wwPDB X-ray Structure Validation Summary Report (i)

Feb 1, 2016 – 02:02 AM GMT

PDB ID	:	2FAH
Title	:	The structure of mitochondrial PEPCK, Complex with Mn and GDP
Authors	:	Holyoak, T.; Sullivan, S.M.; Nowak, T.
Deposited on	:	2005-12-07
Resolution	:	2.09 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 (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

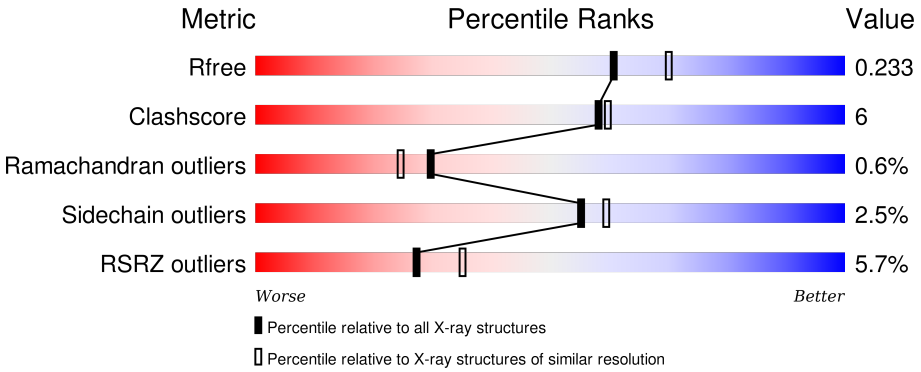
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	trunk26865

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.09 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	3939 (2.10-2.10)
Clashscore	102246	4460 (2.10-2.10)
Ramachandran outliers	100387	4413 (2.10-2.10)
Sidechain outliers	100360	4414 (2.10-2.10)
RSRZ outliers	91569	3948 (2.10-2.10)

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 <=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	608	4% 87% 12%
1	B	608	8% 85% 13%
1	C	608	6% 87% 13%
1	D	608	5% 88% 11%

2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 20770 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 Phosphoenolpyruvate carboxykinase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	608	Total	C	N	O	S	0	11	0
			4804	3048	865	858	33			
1	B	608	Total	C	N	O	S	0	13	0
			4786	3039	855	859	33			
1	C	608	Total	C	N	O	S	0	6	0
			4762	3021	857	851	33			
1	D	608	Total	C	N	O	S	0	5	0
			4749	3017	848	851	33			

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	129	GLY	-	INSERTION	UNP P21642
A	131	PRO	SER	SEE REMARK 999	UNP P21642
A	233	PRO	ARG	SEE REMARK 999	UNP P21642
A	268	ARG	ALA	SEE REMARK 999	UNP P21642
A	339	GLU	ARG	SEE REMARK 999	UNP P21642
A	502	ARG	SER	SEE REMARK 999	UNP P21642
B	129	GLY	-	INSERTION	UNP P21642
B	131	PRO	SER	SEE REMARK 999	UNP P21642
B	233	PRO	ARG	SEE REMARK 999	UNP P21642
B	268	ARG	ALA	SEE REMARK 999	UNP P21642
B	339	GLU	ARG	SEE REMARK 999	UNP P21642
B	502	ARG	SER	SEE REMARK 999	UNP P21642
C	129	GLY	-	INSERTION	UNP P21642
C	131	PRO	SER	SEE REMARK 999	UNP P21642
C	233	PRO	ARG	SEE REMARK 999	UNP P21642
C	268	ARG	ALA	SEE REMARK 999	UNP P21642
C	339	GLU	ARG	SEE REMARK 999	UNP P21642
C	502	ARG	SER	SEE REMARK 999	UNP P21642
D	129	GLY	-	INSERTION	UNP P21642
D	131	PRO	SER	SEE REMARK 999	UNP P21642
D	233	PRO	ARG	SEE REMARK 999	UNP P21642

Continued on next page...

