



wwPDB X-ray Structure Validation Summary Report

Mar 1, 2014 – 12:32 AM GMT

PDB ID : 3KRO
Title : Mint heterotetrameric geranyl pyrophosphate synthase in complex with magnesium, IPP, and DMASPP (II)
Authors : Chang, T.-H.; Hsieh, F.-L.; Ko, T.-P.; Wang, A.H.-J.
Deposited on : 2009-11-19
Resolution : 1.95 Å(reported)

This is a wwPDB 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/ValidationPDFNotes.html>

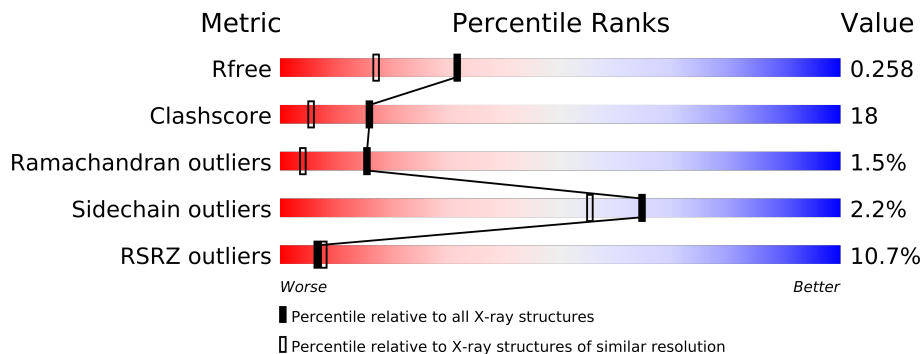
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.15 2013
Xtriage (Phenix)	:	dev-1323
EDS	:	stable22639
Percentile statistics	:	21963
Refmac	:	5.8.0049
CCP4	:	6.3.0 (Settle)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP)	:	stable22683

1 Overall quality at a glance

The reported resolution of this entry is 1.95 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}	66092	1321 (1.96-1.96)
Clashscore	79885	1488 (1.96-1.96)
Ramachandran outliers	78287	1475 (1.96-1.96)
Sidechain outliers	78261	1475 (1.96-1.96)
RSRZ outliers	66119	1321 (1.96-1.96)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	295	
1	D	295	
2	B	274	
2	C	274	

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 9441 atoms, of which 0 are hydrogen and 0 are deuterium.

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 Geranyl diphosphate synthase large subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	279	Total	C	N	O	S	0	0	0
			2120	1338	372	392	18			
1	D	295	Total	C	N	O	S	0	0	0
			2232	1406	391	417	18			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	EXPRESSION TAG	UNP Q9SBR3
D	1	MET	-	EXPRESSION TAG	UNP Q9SBR3

- Molecule 2 is a protein called Geranyl diphosphate synthase small subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	259	Total	C	N	O	S	0	0	0
			1954	1233	339	368	14			
2	C	259	Total	C	N	O	S	0	0	0
			1954	1233	339	368	14			

There are 18 discrepancies between the modelled and reference sequences:

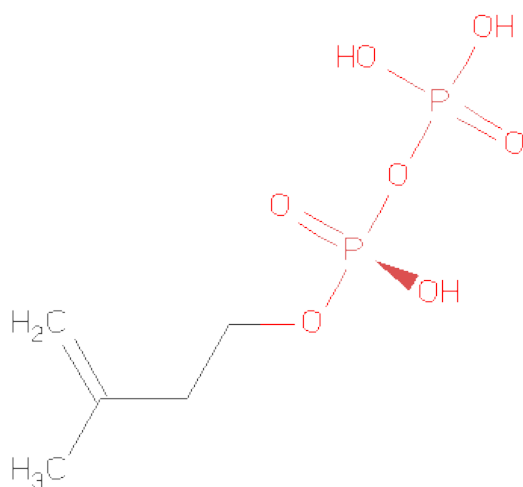
Chain	Residue	Modelled	Actual	Comment	Reference
B	1	MET	-	EXPRESSION TAG	UNP Q9SBR4
B	267	HIS	-	EXPRESSION TAG	UNP Q9SBR4
B	268	HIS	-	EXPRESSION TAG	UNP Q9SBR4
B	269	HIS	-	EXPRESSION TAG	UNP Q9SBR4
B	270	HIS	-	EXPRESSION TAG	UNP Q9SBR4
B	271	HIS	-	EXPRESSION TAG	UNP Q9SBR4
B	272	HIS	-	EXPRESSION TAG	UNP Q9SBR4
B	273	HIS	-	EXPRESSION TAG	UNP Q9SBR4
B	274	HIS	-	EXPRESSION TAG	UNP Q9SBR4
C	1	MET	-	EXPRESSION TAG	UNP Q9SBR4

