



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 19, 2016 – 09:38 PM GMT

PDB ID : 5AVV
Title : Kinetics by X-ray crystallography: Tl⁺-substitution of bound K⁺ in the E2.MgF42-.2K⁺ crystal after 8.5 min
Authors : Ogawa, H.; Cornelius, F.; Hirata, A.; Toyoshima, C.
Deposited on : 2015-07-01
Resolution : 2.90 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 : 1.7.1 (RC1), CSD as537be (2016)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026982
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
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) : rb-20026982

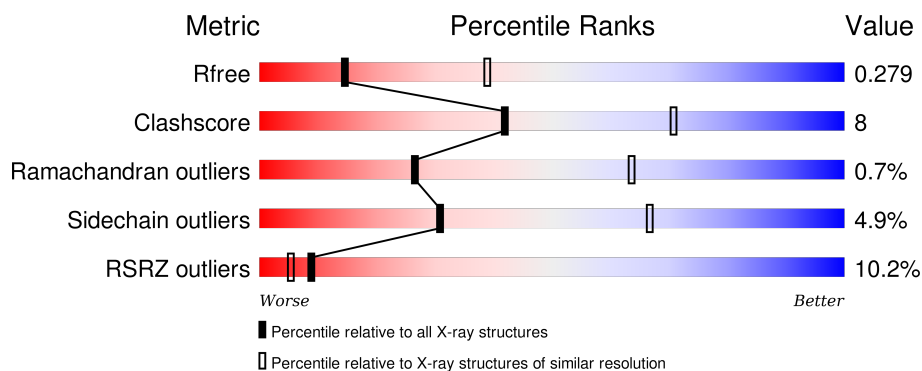
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.90 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}	91344	1451 (2.90-2.90)
Clashscore	102246	1668 (2.90-2.90)
Ramachandran outliers	100387	1630 (2.90-2.90)
Sidechain outliers	100360	1632 (2.90-2.90)
RSRZ outliers	91569	1456 (2.90-2.90)

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	1028	
2	B	305	
3	G	74	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	MF4	A	2001	-	-	-	X
5	MG	A	2002	-	-	-	X
8	CLR	B	3001	-	-	-	X

2 Entry composition [i](#)

There are 10 unique types of molecules in this entry. The entry contains 10235 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 Na, K-ATPase alpha subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	992	Total	C	N	O	S	0	0	0
			7675	4886	1290	1453	46			

- Molecule 2 is a protein called Na⁺,K⁺-ATPase beta subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	268	Total	C	N	O	S	0	0	0
			2174	1409	358	396	11			

- Molecule 3 is a protein called Phospholemman-like protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	G	39	Total	C	N	O	S	0	0	0
			305	200	50	54	1			

- Molecule 4 is TETRAFLUOROMAGNESATE(2-) (three-letter code: MF4) (formula: F₄Mg).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total F Mg 5 4 1	0	0

- Molecule 5 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total Mg 1 1	0	0

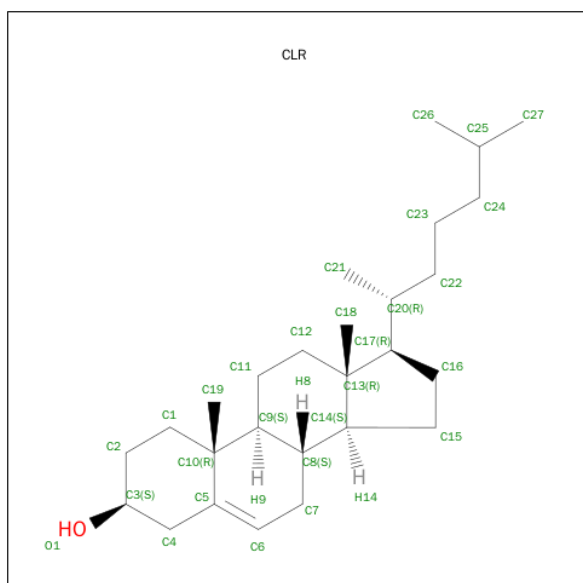
- Molecule 6 is THALLIUM (I) ION (three-letter code: TL) (formula: Tl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	3	Total Tl 3 3	0	1

- Molecule 7 is POTASSIUM ION (three-letter code: K) (formula: K).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	1	Total K 1 1	0	1

- Molecule 8 is CHOLESTEROL (three-letter code: CLR) (formula: C₂₇H₄₆O).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	B	1	Total C O 28 27 1	0	0

- Molecule 9 is N-ACETYL-D-GLUCOSAMINE (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
9	B	1	Total	C	N	O	0	0
			14	8	1	5		
9	B	1	Total	C	N	O	0	0
			14	8	1	5		
9	B	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 10 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	A	1	Total	O	0	0
			1	1		

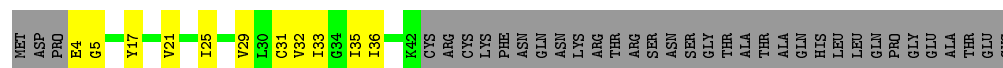
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according 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.

