



Full wwPDB X-ray Structure Validation Report ⓘ

Sep 7, 2020 – 02:44 PM BST

PDB ID : 6W2L
Title : Crystal structure of human dehydrodolichyl diphosphate synthase (NgBR/DHDDS) in complex with Mg and IPP
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Deposited on : 2020-03-06
Resolution : 2.31 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

<https://www.wwpdb.org/validation/2017/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 : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.14.2
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.14.2

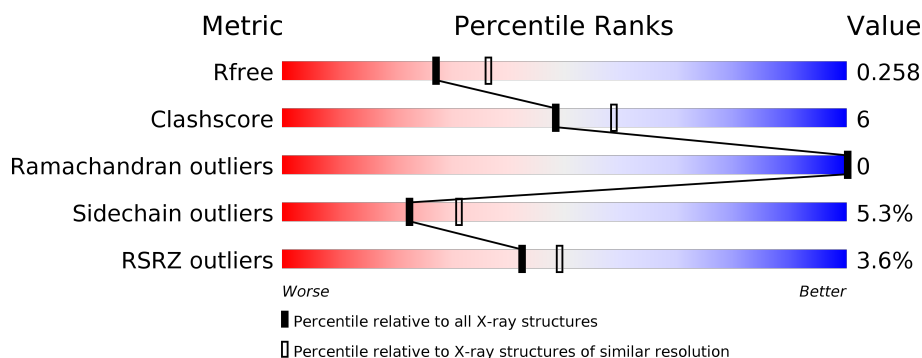
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.31 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}	130704	5042 (2.30-2.30)
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)
RSRZ outliers	127900	4938 (2.30-2.30)

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 respectively. 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	330	<div> <div>4%</div> <div> <div></div> <div>86%</div> <div>12%</div> <div>••</div> </div> </div>
2	B	214	<div> <div>2%</div> <div> <div></div> <div>78%</div> <div>12%</div> <div>• 9%</div> </div> </div>

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 4036 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 Dehydrodolichyl diphosphate synthase complex subunit DHDDS.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	328	Total	C	N	O	S	0	0	0
			2456	1564	440	438	14			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	ALA	-	expression tag	UNP Q86SQ9
A	253	MET	VAL	variant	UNP Q86SQ9

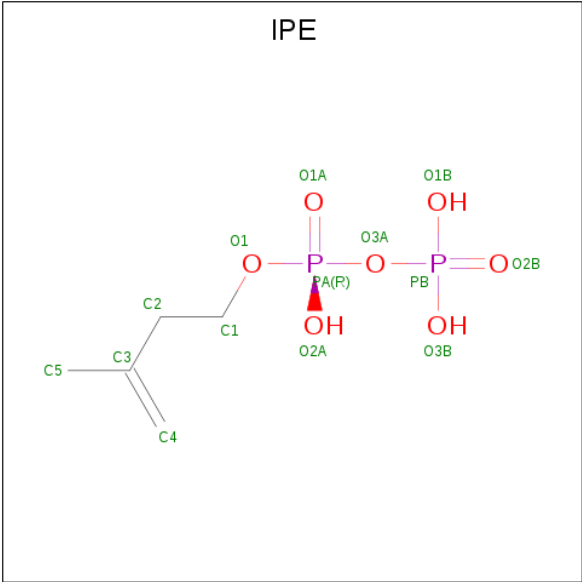
- Molecule 2 is a protein called Dehydrodolichyl diphosphate synthase complex subunit NUS1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	195	Total	C	N	O	S	0	0	0
			1444	919	248	269	8			

- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

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

- Molecule 4 is 3-METHYLBUT-3-ENYL TRIHYDROGEN DIPHOSPHATE (three-letter code: IPE) (formula: C₅H₁₂O₇P₂).



