



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 19, 2016 – 09:39 PM GMT

PDB ID : 5AW4
Title : Kinetics by X-ray crystallography: Rb⁺-substitution of bound K⁺ in the E2.MgF42-.2K⁺ crystal after 1.5 min
Authors : Ogawa, H.; Cornelius, F.; Hirata, A.; Toyoshima, C.
Deposited on : 2015-07-01
Resolution : 2.80 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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

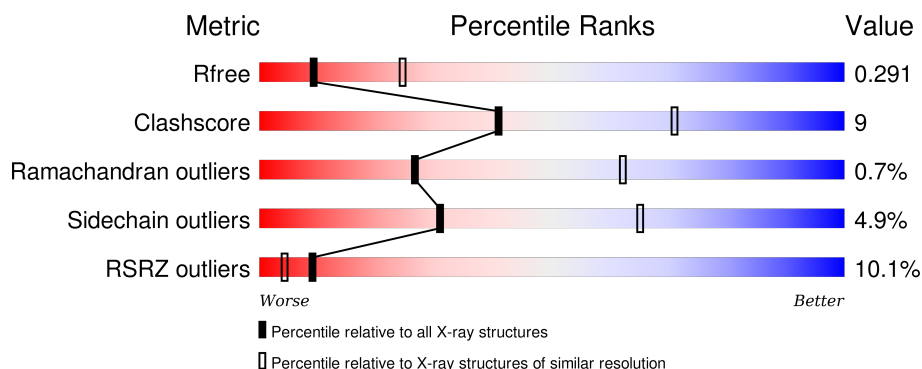
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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	2393 (2.80-2.80)
Clashscore	102246	2827 (2.80-2.80)
Ramachandran outliers	100387	2782 (2.80-2.80)
Sidechain outliers	100360	2784 (2.80-2.80)
RSRZ outliers	91569	2404 (2.80-2.80)

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	<div> <div>7%</div> <div>74%</div> <div>21%</div> <div>• •</div> </div>
2	B	305	<div> <div>18%</div> <div>67%</div> <div>19%</div> <div>• 12%</div> </div>
3	G	74	<div> <div>%</div> <div>36%</div> <div>16%</div> <div>47%</div> </div>

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

2 Entry composition [i](#)

There are 10 unique types of molecules in this entry. The entry contains 10237 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	0	0
			5	4	1		

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

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

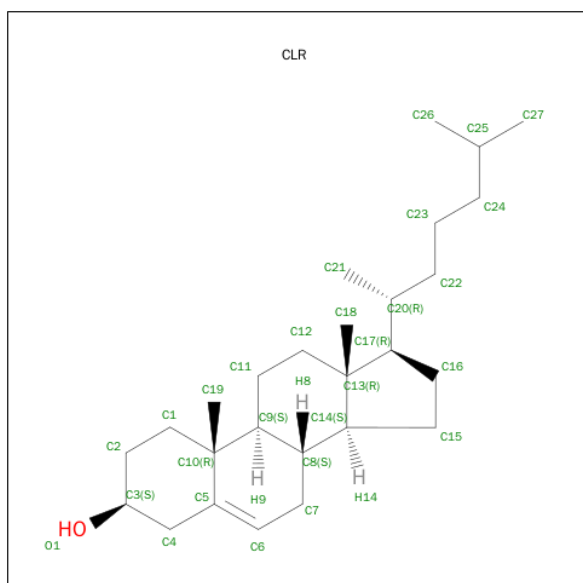
- Molecule 6 is POTASSIUM ION (three-letter code: K) (formula: K).

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	3	Total	K		0	3
			3	3			

- Molecule 7 is RUBIDIUM ION (three-letter code: RB) (formula: Rb).