- Chain A: 74% 21% 7%

Sequence Logo for Chain A (Amino Acid Conservation):

Position	Amino Acid	Conservation Score
1	Met	0.05
2	Gly	0.05
3	Lys	0.05
4	Gly	0.05
5	Thr	0.05
6	Ala	0.05
7	Ser	0.05
8	Asp	0.05
9	Lys	0.05
10	Tyr	0.05
11	Glu	0.05
12	Pro	0.05
13	Ala	0.05
14	Ala	0.05
15	Thr	0.05
16	Ser	0.05
17	Glu	0.05
18	Asn	0.05
19	Ala	0.05
20	Lys	0.05
21	Ser	0.05
22	Lys	0.05
23	Lys	0.05
24	Gly	0.05
25	Lys	0.05
26	Lys	0.05
27	Asp	0.05
28	Lys	0.05
29	Ile	0.05
30	Asp	0.05
31	Lys	0.05
32	Lys	0.05
33	Arg	0.05
34	Asp	0.05
35	Lys	0.05
36	D33	0.05
37	E34	0.05
38	L35	0.05
39	K36	0.05
40	M41	0.05
41	D42	0.05
42	D43	0.05
43	H44	0.05
44	L48	0.05
45	L51	0.05
46	H52	0.05
47	T57	0.05
48	S58	0.05
49	L59	0.05
50	T60	0.05
51	R61	0.05
52	G62	0.05
53	L63	0.05
54	T64	0.05
55	K177	0.05
56	H181	0.05
57	A182	0.05
58	E183	0.05
59	D189	0.05
60	V191	0.05
61	I199	0.05
62	P200	0.05
63	A201	0.05
64	R204	0.05
65	I205	0.05
66	I206	0.05
67	H209	0.05
68	K212	0.05
69	V213	0.05
70	I106	0.05
71	L110	0.05
72	A114	0.05
73	Y115	0.05
74	G116	0.05
75	I117	0.05
76	A120	0.05
77	T121	0.05
78	E122	0.05
79	D123	0.05
80	E124	0.05
81	P125	0.05
82	A126	0.05
83	N127	0.05
84	D128	0.05
85	Y131	0.05
86	L132	0.05
87	Y149	0.05
88	I157	0.05
89	M158	0.05
90	S160	0.05
91	F161	0.05
92	M164	0.05
93	V165	0.05
94	L170	0.05
95	V171	0.05
96	R172	0.05
97	I173	0.05
98	D174	0.05
99	T188	0.05
100	F291	0.05
101	I294	0.05
102	V300	0.05
103	F301	0.05
104	L302	0.05
105	G303	0.05
106	V304	0.05
107	S305	0.05
108	L309	0.05
109	I312	0.05
110	V317	0.05
111	F323	0.05
112	L324	0.05
113	I327	0.05
114	I328	0.05
115	L336	0.05
116	T339	0.05
117	V342	0.05
118	C343	0.05
119	L344	0.05
120	T345	0.05
121	I242	0.05
122	K351	0.05
123	K354	0.05
124	S246	0.05
125	T247	0.05
126	N248	0.05
127	K360	0.05
128	C249	0.05
129	L361	0.05
130	E251	0.05
131	C352	0.05
132	A363	0.05
133	T253	0.05
134	A254	0.05

- Chain B: 



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	220.99Å 50.84Å 163.36Å 90.00° 104.02° 90.00°	Depositor
Resolution (Å)	14.99 – 2.90 47.41 – 2.90	Depositor EDS
% Data completeness (in resolution range)	72.4 (14.99-2.90) 87.9 (47.41-2.90)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.94 (at 2.91Å)	Xtriage
Refinement program	CNS 1.2	Depositor
R, R_{free}	0.279 , 0.293 0.281 , 0.279	Depositor DCC
R_{free} test set	1842 reflections (5.59%)	DCC
Wilson B-factor (Å ²)	68.6	Xtriage
Anisotropy	0.420	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 52.7	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Outliers	0 of 36329 reflections	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	10235	wwPDB-VP
Average B, all atoms (Å ²)	99.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.12% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: MG, NAG, K, TL, MF4, CLR