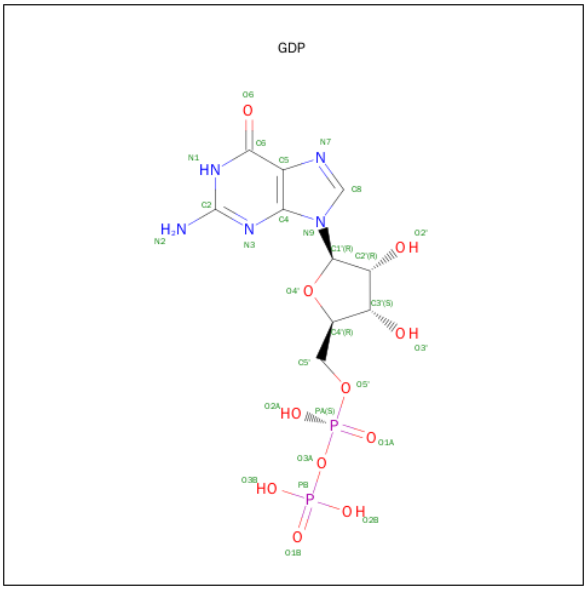
Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
D	268	ARG	ALA	SEE REMARK 999	UNP P21642
D	339	GLU	ARG	SEE REMARK 999	UNP P21642
D	502	ARG	SER	SEE REMARK 999	UNP P21642

- Molecule 2 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	B	2	Total Mn 2 2	0	0
2	A	2	Total Mn 2 2	0	0
2	D	2	Total Mn 2 2	0	0
2	C	2	Total Mn 2 2	0	0

- Molecule 3 is GUANOSINE-5'-DIPHOSPHATE (three-letter code: GDP) (formula: $C_{10}H_{15}N_5O_{11}P_2$).



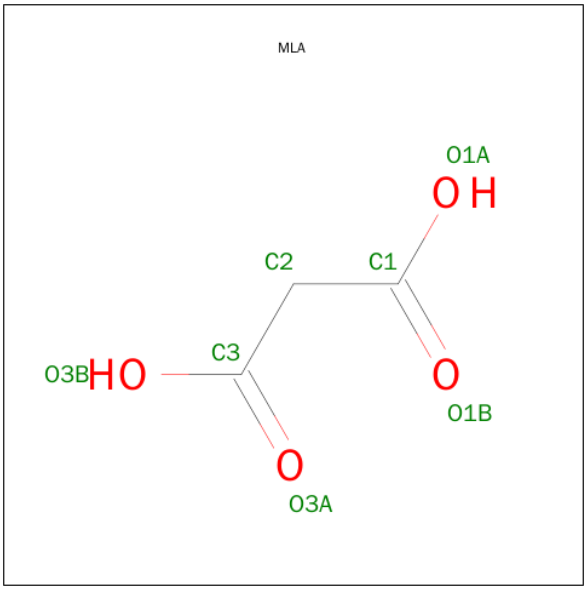
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C N O P 28 10 5 11 2	0	0
3	B	1	Total C N O P 28 10 5 11 2	0	0
3	C	1	Total C N O P 28 10 5 11 2	0	0

Continued on next page...

Continued from previous page...

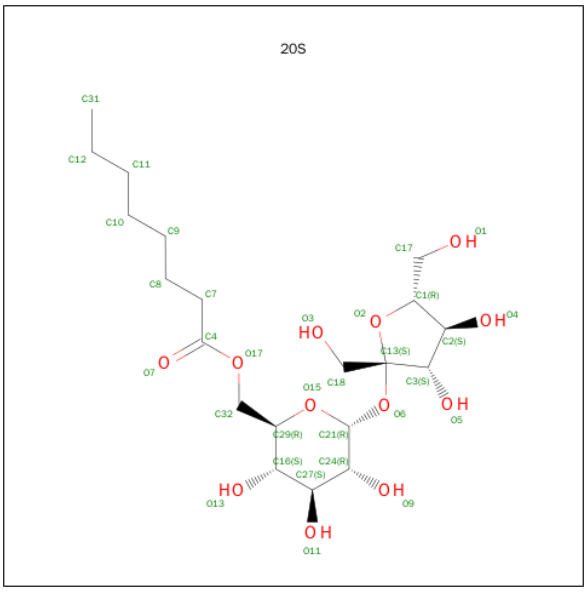
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	D	1	Total	C	N	O	P	0	0
			28	10	5	11	2		

- Molecule 4 is MALONIC ACID (three-letter code: MLA) (formula: $C_3H_4O_4$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	O		0	0
			7	3	4			
4	B	1	Total	C	O		0	0
			7	3	4			
4	C	1	Total	C	O		0	0
			7	3	4			
4	D	1	Total	C	O		0	0
			7	3	4			
4	B	1	Total	C	O		0	0
			7	3	4			

- Molecule 5 is BETA-D-FRUCTOFURANOSYL 6-O-OCTANOYL-ALPHA-D-GLUCOPYRANOSIDE (three-letter code: 20S) (formula: $C_{20}H_{36}O_{12}$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	D	1	Total C O 32 20 12	0	0
5	C	1	Total C O 32 20 12	0	0

- Molecule 6 is water.