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

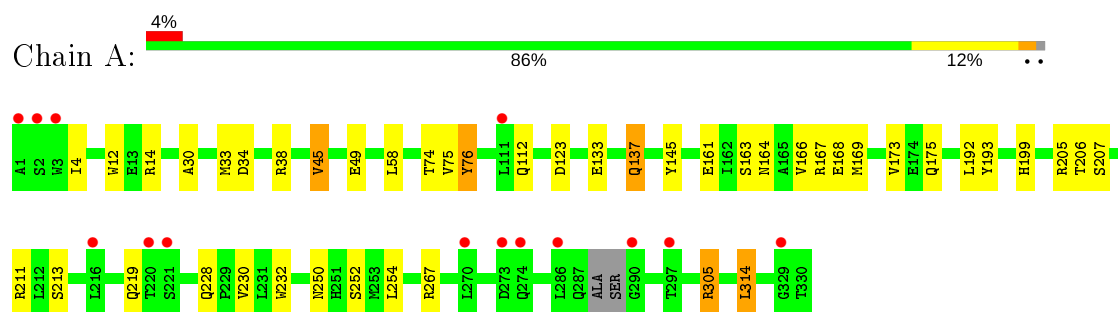
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	68	Total	O	0	0
			68	68		
5	B	39	Total	O	0	0
			39	39		

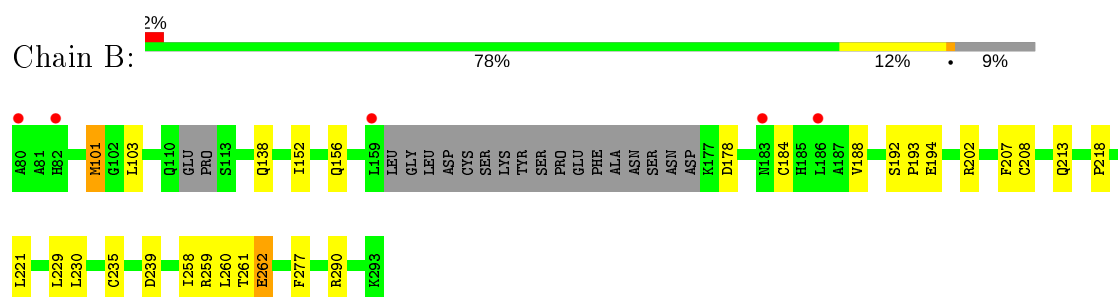
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide 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: Dehydrodolichyl diphosphate synthase complex subunit DHDDS



- Molecule 2: Dehydrodolichyl diphosphate synthase complex subunit NUS1



4 Data and refinement statistics

Property	Value	Source
Space group	H 3 2	Depositor
Cell constants a, b, c, α , β , γ	185.67Å 185.67Å 113.35Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	37.92 – 2.31 37.89 – 2.31	Depositor EDS
% Data completeness (in resolution range)	94.9 (37.92-2.31) 95.0 (37.89-2.31)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.26 (at 2.31Å)	Xtriage
Refinement program	REFMAC 5.8.0258	Depositor
R, R_{free}	0.212 , 0.255 0.216 , 0.258	Depositor DCC
R_{free} test set	1611 reflections (5.14%)	wwPDB-VP
Wilson B-factor (Å ²)	66.8	Xtriage
Anisotropy	0.034	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 60.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.023 for -2/3*h-1/3*k-4/3*l,-1/3*h-2/3*k+4/3*l,-1/3*h+1/3*k+1/3*l 0.019 for -h,1/3*h-1/3*k-4/3*l,-1/3*h-2/3*k+1/3*l 0.016 for -1/3*h+1/3*k+4/3*l,-k,2/3*h+1/3*k+1/3*l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	4036	wwPDB-VP
Average B, all atoms (Å ²)	78.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.71% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: MG, 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	0.28	0/2506	0.60	0/3403
2	B	0.33	1/1471 (0.1%)	0.57	0/2002
All	All	0.30	1/3977 (0.0%)	0.59	0/5405

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	138	GLN	C-O	5.66	1.34	1.23

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

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	2456	0	2239	33	0
2	B	1444	0	1340	15	0
3	A	1	0	0	0	0
4	A	28	0	18	4	0
5	A	68	0	0	2	0
5	B	39	0	0	1	0
All	All	4036	0	3597	45	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.