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	0.38	0/7825	0.51	0/10616
2	B	0.36	0/2229	0.49	0/3002
3	G	0.36	0/309	0.46	0/419
All	All	0.38	0/10363	0.51	0/14037

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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	7675	0	7699	124	0
2	B	2174	0	2146	46	0
3	G	305	0	318	7	0
4	A	5	0	0	0	0
5	A	1	0	0	0	0
6	A	3	0	0	0	0
7	A	1	0	0	0	0
8	B	28	0	46	1	0
9	B	42	0	38	0	0
10	A	1	0	0	0	0
All	All	10235	0	10247	172	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 (172) 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:B:74:ALA:HB3	2:B:75:PRO:HD3	1.47	0.94
1:A:478:VAL:HG21	1:A:571:PHE:HB2	1.64	0.79
1:A:905:GLN:NE2	2:B:182:ASN:HA	2.00	0.77
1:A:497:LYS:HE2	1:A:499:SER:HB2	1.68	0.75
1:A:868:SER:O	1:A:872:ILE:HG12	1.86	0.75
1:A:61:ARG:HH11	1:A:61:ARG:HB3	1.52	0.73
1:A:261:THR:HG22	1:A:264:ARG:NH2	2.02	0.73
1:A:51:LEU:HD13	1:A:204:ARG:HG3	1.69	0.71
2:B:270:GLN:HG2	2:B:271:ASN:HD22	1.58	0.68
1:A:766:ARG:HD2	1:A:832:MET:CE	2.24	0.68
1:A:339:THR:HG23	1:A:820:ILE:HD13	1.77	0.66
2:B:213:LEU:HD11	2:B:278:CYS:HB3	1.78	0.65
1:A:935:ILE:HG23	1:A:944:ILE:HD12	1.77	0.65
1:A:78:ASN:HA	1:A:261:THR:HG23	1.79	0.64
2:B:74:ALA:CB	2:B:75:PRO:HD3	2.23	0.63
1:A:160:SER:HB3	1:A:741:VAL:HG22	1.80	0.63
1:A:816:MET:O	1:A:820:ILE:HG12	1.97	0.63
1:A:52:HIS:HA	1:A:57:THR:HG23	1.80	0.63
2:B:28:ARG:HB2	2:B:32:SER:HB3	1.81	0.63
1:A:673:LEU:HD22	1:A:677:VAL:HG11	1.80	0.62
2:B:193:LYS:HA	2:B:207:ASN:HD21	1.65	0.62
1:A:905:GLN:HE21	2:B:182:ASN:HA	1.62	0.61
1:A:323:PHE:O	1:A:327:ILE:HG12	2.01	0.61
1:A:64:THR:HG22	1:A:66:ALA:H	1.65	0.61
3:G:29:VAL:O	3:G:33:ILE:HG12	2.00	0.61
1:A:483:ASN:HB2	1:A:486:ASN:HB2	1.82	0.60
2:B:270:GLN:HG2	2:B:271:ASN:ND2	2.16	0.60
1:A:363:ALA:HB1	1:A:730:ILE:HD12	1.83	0.60
2:B:31:SER:O	2:B:35:LYS:HG3	2.01	0.60
1:A:344:LEU:HB3	1:A:361:LEU:HG	1.85	0.59
1:A:392:TRP:HB3	1:A:588:LEU:HB2	1.84	0.59
2:B:84:ALA:HB1	2:B:88:GLU:H	1.67	0.59
3:G:21:VAL:O	3:G:25:ILE:HG12	2.02	0.59
1:A:106:ILE:O	1:A:110:LEU:HB2	2.03	0.59
1:A:212:LYS:HB2	1:A:251:GLU:HG2	1.85	0.59