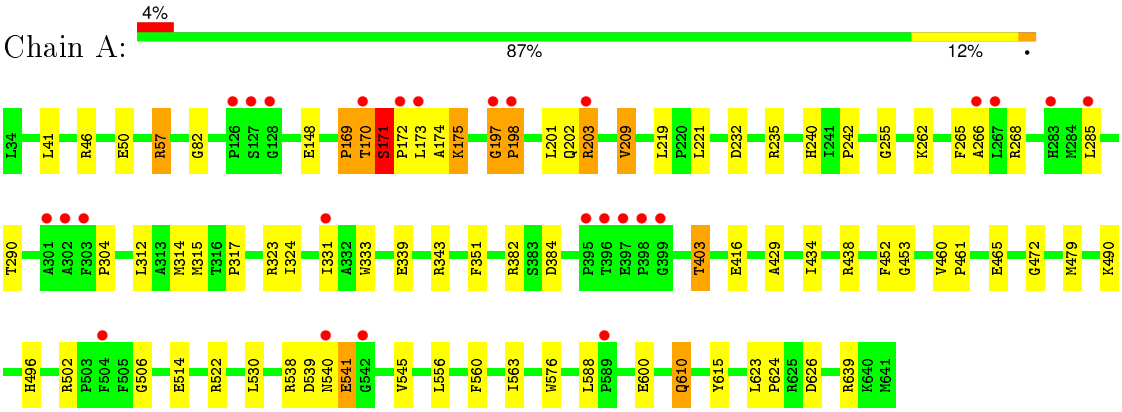
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	384	Total O 384 384	0	0
6	B	305	Total O 305 305	0	0
6	C	417	Total O 417 417	0	0
6	D	344	Total O 344 344	0	0

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 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.

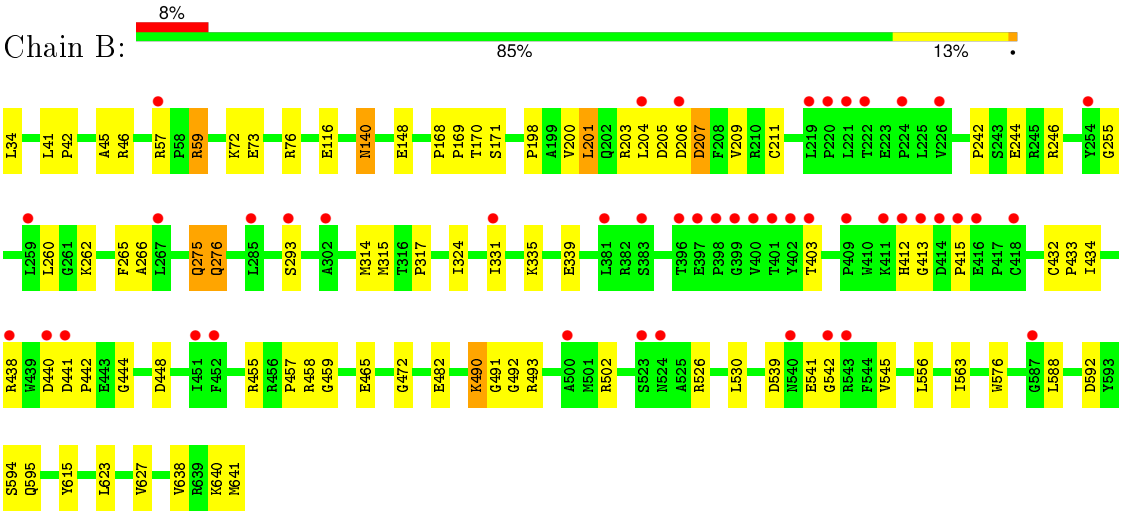
- Molecule 1: Phosphoenolpyruvate carboxykinase

Chain A:



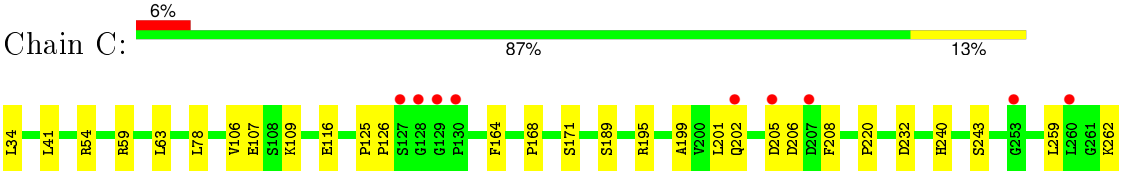
- Molecule 1: Phosphoenolpyruvate carboxykinase

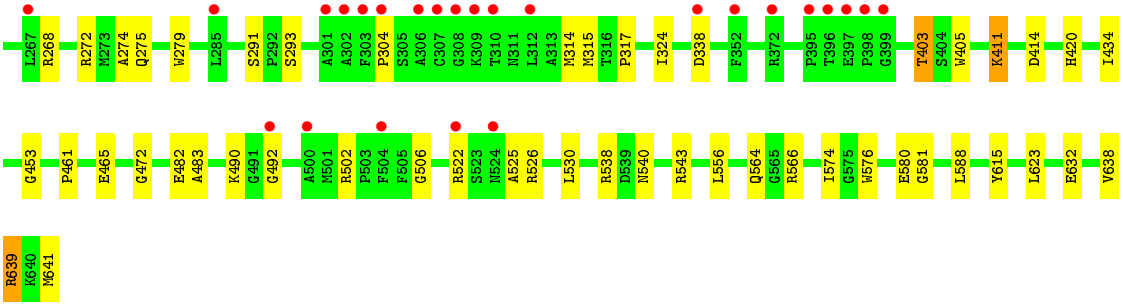
Chain B:



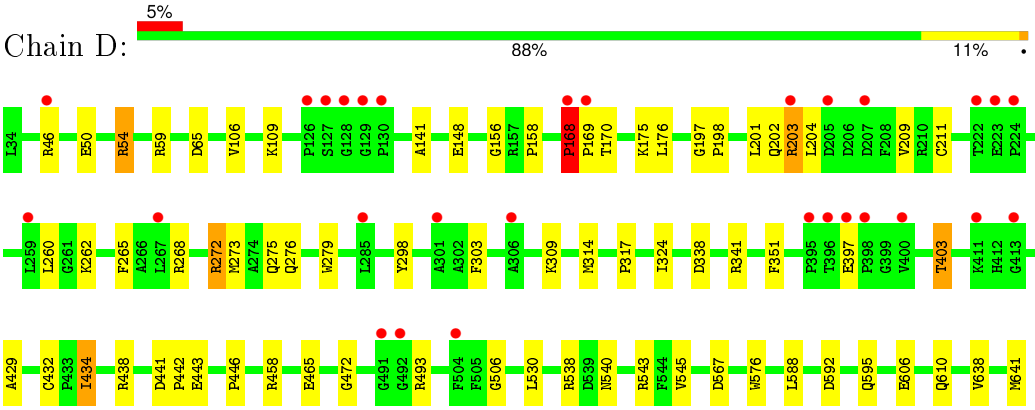
- Molecule 1: Phosphoenolpyruvate carboxykinase

Chain C:





- Molecule 1: Phosphoenolpyruvate carboxykinase



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α, β, γ	74.59Å 90.85Å 103.34Å 64.23° 73.74° 71.18°	Depositor
Resolution (Å)	32.81 – 2.09 32.80 – 2.09	Depositor EDS
% Data completeness (in resolution range)	94.7 (32.81-2.09) 84.1 (32.80-2.09)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.29 (at 2.10Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.187 , 0.234 0.187 , 0.233	Depositor DCC
R_{free} test set	6402 reflections (5.29%)	DCC
Wilson B-factor (Å^2)	24.8	Xtriage
Anisotropy	0.218	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.37 , 42.7	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.34$	Xtriage
Outliers	0 of 127383 reflections	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	20770	wwPDB-VP
Average B, all atoms (Å^2)	16.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 16.66% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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: GDP, 20S, MLA, MN

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	0.52	0/4975	0.64	0/6766
1	B	0.49	0/4969	0.62	1/6761 (0.0%)
1	C	0.52	0/4923	0.63	1/6697 (0.0%)
1	D	0.50	0/4905	0.61	1/6677 (0.0%)
All	All	0.51	0/19772	0.62	3/26901 (0.0%)