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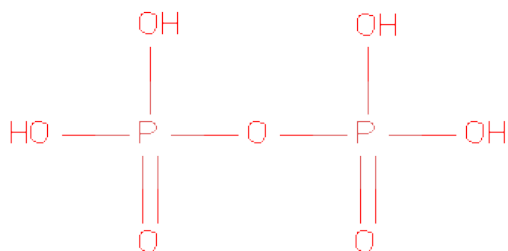
Chain	Residue	Modelled	Actual	Comment	Reference
C	267	HIS	-	EXPRESSION TAG	UNP Q9SBR4
C	268	HIS	-	EXPRESSION TAG	UNP Q9SBR4
C	269	HIS	-	EXPRESSION TAG	UNP Q9SBR4
C	270	HIS	-	EXPRESSION TAG	UNP Q9SBR4
C	271	HIS	-	EXPRESSION TAG	UNP Q9SBR4
C	272	HIS	-	EXPRESSION TAG	UNP Q9SBR4
C	273	HIS	-	EXPRESSION TAG	UNP Q9SBR4
C	274	HIS	-	EXPRESSION TAG	UNP Q9SBR4

- Molecule 3 is 3-METHYLBUT-3-ENYL TRIHYDROGEN DIPHOSPHATE (three-letter code: IPE) (formula: $C_5H_{12}O_7P_2$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	O	P	0	0
			14	5	7	2		
3	D	1	Total	C	O	P	0	0
			14	5	7	2		

- Molecule 4 is PYROPHOSPHATE (three-letter code: PPV) (formula: $H_4O_7P_2$).

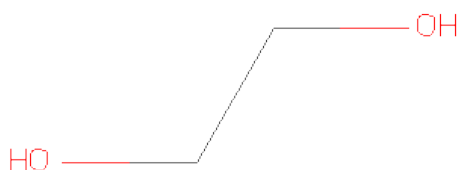


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	O	P	0	0
			9	7	2		

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

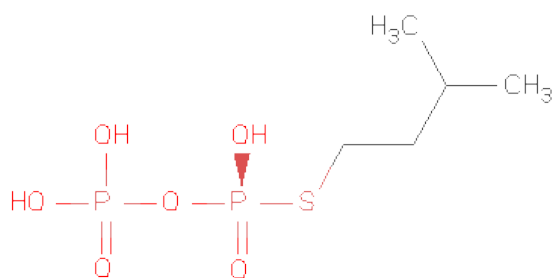
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	2	Total	Mg	0	0
			2	2		
5	D	2	Total	Mg	0	0
			2	2		

- Molecule 6 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C₂H₆O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	C	1	Total	C	O	0	0
			4	2	2		

- Molecule 7 is DIMETHYLALLYL S-THIOLODIPHOSPHATE (three-letter code: DST) (formula: $C_5H_{14}O_6P_2S$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
7	D	1	Total	C	O	P	S	0	0
			14	5	6	2	1		

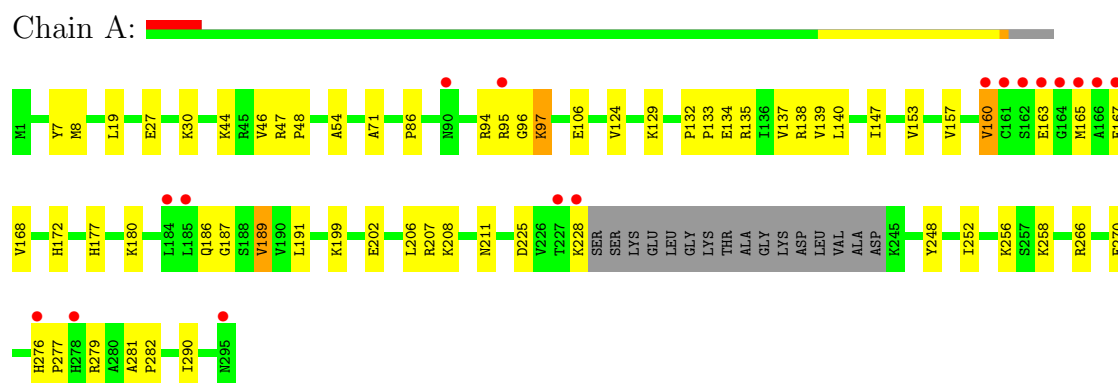
- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	268	Total	O	0	0
			268	268		
8	B	243	Total	O	0	0
			243	243		
8	C	294	Total	O	0	0
			294	294		
8	D	317	Total	O	0	0
			317	317		