2:B:106:MET:O	2:B:110:MET:HG2	2.03	0.58
1:A:345:THR:HA	1:A:361:LEU:HD11	1.84	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:75:PRO:HG2	2:B:294:ARG:HH21	1.68	0.57
2:B:74:ALA:HB3	2:B:75:PRO:CD	2.29	0.57
2:B:193:LYS:HA	2:B:207:ASN:ND2	2.20	0.57
1:A:491:SER:HB3	1:A:493:HIS:NE2	2.20	0.57
2:B:137:ARG:HD2	2:B:147:LYS:HB3	1.87	0.56
2:B:52:ILE:O	2:B:56:GLN:HG2	2.05	0.56
1:A:818:PRO:HB3	1:A:934:LEU:HD22	1.87	0.56
1:A:172:ILE:HD13	1:A:177:LYS:HB3	1.87	0.56
1:A:933:ASP:HA	1:A:936:ILE:HG12	1.86	0.56
1:A:190:LEU:HD11	1:A:206:ILE:HD11	1.88	0.55
2:B:93:ILE:H	2:B:305:SER:HB2	1.72	0.55
1:A:157:ILE:HD11	1:A:745:ALA:HA	1.88	0.55
1:A:994:TYR:O	1:A:997:ILE:HG22	2.06	0.55
1:A:351:MET:HA	1:A:354:LYS:HG2	1.88	0.55
1:A:596:ARG:HB2	1:A:599:VAL:HG23	1.89	0.55
1:A:261:THR:HG22	1:A:264:ARG:HH21	1.71	0.54
1:A:924:ILE:HD12	1:A:983:LEU:HD12	1.89	0.54
1:A:64:THR:HG22	1:A:66:ALA:N	2.23	0.54
1:A:994:TYR:HA	1:A:997:ILE:HG22	1.89	0.54
1:A:921:SER:HA	1:A:983:LEU:HD11	1.90	0.54
1:A:51:LEU:CD1	1:A:204:ARG:HG3	2.36	0.53
1:A:424:ILE:HG23	1:A:506:VAL:HB	1.90	0.53
2:B:213:LEU:HD23	2:B:261:LEU:HD13	1.89	0.53
1:A:161:PHE:HA	1:A:164:MET:HE3	1.90	0.53
1:A:324:LEU:O	1:A:328:ILE:HG12	2.09	0.52
1:A:161:PHE:HA	1:A:164:MET:CE	2.39	0.52
1:A:808:LEU:O	1:A:812:LEU:HB2	2.10	0.52
2:B:75:PRO:HG2	2:B:294:ARG:NH2	2.25	0.52
1:A:766:ARG:HD2	1:A:832:MET:HE2	1.91	0.52
1:A:212:LYS:HD3	1:A:224:PRO:HB2	1.90	0.52
3:G:32:VAL:O	3:G:36:ILE:HG12	2.09	0.52
1:A:82:PRO:HA	1:A:158:MET:HG2	1.92	0.51
3:G:25:ILE:O	3:G:29:VAL:HG23	2.11	0.51
1:A:572:ASP:HB3	1:A:577:ASN:HB2	1.92	0.51
1:A:788:THR:N	1:A:789:PRO:HD2	2.26	0.51
1:A:417:THR:HA	1:A:522:LEU:HD22	1.93	0.51
2:B:288:SER:HB2	2:B:294:ARG:HH11	1.76	0.50
1:A:571:PHE:HA	1:A:577:ASN:HD22	1.76	0.50
2:B:28:ARG:NH1	8:B:3001:CLR:H22	2.27	0.50
1:A:359:LYS:HE2	1:A:746:ALA:O	2.12	0.49
2:B:232:PHE:HB2	2:B:262:ALA:HB3	1.93	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:826:GLN:HE22	1:A:950:LYS:HE3	1.78	0.49
1:A:1005:ARG:NH1	1:A:1006:ARG:HG3	2.28	0.49
2:B:209:TYR:HA	2:B:242:LEU:HD22	1.95	0.48
1:A:1016:TRP:HE1	2:B:35:LYS:HE3	1.79	0.48