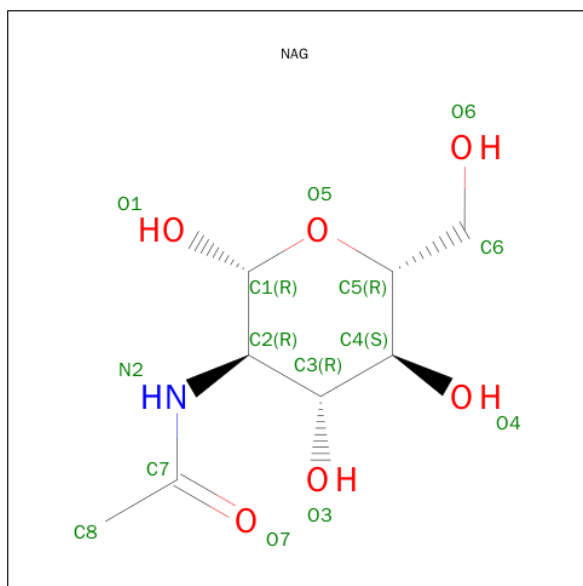
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	A	3	Total	Rb		0	3
			3	3			

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



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

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

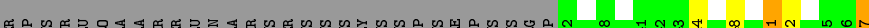


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
9	B	1	Total	C	N	O	0	0
			14	8	1	5		
9	B	1	Total	C	N	O	0	0
			14	8	1	5		
9	B	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 10 is water.

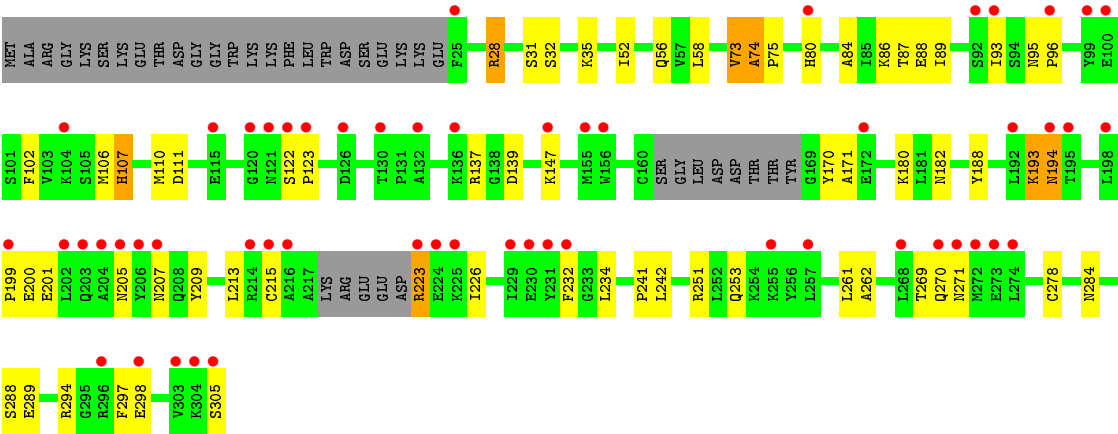
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	A	1	Total	O	0	0
			1	1		

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.

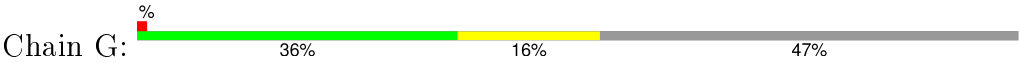
- Chain A: 