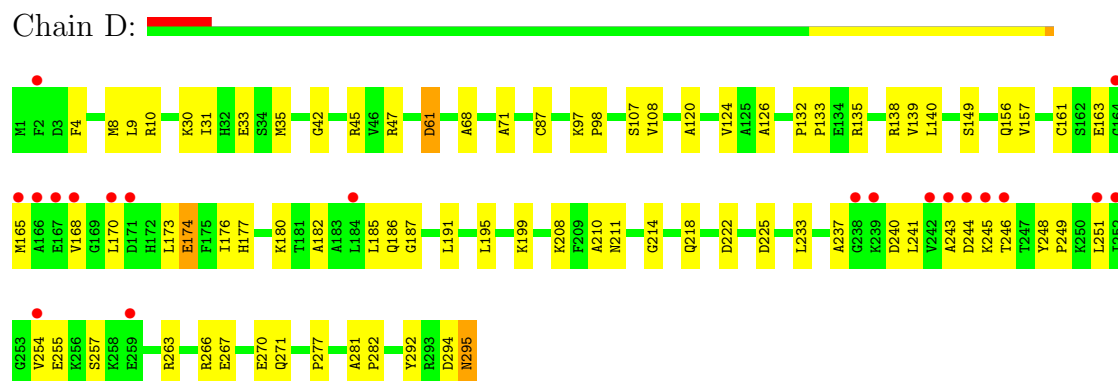
3 Residue-property plots

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.

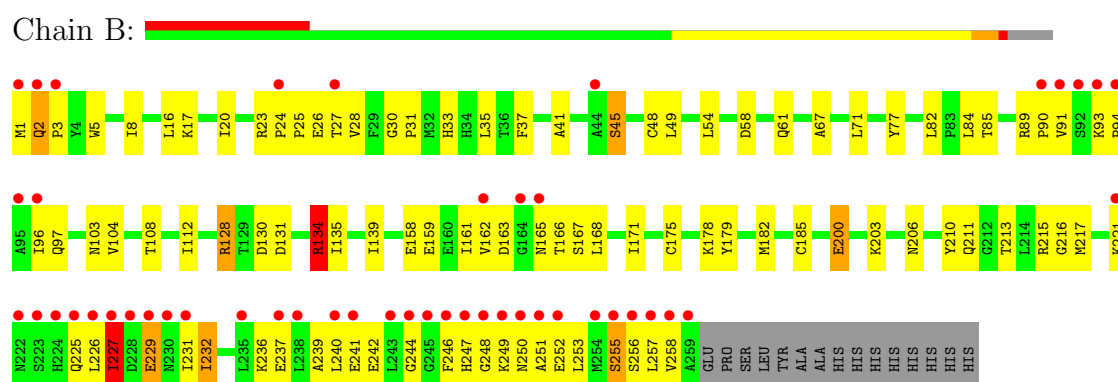
- Molecule 1: Geranyl diphosphate synthase large subunit



- Molecule 1: Geranyl diphosphate synthase large subunit

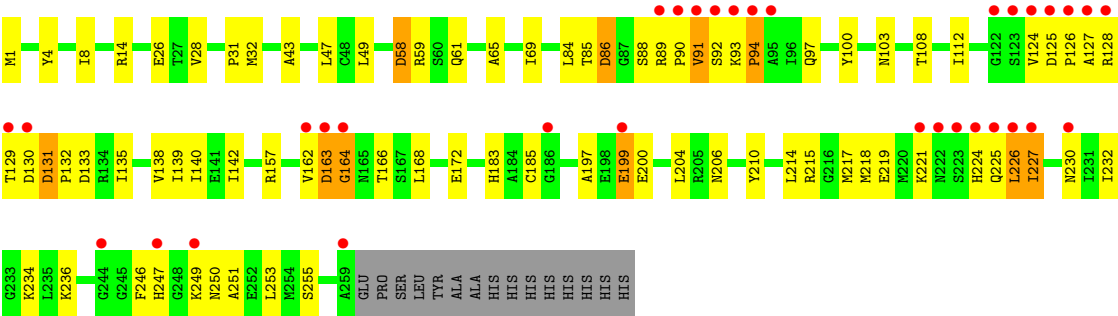


- Molecule 2: Geranyl diphosphate synthase small subunit



● Molecule 2: Geranyl diphosphate synthase small subunit

Chain C: 