1:A:502:ARG:CG	1:A:503:TYR:H	2.27	0.48
1:A:442:ILE:O	1:A:445:ARG:HG2	2.14	0.48
1:A:323:PHE:CE1	1:A:793:PHE:HE2	2.32	0.47
1:A:171:VAL:HG12	1:A:191:VAL:HG22	1.97	0.47
1:A:797:ASN:HD22	1:A:887:ARG:HD3	1.79	0.47
1:A:814:THR:HB	1:A:961:GLU:HG3	1.96	0.47
1:A:132:LEU:HD21	1:A:804:THR:HG21	1.97	0.47
2:B:87:THR:HB	2:B:298:GLU:O	2.14	0.47
3:G:31:CYS:O	3:G:35:ILE:HG12	2.14	0.47
2:B:215:CYS:HA	2:B:278:CYS:HA	1.96	0.47
2:B:80:HIS:HB3	2:B:297:PHE:CZ	2.50	0.46
1:A:127:ASN:HB3	1:A:131:TYR:CD1	2.50	0.46
1:A:336:LEU:HD11	1:A:776:ILE:HG12	1.96	0.46
2:B:226:ILE:HG22	2:B:269:THR:HB	1.96	0.46
1:A:924:ILE:HD12	1:A:983:LEU:CD1	2.45	0.46
2:B:122:SER:HA	2:B:123:PRO:HA	1.75	0.46
1:A:631:VAL:HG23	1:A:633:ILE:HG12	1.96	0.46
1:A:63:LEU:HD22	1:A:189:ASP:HB3	1.96	0.46
1:A:303:GLY:HA2	1:A:327:ILE:HG21	1.97	0.46
1:A:670:LEU:HD23	1:A:678:LEU:HD21	1.96	0.46
1:A:784:ILE:HD11	1:A:854:TYR:CG	2.51	0.46
1:A:475:PRO:HD2	1:A:494:GLU:HB2	1.98	0.45
1:A:209:HIS:HB3	1:A:253:THR:HG22	1.98	0.45
1:A:889:ARG:HD2	1:A:895:ILE:CD1	2.46	0.45
2:B:84:ALA:HB1	2:B:88:GLU:N	2.32	0.45
1:A:847:GLU:H	1:A:847:GLU:CD	2.20	0.45
1:A:676:GLU:H	1:A:676:GLU:CD	2.20	0.45
1:A:631:VAL:CG2	1:A:633:ILE:HG12	2.46	0.45
1:A:722:SER:OG	1:A:723:PRO:HD3	2.17	0.45
1:A:52:HIS:HE2	1:A:59:LEU:HD12	1.82	0.45
1:A:806:THR:HG22	1:A:923:PHE:HB2	1.99	0.44
1:A:915:GLU:O	1:A:918:CYS:HB2	2.17	0.44
2:B:194:ASN:N	2:B:194:ASN:HD22	2.15	0.44
2:B:234:LEU:HG	2:B:241:PRO:HG3	1.99	0.44
2:B:107:HIS:O	2:B:111:ASP:HB2	2.18	0.44
1:A:246:SER:OG	1:A:267:MET:HG3	2.18	0.44
1:A:354:LYS:HB2	1:A:354:LYS:HZ2	1.81	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:107:HIS:ND1	2:B:170:TYR:HE1	2.17	0.43
1:A:273:LEU:O	1:A:277:LEU:HG	2.19	0.43
1:A:110:LEU:HD22	1:A:324:LEU:HD12	1.99	0.43
1:A:790:PHE:O	1:A:794:ILE:HG12	2.19	0.43
1:A:87:PRO:HD2	1:A:90:ILE:HD12	1.99	0.43
2:B:147:LYS:HB2	2:B:253:GLN:HG3	1.99	0.43
3:G:4:GLU:CD	3:G:5:GLY:H	2.23	0.43
1:A:661:LYS:HA	1:A:661:LYS:HE2	2.00	0.43
1:A:511:PRO:HG2	1:A:542:TYR:CE1	2.53	0.43
1:A:64:THR:HA	1:A:174:ASP:OD1	2.19	0.42
1:A:300:VAL:O	1:A:304:VAL:HG22	2.19	0.42