Chain A	Chain B	Chain C	Chain D	Chain E	Chain F	Chain G	Chain H	Chain I	Chain J	Chain K	Chain L	Chain M	Chain N	Chain O	Chain P	Chain Q	Chain R	Chain S	Chain T	Chain U	Chain V	Chain W	Chain X	Chain Y	Chain Z																																																																																																																																																																																																																																																																																																																																																																																																													
R940	I820	E676	P529	A426	V300	M65	D189	A66	L72	M78	P200	P82	P83	P84	T85	T86	E88	W89	I90	R94	I106	L110	L113	A114	L117	T121	D122	N248	A126	M127	D128	Y131	L132	E38	R41	D42	H44	L48	L51	H52	Y55	G56	T57	P58	L59	T60	R61	G62	L63	T64																																																																																																																																																																																																																																																																																																																																																																																				
I944	Q826	L678	K531	L427	L302	A66	V191	L72	M78	P200	A201	R204	I205	I206	H209	K212	V213	S217	L218	P224	Q225	T226	F231	I242	F245	S246	N248	C249	V250	E251	G252	T253	A254	L255	Y260	T261	R264	M267	L273	L277	I284	I288	F291	I294	E298	L300	L302	G303	V304	S305	L308	L309	T312	L313	W317	F323	L324	I327	L328	L336	T339	V342	C343	L344	T345	M351	K354	K359	M360	L361	E362	A363	L367	S368	S499	E500	G379	S501	T380	L381	T382	M391	K392	F411	D412	K413	T417	R423	L424	L425	A426	L427	G430	Q434	L442	R445	A441	Y442	H457	K458	L462	C463	C464	N470	R471	P475	D572	A573	E479	L480	P481	F482	N483	N486	L490	S491	L492	H493	E494	K497	S496	Y599	E500	S501	R502	G503	L503	L504	V506	P511	L515	L521	L522	L523	S524	T525	L526	L527	L528	L529	L530	L531	L532	L533	L534	L535	L536	L537	L538	L539	L540	L541	L542	L543	L544	L545	L546	L547	L548	L549	L550	L551	L552	L553	L554	L555	L556	L557	L558	L559	L560	L561	L562	L563	L564	L565	L566	L567	L568	L569	L570	L571	L572	L573	L574	L575	L576	L577	L578	L579	L580	L581	L582	L583	L584	L585	L586	L587	L588	L589	L590	L591	L592	L593	L594	L595	L596	L597	L598	L599	L600	L601	L602	L603	L604	L605	L606	L607	L608	L609	L610	L611	L612	L613	L614	L615	L616	L617	L618	L619	L620	L621	L622	L623	L624	L625	L626	L627	L628	L629	L630	L631	L632	L633	L634	L635	L636	L637	L638	L639	L640	L641	L642	L643	L644	L645	L646	L647	L648	L649	L650	L651	L652	L653	L654	L655	L656	L657	L658	L659	L660	L661	L662	L663	L664	L665	L666	L667	L668	L669	L670	L671	L672	L673	L674	L675	L676	L677	L678	L679	L680	L681	L682	L683	L684	L685	L686	L687	L688	L689	L690	L691	L692	L693	L694	L695	L696	L697	L698	L699	L700	L701	L702	L703	L704	L705	L706	L707	L708	L709	L710	L711	L712	L713	L714	L715	L716	L717	L718	L719	L720	L721	L722	L723	L724	L725	L726	L727	L728	L729	L730	L731	L732	L733	L734	L735	L736	L737	L738	L739	L740	L741	L742	L743	L744	L745	L746	L747	L748	L749	L750	L751	L752	L753	L754	L755	L756	L757	L758	L759	L760	L761	L762	L763	L764	L765	L766	L767	L768	L769	L770	L771	L772	L773	L774	L775	L776	L777	L778	L779	L780	L781	L782	L783	L784	L785	L786	L787	L788	L789	L790	L791	L792	L793	L794	L795	L796	L797	L798	L799	L800	L801	L802	L803	L804	L805	L806	L807	L808	L809	L810	L811

- Chain B: 



● Molecule 3: Phospholemman-like protein



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	219.82Å 50.59Å 162.53Å 90.00° 104.42° 90.00°	Depositor
Resolution (Å)	14.96 – 2.80 40.69 – 2.70	Depositor EDS
% Data completeness (in resolution range)	68.2 (14.96-2.80) 83.5 (40.69-2.70)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.47 (at 2.68Å)	Xtriage
Refinement program	CNS 1.2	Depositor
R, R_{free}	0.286 , 0.275 0.288 , 0.291	Depositor DCC
R_{free} test set	1901 reflections (5.40%)	DCC
Wilson B-factor (Å ²)	58.6	Xtriage
Anisotropy	0.198	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 41.6	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 42379 reflections	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	10237	wwPDB-VP
Average B, all atoms (Å ²)	100.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.65% 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, MF4, RB, 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	130	1
2	B	2174	0	2146	49	0
3	G	305	0	318	9	0
4	A	5	0	0	0	0
5	A	1	0	0	0	0
6	A	3	0	0	0	0
7	A	3	0	0	0	0
8	B	28	0	46	0	0
9	B	42	0	38	0	0
10	A	1	0	0	0	0
All	All	10237	0	10247	177	1

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 9.