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

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	502	ARG	NE-CZ-NH2	-5.86	117.37	120.30
1	C	639	ARG	NE-CZ-NH2	-5.70	117.45	120.30
1	D	168	PRO	C-N-CD	-5.58	108.33	120.60

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	169	PRO	Peptide
1	A	170	THR	Peptide

5.2 Too-close contacts (i)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4804	0	4708	63	0
1	B	4786	0	4688	61	0
1	C	4762	0	4663	48	0
1	D	4749	0	4629	54	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
2	C	2	0	0	0	0
2	D	2	0	0	0	0
3	A	28	0	12	0	0
3	B	28	0	12	0	0
3	C	28	0	12	0	0
3	D	28	0	12	1	0
4	A	7	0	2	0	0
4	B	14	0	4	1	0
4	C	7	0	2	1	0
4	D	7	0	2	0	0
5	C	32	0	30	1	0
5	D	32	0	30	2	0
6	A	384	0	0	9	0
6	B	305	0	0	9	0
6	C	417	0	0	13	0
6	D	344	0	0	10	0
All	All	20770	0	18806	224	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 6.

The worst 5 of 224 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:197:GLY:H	1:A:198:PRO:HD3	1.06	1.06
1:D:209:VAL:HG21	1:D:265:PHE:CE2	1.93	1.02
1:D:170:THR:HG22	6:D:6251:HOH:O	1.60	1.01
1:B:209:VAL:HG21	1:B:265:PHE:CE2	2.00	0.96
1:A:197:GLY:H	1:A:198:PRO:CD	1.81	0.93

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	617/608 (102%)	597 (97%)	14 (2%)	6 (1%)	19	13
1	B	619/608 (102%)	596 (96%)	19 (3%)	4 (1%)	30	24
1	C	612/608 (101%)	597 (98%)	14 (2%)	1 (0%)	52	53
1	D	611/608 (100%)	591 (97%)	17 (3%)	3 (0%)	34	30
All	All	2459/2432 (101%)	2381 (97%)	64 (3%)	14 (1%)	30	24

5 of 14 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	170	THR
1	B	207	ASP
1	D	168	PRO
1	A	255	GLY
1	B	255	GLY

5.3.2 Protein sidechains (i)

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	509/499 (102%)	493 (97%)	16 (3%)	47	50
1	B	509/499 (102%)	489 (96%)	20 (4%)	39	39
1	C	503/499 (101%)	495 (98%)	8 (2%)	70	76

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	D	500/499 (100%)	488 (98%)	12 (2%)	57 61
All	All	2021/1996 (101%)	1965 (97%)	56 (3%)	55 55

5 of 56 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	203	ARG
1	B	403	THR
1	D	403	THR
1	B	205	ASP
1	B	276[A]	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 23 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	311	ASN
1	C	135	ASN
1	D	311	ASN
1	B	524	ASN
1	C	202	GLN

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 19 ligands modelled in this entry, 8 are monoatomic - leaving 11 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	$\#\|Z\| > 2$
3	GDP	A	2000	2	23,30,30	1.18	3 (13%)	30,47,47	2.04	7 (23%)
4	MLA	A	2001	2	0,6,6	0.00	-	0,7,7	0.00	-
3	GDP	B	3000	2	23,30,30	1.07	2 (8%)	30,47,47	1.85	8 (26%)
4	MLA	B	3001	2	0,6,6	0.00	-	0,7,7	0.00	-
4	MLA	B	6001	-	0,6,6	0.00	-	0,7,7	0.00	-
3	GDP	C	4000	2	23,30,30	1.26	3 (13%)	30,47,47	1.87	9 (30%)
4	MLA	C	4003	2	0,6,6	0.00	-	0,7,7	0.00	-
5	20S	C	6003	-	33,33,33	1.35	3 (9%)	46,46,46	2.05	4 (8%)
3	GDP	D	5000	2	23,30,30	1.44	3 (13%)	30,47,47	2.04	8 (26%)
4	MLA	D	5001	2	0,6,6	0.00	-	0,7,7	0.00	-
5	20S	D	6002	-	33,33,33	1.33	3 (9%)	46,46,46	2.04	3 (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
3	GDP	A	2000	2	-	0/12/32/32	0/3/3/3
4	MLA	A	2001	2	-	0/0/4/4	0/0/0/0
3	GDP	B	3000	2	-	0/12/32/32	0/3/3/3
4	MLA	B	3001	2	-	0/0/4/4	0/0/0/0
4	MLA	B	6001	-	-	0/0/4/4	0/0/0/0
3	GDP	C	4000	2	-	0/12/32/32	0/3/3/3
4	MLA	C	4003	2	-	0/0/4/4	0/0/0/0
5	20S	C	6003	-	-	0/22/61/61	0/2/2/2
3	GDP	D	5000	2	-	0/12/32/32	0/3/3/3
4	MLA	D	5001	2	-	0/0/4/4	0/0/0/0
5	20S	D	6002	-	-	0/22/61/61	0/2/2/2