2:B:74:ALA:CB	2:B:75:PRO:CD	2.92	0.42
1:A:797:ASN:HB3	1:A:885:GLY:HA2	2.01	0.42
2:B:188:TYR:O	2:B:284:ASN:ND2	2.53	0.42
1:A:170:LEU:HD21	1:A:177:LYS:HD3	2.00	0.42
1:A:291:PHE:HA	1:A:294:ILE:HD12	2.01	0.42
1:A:940:ARG:HE	1:A:1023:TYR:HB2	1.84	0.42
2:B:95:ASN:HA	2:B:96:PRO:HD3	1.86	0.42
2:B:223:ARG:HH11	2:B:223:ARG:HB2	1.85	0.42
2:B:89:ILE:HG22	2:B:102:PHE:CE2	2.55	0.42
1:A:291:PHE:HB3	1:A:845:VAL:HB	2.02	0.42
2:B:194:ASN:HB3	2:B:205:ASN:OD1	2.20	0.42
1:A:367:LEU:HD23	1:A:761:GLY:HA3	2.01	0.42
2:B:137:ARG:HB3	2:B:147:LYS:HD2	2.01	0.42
1:A:784:ILE:N	1:A:785:PRO:HD2	2.35	0.42
1:A:378:THR:HA	1:A:382:THR:OG1	2.20	0.42
1:A:110:LEU:CD2	1:A:324:LEU:HD12	2.50	0.41
1:A:48:LEU:HD23	1:A:59:LEU:HD11	2.01	0.41
1:A:502:ARG:HE	1:A:562:GLU:HG2	1.85	0.41
1:A:785:PRO:HB2	1:A:926:ILE:CD1	2.50	0.41
2:B:271:ASN:HD21	2:B:305:SER:N	2.19	0.41
1:A:859:MET:HG2	2:B:44:TYR:CE2	2.55	0.41
1:A:920:THR:HG21	1:A:981:TYR:O	2.20	0.41
1:A:846:ASN:ND2	1:A:848:ARG:HB2	2.35	0.41
1:A:44:HIS:HB3	1:A:242:ILE:HD11	2.02	0.41
1:A:647:ARG:HH21	1:A:648:LEU:HD11	1.86	0.41
1:A:426:ALA:O	1:A:471:ARG:HD2	2.20	0.41
3:G:17:TYR:O	3:G:21:VAL:HG23	2.21	0.41
1:A:540:ASN:N	1:A:540:ASN:HD22	2.18	0.41
1:A:894:TRP:CH2	2:B:86:LYS:HG2	2.55	0.41
1:A:342:VAL:HB	1:A:820:ILE:HD12	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:502:ARG:HG3	1:A:562:GLU:HG2	2.02	0.41
1:A:423:ARG:O	1:A:427:LEU:HB2	2.21	0.41
1:A:301:PHE:O	1:A:305:SER:HB2	2.20	0.41
1:A:458:LYS:O	1:A:462:LEU:HB2	2.21	0.41
1:A:284:ILE:O	1:A:288:ILE:HG12	2.21	0.41
1:A:702:VAL:HG13	1:A:712:VAL:HG21	2.03	0.41
1:A:925:SER:O	1:A:929:VAL:HG22	2.21	0.40
1:A:831:ILE:O	1:A:834:ARG:HG2	2.22	0.40
1:A:354:LYS:HE2	1:A:760:THR:HB	2.02	0.40
1:A:989:PHE:HA	1:A:992:PHE:CD2	2.56	0.40
1:A:900:ASP:OD1	1:A:904:GLN:HB2	2.21	0.40
1:A:199:ILE:HG22	1:A:201:ALA:O	2.22	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	990/1028 (96%)	942 (95%)	43 (4%)	5 (0%)	34	71
2	B	262/305 (86%)	223 (85%)	35 (13%)	4 (2%)	13	42
3	G	37/74 (50%)	33 (89%)	4 (11%)	0	100	100
All	All	1289/1407 (92%)	1198 (93%)	82 (6%)	9 (1%)	26	63

