



# Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 09:56 PM UTC

PDB ID : 4LFE / pdb\_00004lfe  
Title : Crystal structure of geranylgeranyl diphosphate synthase sub1274 (target efi-509455) from streptococcus uberis 0140j with bound magnesium and isopentyl diphosphate, partially liganded complex;  
Authors : Patskovsky, Y.; Toro, R.; Bhosle, R.; Hillerich, B.; Seidel, R.D.; Washington, E.; Scott Glenn, A.; Chowdhury, S.; Evans, B.; Hammonds, J.; Imker, H.J.; Al Obaidi, N.; Stead, M.; Love, J.; Poulter, C.D.; Gerlt, J.A.; Almo, S.C.; Enzyme Function Initiative (EFI)  
Deposited on : 2013-06-26  
Resolution : 1.95 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](mailto: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 types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : 4-5-2 with Phenix2.0  
Mogul : 2022.3.0, CSD as543be (2022)  
Xtriage (Phenix) : 2.0  
EDS : 3.0  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
CCP4 : 9.0.010 (Gargrove)  
Density-Fitness : 1.0.12  
Ideal geometry (proteins) : Engh & Huber (2001)

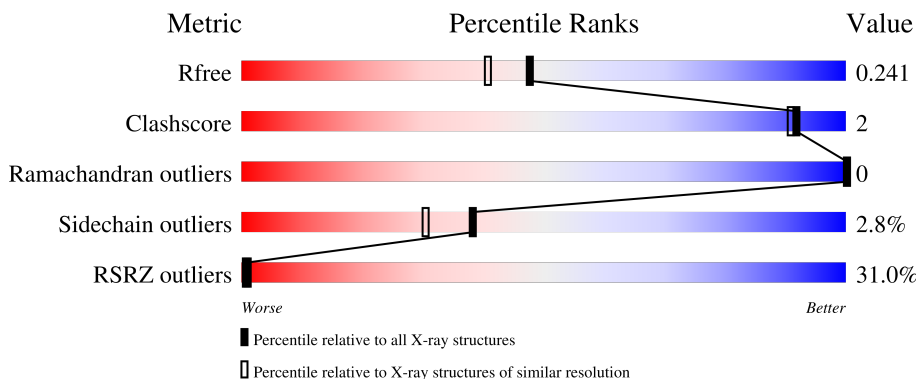
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 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))
$R_{free}$	180053	3494 (1.96-1.96)
Clashscore	190562	3612 (1.96-1.96)
Ramachandran outliers	187476	3587 (1.96-1.96)
Sidechain outliers	187428	3587 (1.96-1.96)
RSRZ outliers	180081	3495 (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 of the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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	290	 33% 88% 7% 6%
1	B	290	 27% 95% ..

Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
 Validation Pipeline (wwPDB-VP) : 2.49

## 2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 4662 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.

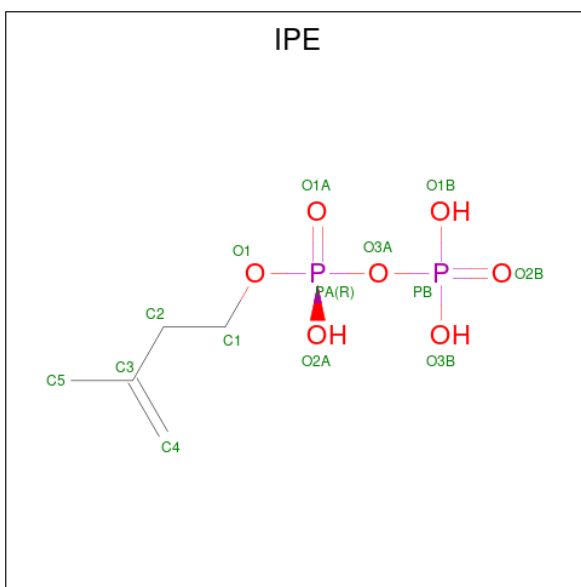
- Molecule 1 is a protein called Geranylgeranyl diphosphate synthase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	274	Total 2125	C 1356	N 353	O 405	S 11	0	2	0
1	B	288	Total 2264	C 1445	N 380	O 429	S 10	0	2	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	SER	-	expression tag	UNP B9DUT7
B	0	SER	-	expression tag	UNP B9DUT7

- Molecule 2 is 3-METHYLBUT-3-ENYL TRIHYDROGEN DIPHOSPHATE (CCD ID: IPE) (formula: C<sub>5</sub>H<sub>12</sub>O<sub>7</sub>P<sub>2</sub>).



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

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

- Molecule 3 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	2	Total	Mg	0	0
			2	2		
3	B	3	Total	Mg	0	0
			3	3		

