15	-	41,45,48,49	0
1	PTR	C	185	16/17	0.98	0.13	-	45,48,53,53	0
1	TPO	A	183	11/12	0.99	0.16	-	35,43,46,49	0

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(\AA^2)	Q<0.9
3	SO4	A	1359	5/5	0.93	0.23	-	95,96,98,99	0
3	SO4	C	1359	5/5	0.88	0.20	-	106,106,107,109	0

6.5 Other polymers [i](#)

There are no such residues in this entry.