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	121	THR
1	A	128	ASP
1	A	576	PRO
2	B	74	ALA
2	B	171	ALA

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Mol	Chain	Res	Type
2	B	201	GLU
1	A	123	ASP
1	A	1014	GLY
2	B	199	PRO

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	840/869 (97%)	796 (95%)	44 (5%)	29	64
2	B	234/266 (88%)	224 (96%)	10 (4%)	35	71
3	G	32/62 (52%)	32 (100%)	0	100	100
All	All	1106/1197 (92%)	1052 (95%)	54 (5%)	31	67

All (54) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	51	LEU
1	A	57	THR
1	A	61	ARG
1	A	63	LEU
1	A	72	LEU
1	A	128	ASP
1	A	165	VAL
1	A	213	VAL
1	A	217	SER
1	A	218	LEU
1	A	226	THR
1	A	231	PHE
1	A	245	PHE
1	A	248	ASN
1	A	250	VAL
1	A	255	ARG
1	A	261	THR
1	A	284	ILE

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Mol	Chain	Res	Type
1	A	309	LEU
1	A	344	LEU
1	A	354	LYS
1	A	391	MET
1	A	413	LYS
1	A	434	GLN
1	A	454	SER
1	A	457	LEU
1	A	524	ASN
1	A	540	ASN
1	A	557	HIS
1	A	581	THR
1	A	636	GLU
1	A	670	LEU
1	A	682	LEU
1	A	712	VAL
1	A	719	VAL
1	A	726	LYS
1	A	806	THR
1	A	811	ASP
1	A	833	LYS
1	A	847	GLU
1	A	880	PRO
1	A	974	THR
1	A	987	TRP
1	A	1019	GLN
2	B	28	ARG
2	B	73	VAL
2	B	107	HIS
2	B	139	ASP
2	B	193	LYS
2	B	194	ASN
2	B	200	GLU
2	B	223	ARG
2	B	251	ARG
2	B	289	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (21) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	118	GLN
1	A	129	ASN

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Mol	Chain	Res	Type
1	A	163	ASN
1	A	225	GLN
1	A	290	HIS
1	A	434	GLN
1	A	524	ASN
1	A	540	ASN
1	A	557	HIS
1	A	577	ASN
1	A	754	ASN
1	A	797	ASN
1	A	826	GLN
1	A	905	GLN
1	A	1019	GLN
2	B	80	HIS
2	B	194	ASN
2	B	207	ASN
2	B	264	GLN
2	B	271	ASN
2	B	284	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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](#)

Of 10 ligands modelled in this entry, 5 are monoatomic - leaving 5 for Mogul analysis.

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	$\# Z > 2$
4	MF4	A	2001	1	0,4,4	0.00	-	0,6,6	0.00	-
8	CLR	B	3001	-	31,31,31	0.43	0	48,48,48	1.05	4 (8%)
9	NAG	B	4001	9,2	14,14,15	0.50	0	15,19,21	0.93	1 (6%)
9	NAG	B	4002	9	14,14,15	0.64	0	15,19,21	1.44	1 (6%)
9	NAG	B	4021	2	14,14,15	0.59	0	15,19,21	1.07	1 (6%)

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
4	MF4	A	2001	1	-	0/0/0/0	0/0/0/0
8	CLR	B	3001	-	-	0/10/68/68	0/4/4/4
9	NAG	B	4001	9,2	-	0/6/23/26	0/1/1/1
9	NAG	B	4002	9	-	0/6/23/26	0/1/1/1
9	NAG	B	4021	2	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	B	3001	CLR	C4-C5-C6	-2.18	117.00	120.60
8	B	3001	CLR	C4-C5-C10	2.25	119.67	116.41
9	B	4021	NAG	C1-O5-C5	2.40	115.67	112.14
9	B	4001	NAG	C1-O5-C5	2.46	115.75	112.14
8	B	3001	CLR	C1-C2-C3	2.52	113.77	110.41
8	B	3001	CLR	C15-C14-C13	3.02	107.37	103.83
9	B	4002	NAG	C2-N2-C7	4.20	128.57	123.11

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
8	B	3001	CLR	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	992/1028 (96%)	0.61	74 (7%) 17 11	64, 85, 126, 151	0
2	B	268/305 (87%)	1.03	58 (21%) 1 0	84, 135, 159, 169	0
3	G	39/74 (52%)	0.36	0 100 100	81, 89, 133, 136	0
All	All	1299/1407 (92%)	0.69	132 (10%) 9 5	64, 91, 147, 169	0

All (132) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	534	MET	6.3
2	B	93	ILE	6.2
2	B	123	PRO	6.0
1	A	562	GLU	5.5
1	A	317	TRP	5.4
1	A	894	TRP	5.4
2	B	214	ARG	5.2
1	A	573	ALA	4.9
1	A	42	ASP	4.8
1	A	41	MET	4.8
1	A	585	PHE	4.8
1	A	579	PRO	4.6
1	A	567	GLU	4.6
1	A	498	SER	4.5
1	A	79	SER	4.3
2	B	121	ASN	4.2
1	A	260	TYR	4.1
1	A	504	LEU	4.0
2	B	194	ASN	4.0
1	A	32	LEU	4.0
2	B	195	THR	3.8
1	A	521	ILE	3.6
1	A	502	ARG	3.5