The worst 5 of 17 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	C	6003	20S	C11-C10	-5.54	1.19	1.51
5	D	6002	20S	C11-C10	-5.31	1.20	1.51

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	C	6003	20S	C12-C11	-3.21	1.27	1.51
5	D	6002	20S	C12-C11	-3.18	1.27	1.51
3	C	4000	GDP	O4'-C1'	2.19	1.44	1.41

The worst 5 of 39 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	A	2000	GDP	C6-C5-C4	-4.52	115.50	120.90
3	D	5000	GDP	C5-C6-N1	-4.50	117.43	123.59
3	A	2000	GDP	N3-C2-N1	-4.37	120.79	127.44
3	C	4000	GDP	C6-C5-C4	-4.21	115.87	120.90
3	B	3000	GDP	C5-C6-N1	-3.73	118.49	123.59

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	6001	MLA	1	0
4	C	4003	MLA	1	0
5	C	6003	20S	1	0
3	D	5000	GDP	1	0
5	D	6002	20S	2	0

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, 95^{th} 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	608/608 (100%)	0.28	26 (4%) 39 48	9, 15, 19, 25	0
1	B	608/608 (100%)	0.39	46 (7%) 17 23	11, 15, 19, 26	0
1	C	608/608 (100%)	0.33	34 (5%) 28 36	12, 15, 19, 25	0
1	D	608/608 (100%)	0.29	33 (5%) 29 38	11, 15, 19, 24	0
All	All	2432/2432 (100%)	0.32	139 (5%) 27 35	9, 15, 19, 26	0

The worst 5 of 139 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	398	PRO	6.8
1	B	400	VAL	6.8
1	C	396	THR	5.8
1	A	396	THR	5.3
1	C	130	PRO	5.1

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, 95^{th} 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
2	MN	A	2003	1/1	0.97	0.21	1.53	21,21,21,21	1
2	MN	D	5003	1/1	0.97	0.21	0.34	14,14,14,14	1
4	MLA	B	6001	7/7	0.91	0.16	0.19	30,32,34,36	0
4	MLA	A	2001	7/7	0.86	0.18	0.01	34,36,38,38	0
3	GDP	D	5000	28/28	0.96	0.09	-1.10	16,18,23,24	0
5	20S	C	6003	32/32	0.95	0.09	-1.14	8,12,18,18	0
4	MLA	D	5001	7/7	0.94	0.15	-1.19	27,30,32,32	0
4	MLA	B	3001	7/7	0.91	0.15	-1.20	27,27,29,29	0
3	GDP	C	4000	28/28	0.97	0.08	-1.40	9,11,13,14	0
5	20S	D	6002	32/32	0.95	0.08	-1.64	11,15,19,20	0
3	GDP	A	2000	28/28	0.98	0.07	-1.90	9,11,14,15	0
3	GDP	B	3000	28/28	0.97	0.07	-2.25	15,18,18,19	0
4	MLA	C	4003	7/7	0.95	0.13	-2.40	21,21,26,30	0
2	MN	C	4001	1/1	1.00	0.03	-2.80	9,9,9,9	0
2	MN	B	3002	1/1	0.98	0.05	-4.83	28,28,28,28	1
2	MN	D	5002	1/1	0.95	0.07	-5.73	38,38,38,38	1
2	MN	C	4002	1/1	0.95	0.19	-	9,9,9,9	1
2	MN	B	3003	1/1	0.96	0.16	-	23,23,23,23	1
2	MN	A	2002	1/1	0.99	0.04	-	15,15,15,15	1

6.5 Other polymers (i)

There are no such residues in this entry.