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	53.44Å 108.70Å 182.28Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 1.95 29.02 – 1.94	Depositor EDS
% Data completeness (in resolution range)	90.1 (30.00-1.95) 89.7 (29.02-1.94)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.34 (at 1.95Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.205 , 0.256 0.205 , 0.258	Depositor DCC
R_{free} test set	3588 reflections (5.08%)	DCC
Wilson B-factor (Å ²)	30.2	Xtriage
Anisotropy	0.820	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 60.3	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	1 of 70905 reflections (0.001%)	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	9441	wwPDB-VP
Average B, all atoms (Å ²)	51.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.96% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

5 Model quality i

5.1 Standard geometry i

Bond lengths and bond angles in the following residue types are not validated in this section: PPV, MG, EDO, DST, IPE

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	0.96	2/2155 (0.1%)	0.85	0/2903
1	D	0.93	0/2268	0.87	3/3055 (0.1%)
2	B	0.83	2/1993 (0.1%)	0.82	1/2695 (0.0%)
2	C	0.84	1/1993 (0.1%)	0.83	1/2695 (0.0%)
All	All	0.89	5/8409 (0.1%)	0.84	5/11348 (0.0%)

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	175	CYS	CB-SG	5.74	1.92	1.82
1	A	27	GLU	CG-CD	5.23	1.59	1.51
1	A	46	VAL	CA-CB	5.20	1.65	1.54
2	B	200	GLU	CG-CD	5.15	1.59	1.51
2	C	185	CYS	CB-SG	-5.05	1.73	1.81

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	47	ARG	NE-CZ-NH2	-6.67	116.96	120.30
2	C	157	ARG	NE-CZ-NH1	-6.08	117.26	120.30
1	D	45	ARG	NE-CZ-NH2	-5.75	117.43	120.30
1	D	61	ASP	CB-CG-OD2	-5.44	113.41	118.30
2	B	134	ARG	NE-CZ-NH1	5.32	122.96	120.30

There are no chirality outliers.

There are no planarity outliers.

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2120	0	2146	51	0
1	D	2232	0	2264	79	0
2	B	1954	0	1948	103	0
2	C	1954	0	1948	83	0
3	A	14	0	9	1	0
3	D	14	0	9	0	0
4	A	9	0	0	0	0
5	A	2	0	0	0	0
5	D	2	0	0	0	0
6	C	4	0	6	0	0
7	D	14	0	10	3	0
8	A	268	0	0	14	1
8	B	243	0	0	13	1
8	C	294	0	0	15	1
8	D	317	0	0	15	1
All	All	9441	0	8340	307	2

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 18.

The worst 5 of 307 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:B:2:GLN:HB2	2:B:3:PRO:HD3	1.21	1.20
2:B:229:GLU:HG3	8:B:289:HOH:O	1.39	1.17
2:C:250:ASN:HB3	8:C:1039:HOH:O	1.57	1.03
2:C:230:ASN:O	2:C:234:LYS:HG3	1.58	1.02
2:C:28:VAL:HG22	1:D:157:VAL:CG2	1.96	0.94

All (2) 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	Distance(Å)	Clash(Å)
8:A:843:HOH:O	8:C:805:HOH:O[4_555]	1.99	0.21
8:B:589:HOH:O	8:D:588:HOH:O[3_555]	2.07	0.13

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	275/295 (93%)	263 (96%)	12 (4%)	0	100	100
1	D	293/295 (99%)	280 (96%)	12 (4%)	1 (0%)	50	38
2	B	257/274 (94%)	237 (92%)	14 (5%)	6 (2%)	10	2
2	C	257/274 (94%)	230 (90%)	18 (7%)	9 (4%)	6	1
All	All	1082/1138 (95%)	1010 (93%)	56 (5%)	16 (2%)	15	4