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Mol	Chain	Res	Type	RSRZ
1	A	82	PRO	3.4
1	A	675	THR	3.4
2	B	268	LEU	3.4
1	A	571	PHE	3.4
1	A	515	LEU	3.4
1	A	121	THR	3.4
1	A	411	PHE	3.3
2	B	269	THR	3.3
1	A	89	TRP	3.3
2	B	96	PRO	3.3
2	B	99	TYR	3.3
1	A	563	ASP	3.3
1	A	499	SER	3.3
2	B	122	SER	3.2
2	B	255	LYS	3.2
2	B	274	LEU	3.2
1	A	578	PHE	3.2
2	B	85	ILE	3.2
1	A	57	THR	3.1
2	B	205	ASN	3.1
2	B	140	LEU	3.1
2	B	104	LYS	3.1
2	B	231	TYR	3.0
1	A	117	ILE	3.0
2	B	216	ALA	2.9
1	A	149	TYR	2.9
2	B	298	GLU	2.9
1	A	496	GLU	2.9
1	A	72	LEU	2.8
1	A	122	GLU	2.8
2	B	207	ASN	2.8
1	A	84	PRO	2.8
1	A	125	PRO	2.8
1	A	815	ASP	2.8
1	A	183	GLU	2.8
2	B	210	VAL	2.8
1	A	482	PHE	2.8
2	B	270	GLN	2.8
1	A	87	PRO	2.7
1	A	126	ALA	2.7
1	A	533	ASP	2.7
1	A	503	TYR	2.6

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Mol	Chain	Res	Type	RSRZ
1	A	114	ALA	2.6
1	A	35	LEU	2.6
1	A	80	LEU	2.6
2	B	202	LEU	2.6
2	B	124	PHE	2.6
1	A	36	LYS	2.6
2	B	203	GLN	2.6
2	B	304	LYS	2.6
2	B	97	LYS	2.5
1	A	492	ILE	2.5
1	A	536	GLU	2.5
1	A	414	THR	2.5
2	B	172	GLU	2.5
2	B	237	TYR	2.5
2	B	25	PHE	2.5
1	A	557	HIS	2.5
1	A	804	THR	2.5
2	B	234	LEU	2.5
2	B	272	MET	2.4
1	A	814	THR	2.4
2	B	303	VAL	2.4
2	B	120	GLY	2.4
1	A	90	ILE	2.4
1	A	97	PHE	2.4
1	A	120	ALA	2.4
1	A	86	THR	2.4
2	B	212	PRO	2.4
1	A	33	ASP	2.3
2	B	89	ILE	2.3
2	B	211	LEU	2.3
2	B	197	ASP	2.3
2	B	179	ALA	2.3
1	A	116	GLY	2.3
1	A	127	ASN	2.3
1	A	529	PRO	2.3
2	B	204	ALA	2.3
2	B	100	GLU	2.3
2	B	158	LYS	2.3
2	B	276	ILE	2.2
2	B	175	PRO	2.2
1	A	427	LEU	2.2
1	A	654	GLN	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	439	ASN	2.2
2	B	265	PHE	2.2
1	A	514	ILE	2.1
2	B	147	LYS	2.1
2	B	230	GLU	2.1
2	B	271	ASN	2.1
1	A	518	CYS	2.1
2	B	305	SER	2.1
1	A	558	PHE	2.1
2	B	296	ARG	2.1
1	A	779	THR	2.1
1	A	470	MET	2.1
1	A	443	LEU	2.1
1	A	530	LEU	2.1
2	B	155	MET	2.1
1	A	826	GLN	2.0
1	A	312	ILE	2.0
2	B	215	CYS	2.0
1	A	181	ASN	2.0
2	B	142	ASP	2.0
2	B	273	GLU	2.0
1	A	566	ASN	2.0
2	B	92	SER	2.0
2	B	87	THR	2.0
2	B	240	PHE	2.0

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

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

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
5	MG	A	2002	1/1	0.93	0.38	4.23	66,66,66,66	0
4	MF4	A	2001	5/5	0.94	0.31	2.52	69,70,71,72	0
8	CLR	B	3001	28/28	0.83	0.32	2.39	127,127,128,128	0
6	TL	A	2006[B]	1/1	0.98	0.03	-4.12	82,82,82,82	1
7	K	A	2005[A]	1/1	0.98	0.03	-4.12	82,82,82,82	1
6	TL	A	2003	1/1	0.92	0.05	-4.15	86,86,86,86	0
6	TL	A	2004	1/1	0.98	0.09	-4.69	86,86,86,86	0
9	NAG	B	4001	14/15	0.79	0.24	-	142,144,145,147	0
9	NAG	B	4021	14/15	0.67	0.51	-	148,148,149,149	0
9	NAG	B	4002	14/15	0.55	0.42	-	148,149,149,150	0

6.5 Other polymers

There are no such residues in this entry.