All (45) 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:14:ARG:HD2	5:A:553:HOH:O	1.84	0.78
1:A:205:ARG:HH12	1:A:213:SER:HB2	1.52	0.75
1:A:4:ILE:HA	5:A:524:HOH:O	1.93	0.69
1:A:38:ARG:NH2	1:A:207:SER:OG	2.26	0.69
1:A:211:ARG:HB3	2:B:262:GLU:OE1	1.94	0.67
1:A:164:ASN:O	1:A:168:GLU:HG2	1.96	0.65
1:A:206:THR:HG21	1:A:232:TRP:HE3	1.61	0.64
2:B:152:ILE:O	2:B:156:GLN:HB2	2.01	0.60
1:A:58:LEU:HD13	1:A:75:VAL:HG11	1.86	0.57
1:A:34:ASP:HA	4:A:402:IPE:H12	1.88	0.55
2:B:258:ILE:O	2:B:258:ILE:HG23	2.08	0.54
1:A:33:MET:O	4:A:402:IPE:H12	2.08	0.53
2:B:192:SER:HB2	2:B:193:PRO:HD2	1.91	0.52
1:A:161:GLU:OE1	1:A:192:LEU:HB3	2.09	0.52
1:A:45:VAL:CG1	1:A:49:GLU:HB3	2.42	0.50
1:A:173:VAL:HG21	2:B:208:CYS:HB3	1.94	0.50
1:A:133:GLU:O	1:A:137:GLN:CG	2.60	0.50
1:A:206:THR:O	1:A:230:VAL:O	2.30	0.49
2:B:207:PHE:CZ	2:B:221:LEU:HB2	2.48	0.49
1:A:133:GLU:O	1:A:137:GLN:HG3	2.13	0.48
1:A:205:ARG:HH12	1:A:213:SER:CB	2.24	0.48
1:A:305:ARG:HD3	1:A:305:ARG:C	2.34	0.48
1:A:123:ASP:OD2	1:A:193:TYR:OH	2.29	0.47
1:A:112:GLN:HA	1:A:145:TYR:CE1	2.51	0.46
2:B:192:SER:HB2	2:B:193:PRO:CD	2.46	0.46
1:A:30:ALA:HA	1:A:74:THR:O	2.15	0.46
1:A:199:HIS:ND1	1:A:219:GLN:HA	2.30	0.46
1:A:45:VAL:HG13	1:A:49:GLU:HB3	1.98	0.46
2:B:184:CYS:O	2:B:188:VAL:HB	2.15	0.45
1:A:167:ARG:HG2	2:B:218:PRO:O	2.15	0.45
2:B:259:ARG:HG3	2:B:260:LEU:HG	1.99	0.45
2:B:101:MET:HE1	2:B:277:PHE:HE2	1.83	0.44
1:A:163:SER:O	1:A:166:VAL:HG22	2.17	0.44
1:A:166:VAL:O	1:A:169:MET:HG2	2.17	0.44
1:A:164:ASN:HA	1:A:167:ARG:NH1	2.33	0.44
1:A:314:LEU:HD12	1:A:314:LEU:HA	1.83	0.43
2:B:258:ILE:HA	2:B:261:THR:OG1	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:76:TYR:O	4:A:403:IPE:H42	2.19	0.43
1:A:250:ASN:HB3	1:A:254:LEU:HD12	2.01	0.42
2:B:202:ARG:NH2	5:B:301:HOH:O	2.53	0.42
2:B:101:MET:HE3	2:B:103:LEU:HD21	2.02	0.42
1:A:206:THR:O	1:A:228:GLN:O	2.38	0.41
1:A:34:ASP:HA	4:A:402:IPE:C1	2.49	0.41
2:B:202:ARG:C	2:B:202:ARG:HD2	2.41	0.41
1:A:205:ARG:NH1	1:A:213:SER:HB2	2.29	0.41

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	324/330 (98%)	313 (97%)	11 (3%)	0	100	100
2	B	189/214 (88%)	178 (94%)	11 (6%)	0	100	100
All	All	513/544 (94%)	491 (96%)	22 (4%)	0	100	100

There are no Ramachandran outliers to report.