5 of 16 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	227	ILE
2	C	91	VAL
2	C	163	ASP
2	C	227	ILE
2	B	2	GLN

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	222/234 (95%)	218 (98%)	4 (2%)	71	64
1	D	234/234 (100%)	231 (99%)	3 (1%)	80	76
2	B	201/214 (94%)	193 (96%)	8 (4%)	42	26
2	C	201/214 (94%)	197 (98%)	4 (2%)	68	59
All	All	858/896 (96%)	839 (98%)	19 (2%)	64	55

5 of 19 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	227	ILE
2	B	232	ILE
2	C	199	GLU
2	B	134	ARG
1	D	174	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 10 such sidechains are listed below:

Mol	Chain	Res	Type
2	C	225	GLN
2	C	230	ASN
1	D	186	GLN
2	C	183	HIS
1	D	156	GLN

5.3.3 RNA ⓘ

There are no RNA chains 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 9 ligands modelled in this entry, 4 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
3	IPE	A	2003	-	13,13,13	2.91	5 (38%)	19,19,19	2.05	7 (36%)
4	PPV	A	2004	5	8,8,8	1.41	0	13,13,13	2.06	1 (7%)
6	EDO	C	2005	-	3,3,3	0.77	0	2,2,2	0.48	0
3	IPE	D	2001	-	13,13,13	3.03	4 (30%)	19,19,19	1.70	5 (26%)
7	DST	D	2002	5	13,13,13	1.89	3 (23%)	17,19,19	2.95	7 (41%)

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	IPE	A	2003	-	-	0/13/13/13	0/0/0/0
4	PPV	A	2004	5	-	0/6/6/6	0/0/0/0
6	EDO	C	2005	-	-	0/1/1/1	0/0/0/0
3	IPE	D	2001	-	-	0/13/13/13	0/0/0/0
7	DST	D	2002	5	-	1/11/13/13	0/0/0/0

The worst 5 of 12 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	D	2001	IPE	C2-C3	-6.81	1.36	1.51
3	A	2003	IPE	C4-C3	6.72	1.55	1.33
3	A	2003	IPE	C2-C3	-6.46	1.36	1.51
3	D	2001	IPE	C4-C3	6.23	1.54	1.33
3	D	2001	IPE	PA-O3A	-4.30	1.52	1.59

The worst 5 of 20 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	2004	PPV	P2-OPP-P1	-7.08	110.91	131.68
7	D	2002	DST	C10-C11-C12	6.97	126.04	115.50
7	D	2002	DST	O8-P3-O7	4.48	124.36	110.34
3	A	2003	IPE	O3A-PA-O1	4.29	122.60	103.41
3	A	2003	IPE	PA-O3A-PB	-4.16	119.49	131.68

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	D	2002	DST	O7-P3-S9-C10

There are no ring outliers.

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	279/295 (94%)	0.18	17 (6%) 21 26	27, 39, 68, 99	0
1	D	295/295 (100%)	0.38	20 (6%) 17 22	26, 41, 91, 109	0
2	B	259/274 (94%)	0.86	48 (18%) 2 1	29, 46, 116, 126	0
2	C	259/274 (94%)	0.71	33 (12%) 4 5	27, 46, 96, 115	0
All	All	1092/1138 (95%)	0.52	118 (10%) 6 7	26, 42, 98, 126	0

The worst 5 of 118 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	257	LEU	9.1
2	B	246	PHE	8.8
1	D	251	LEU	8.7
2	B	248	GLY	8.6
2	B	249	LYS	7.7

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	RSR	LLDF	B-factors(\AA^2)	Q<0.9
6	EDO	C	2005	4/4	0.17	1.82	36,37,37,38	0
3	IPE	A	2003	14/14	0.17	0.89	72,81,88,88	0
7	DST	D	2002	14/14	0.16	0.23	49,55,62,62	0
3	IPE	D	2001	14/14	0.12	-0.18	39,40,45,48	0
5	MG	A	3003	1/1	0.10	-0.25	50,50,50,50	0
5	MG	D	3002	1/1	0.09	-0.73	49,49,49,49	0
4	PPV	A	2004	9/9	0.09	-1.00	76,76,77,78	0
5	MG	D	3001	1/1	0.06	-1.43	53,53,53,53	0
5	MG	A	3004	1/1	0.06	-1.51	58,58,58,58	0

6.5 Other polymers ⓘ

There are no such residues in this entry.