The worst 5 of 177 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:497:LYS:HE2	1:A:499:SER:HB2	1.69	0.75
1:A:868:SER:O	1:A:872:ILE:HG12	1.86	0.75
1:A:61:ARG:HB3	1:A:61:ARG:HH11	1.52	0.73

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:430:ARG:NH2	1:A:648:LEU:O[1_565]	2.04	0.16

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	69
2	B	262/305 (86%)	223 (85%)	35 (13%)	4 (2%)	13	40
3	G	37/74 (50%)	33 (89%)	4 (11%)	0	100	100
All	All	1289/1407 (92%)	1198 (93%)	82 (6%)	9 (1%)	26	62

5 of 9 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	121	THR
1	A	128	ASP
1	A	576	PRO

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Mol	Chain	Res	Type
2	B	74	ALA
2	B	171	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	840/869 (97%)	796 (95%)	44 (5%)	29	62
2	B	234/266 (88%)	224 (96%)	10 (4%)	35	70
3	G	32/62 (52%)	32 (100%)	0	100	100
All	All	1106/1197 (92%)	1052 (95%)	54 (5%)	31	65

5 of 54 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	454	SER
1	A	636	GLU
2	B	194	ASN
1	A	457	LEU
1	A	540	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 21 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	577	ASN
1	A	797	ASN
2	B	207	ASN
1	A	557	HIS
2	B	264	GLN

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 carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 12 ligands modelled in this entry, 7 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	0.44	0	48,48,48	1.05	5 (10%)
9	NAG	B	4001	9,2	14,14,15	0.49	0	15,19,21	0.94	1 (6%)
9	NAG	B	4002	9	14,14,15	0.62	0	15,19,21	1.44	1 (6%)
9	NAG	B	4021	2	14,14,15	0.58	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.

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
8	B	3001	CLR	C4-C5-C6	-2.15	117.05	120.60
8	B	3001	CLR	C12-C11-C9	2.03	116.78	113.09
8	B	3001	CLR	C4-C5-C10	2.22	119.63	116.41
9	B	4021	NAG	C1-O5-C5	2.44	115.73	112.14
8	B	3001	CLR	C1-C2-C3	2.49	113.73	110.41

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	992/1028 (96%)	0.54	75 (7%) 17 9	64, 86, 127, 152	0
2	B	268/305 (87%)	1.14	55 (20%) 1 1	85, 136, 160, 170	0
3	G	39/74 (52%)	0.17	1 (2%) 59 47	81, 90, 133, 137	0
All	All	1299/1407 (92%)	0.65	131 (10%) 9 4	64, 91, 148, 170	0

The worst 5 of 131 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	214	ARG	7.2
2	B	123	PRO	6.5
1	A	894	TRP	5.9
1	A	579	PRO	5.2
1	A	568	GLY	5.0

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

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

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

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
4	MF4	A	2001	5/5	0.92	0.36	2.65	69,71,72,73	0
5	MG	A	2002	1/1	0.78	0.37	2.60	66,66,66,66	0
8	CLR	B	3001	28/28	0.83	0.28	1.72	128,128,128,129	0
6	K	A	2007[A]	1/1	0.95	0.11	-2.52	82,82,82,82	1
7	RB	A	2008[B]	1/1	0.95	0.11	-2.52	82,82,82,82	1
6	K	A	2003[A]	1/1	0.97	0.12	-4.93	87,87,87,87	1
7	RB	A	2004[B]	1/1	0.97	0.12	-4.93	87,87,87,87	1
6	K	A	2005[A]	1/1	0.99	0.18	-5.42	87,87,87,87	1
7	RB	A	2006[B]	1/1	0.99	0.18	-5.42	87,87,87,87	1
9	NAG	B	4002	14/15	0.50	0.38	-	149,149,150,150	0
9	NAG	B	4001	14/15	0.82	0.24	-	142,145,146,147	0
9	NAG	B	4021	14/15	0.69	0.43	-	148,149,149,149	0

6.5 Other polymers

There are no such residues in this entry.