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	218/290 (75%)	209 (96%)	9 (4%)	30	43

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	B	140/189 (74%)	130 (93%)	10 (7%)	14	19
All	All	358/479 (75%)	339 (95%)	19 (5%)	22	31

All (19) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	12	TRP
1	A	45	VAL
1	A	76	TYR
1	A	137	GLN
1	A	175	GLN
1	A	252	SER
1	A	267	ARG
1	A	305	ARG
1	A	314	LEU
2	B	101	MET
2	B	178	ASP
2	B	194	GLU
2	B	213	GLN
2	B	229	LEU
2	B	230	LEU
2	B	235	CYS
2	B	239	ASP
2	B	262	GLU
2	B	290	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	36	ASN
1	A	51	HIS
1	A	175	GLN
1	A	274	GLN
2	B	157	GLN
2	B	215	GLN
2	B	257	HIS

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 monosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 3 ligands modelled in this entry, 1 is monoatomic - leaving 2 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	IPE	A	402	3	11,13,13	2.75	3 (27%)	15,19,19	1.52	3 (20%)
4	IPE	A	403	3	11,13,13	2.68	3 (27%)	15,19,19	1.59	4 (26%)

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	IPE	A	402	3	-	8/13/13/13	-
4	IPE	A	403	3	-	6/13/13/13	-

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	403	IPE	C4-C3	7.02	1.53	1.33
4	A	402	IPE	C4-C3	6.99	1.52	1.33
4	A	403	IPE	PB-O2B	4.06	1.63	1.50
4	A	402	IPE	PB-O2B	4.03	1.63	1.50
4	A	403	IPE	PB-O1B	2.41	1.64	1.54
4	A	402	IPE	PB-O1B	2.29	1.63	1.54

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	402	IPE	PA-O3A-PB	-3.55	120.66	132.83
4	A	402	IPE	O3B-PB-O3A	2.84	114.14	104.64
4	A	403	IPE	O1-PA-O1A	2.76	119.83	109.07
4	A	403	IPE	O3B-PB-O3A	2.61	113.39	104.64
4	A	403	IPE	PA-O3A-PB	-2.58	123.96	132.83
4	A	403	IPE	O1-C1-C2	-2.46	98.58	108.64
4	A	402	IPE	C5-C3-C2	2.14	121.94	115.24

There are no chirality outliers.

All (14) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	403	IPE	C1-O1-PA-O1A
4	A	403	IPE	C1-C2-C3-C4
4	A	403	IPE	C1-C2-C3-C5
4	A	402	IPE	C1-O1-PA-O1A
4	A	402	IPE	C1-C2-C3-C4
4	A	402	IPE	C1-C2-C3-C5
4	A	402	IPE	O1-C1-C2-C3
4	A	403	IPE	C1-O1-PA-O3A
4	A	403	IPE	C1-O1-PA-O2A
4	A	403	IPE	O1-C1-C2-C3
4	A	402	IPE	PB-O3A-PA-O2A
4	A	402	IPE	PB-O3A-PA-O1A
4	A	402	IPE	C1-O1-PA-O3A
4	A	402	IPE	C2-C1-O1-PA

There are no ring outliers.

2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	402	IPE	3	0
4	A	403	IPE	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 [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	328/330 (99%)	-0.04	14 (4%) 35 42	46, 74, 116, 166	0
2	B	195/214 (91%)	-0.03	5 (2%) 56 63	55, 76, 122, 155	0
All	All	523/544 (96%)	-0.04	19 (3%) 42 49	46, 75, 121, 166	0

All (19) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	286	LEU	5.3
2	B	80	ALA	4.7
1	A	3	TRP	4.4
2	B	186	LEU	3.6
2	B	82	HIS	3.4
2	B	159	LEU	3.1
1	A	1	ALA	2.7
2	B	183	ASN	2.6
1	A	297	THR	2.6
1	A	221	SER	2.6
1	A	273	ASP	2.4
1	A	2	SER	2.4
1	A	270	LEU	2.4
1	A	290	GLY	2.4
1	A	216	LEU	2.3
1	A	274	GLN	2.2
1	A	111	LEU	2.2
1	A	329	GLY	2.1
1	A	220	THR	2.0

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 monosaccharides 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. 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	B-factors(\AA^2)	Q<0.9
3	MG	A	401	1/1	0.95	0.16	65,65,65,65	0
4	IPE	A	403	14/14	0.97	0.12	56,63,77,78	0
4	IPE	A	402	14/14	0.99	0.14	59,65,74,75	0

6.5 Other polymers [i](#)

There are no such residues in this entry.