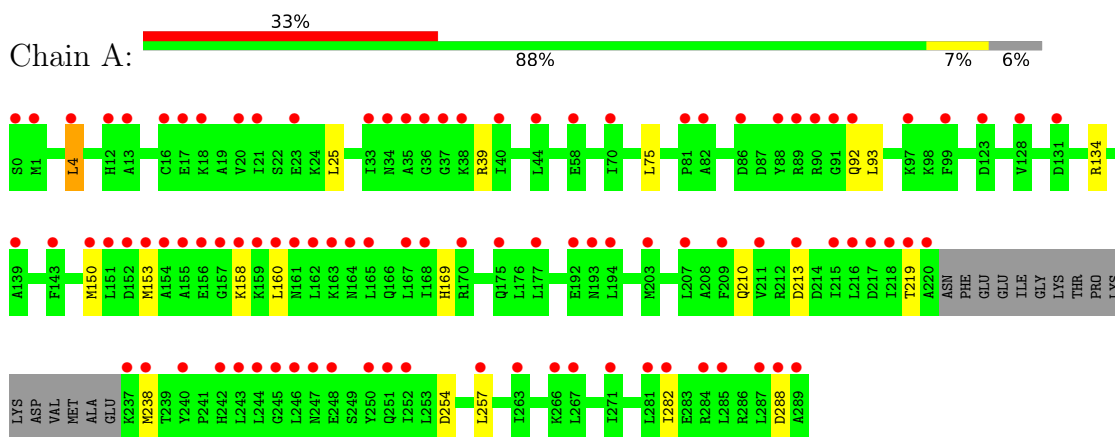
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	103	Total	O	0	0
			103	103		
4	B	123	Total	O	0	0
			123	123		

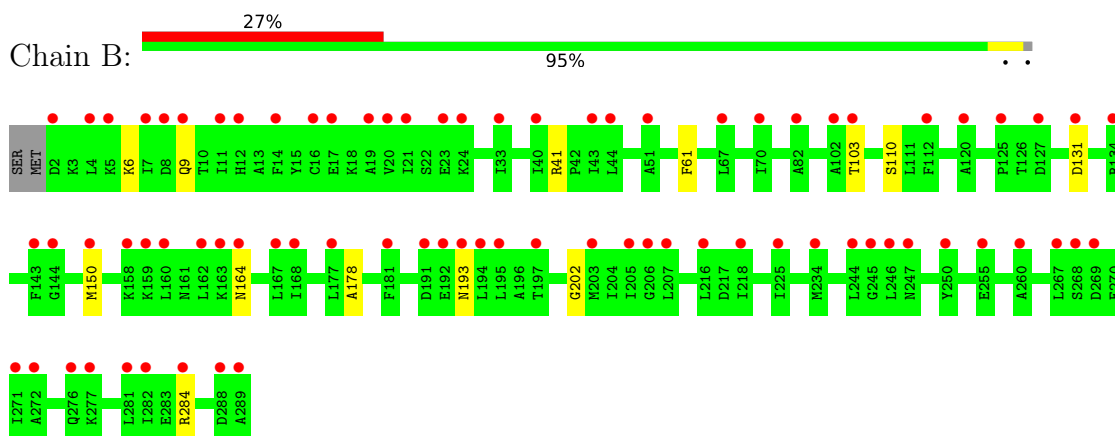
### 3 Residue-property plots [i](#)

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: Geranylgeranyl diphosphate synthase



- Molecule 1: Geranylgeranyl diphosphate synthase



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	70.80Å 75.79Å 124.62Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	46.82 – 1.95 46.82 – 1.95	Depositor EDS
% Data completeness (in resolution range)	97.7 (46.82-1.95) 97.7 (46.82-1.95)	Depositor EDS
$R_{merge}$	0.08	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.64 (at 1.95Å)	Xtrriage
Refinement program	REFMAC 5.7.0032	Depositor
R, $R_{free}$	0.207 , 0.236 0.214 , 0.241	Depositor DCC
$R_{free}$ test set	1519 reflections (3.08%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	25.7	Xtrriage
Anisotropy	0.840	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 39.0	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.51$ , $\langle L^2 \rangle = 0.35$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	4662	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	37.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.80% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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: IPE, MG

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	0/2164	0.77	1/2925 (0.0%)
1	B	0.54	0/2306	0.76	0/3111
All	All	0.53	0/4470	0.77	1/6036 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	158	LYS	N-CA-C	7.42	120.73	109.23

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	2125	0	2132	7	0
1	B	2264	0	2305	9	0
2	A	14	0	9	1	0
2	B	28	0	18	1	0
3	A	2	0	0	0	0
3	B	3	0	0	0	0
4	A	103	0	0	0	0
4	B	123	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	4662	0	4464	14	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 2.

All (14) 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:B:284[B]:ARG:HH21	1:B:284[B]:ARG:HG2	1.20	1.04
1:A:160:LEU:CB	1:A:238:MET:HE1	1.99	0.93
1:B:284[B]:ARG:HG2	1:B:284[B]:ARG:NH2	1.96	0.67
1:A:75:LEU:HD23	2:A:301:IPE:H52	1.89	0.55
1:A:169:HIS:CG	1:A:210:GLN:HG2	2.43	0.53
1:A:257:LEU:HD22	1:A:282:ILE:HG23	1.91	0.52
1:B:41:ARG:NH2	2:B:302:IPE:H52	2.26	0.50
1:B:284[B]:ARG:NH2	1:B:284[B]:ARG:CG	2.69	0.47
1:A:25:LEU:HB2	1:B:150:MET:HG3	1.95	0.47
1:B:178:ALA:HA	1:B:202:GLY:HA3	1.96	0.47
1:A:150[B]:MET:HE1	1:B:103:THR:HG23	1.98	0.44
1:B:164:ASN:ND2	4:B:478:HOH:O	2.50	0.44
1:A:4:LEU:HD23	1:A:39:ARG:HG3	2.02	0.42
1:B:6:LYS:HE3	1:B:61:PHE:CZ	2.54	0.42

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	272/290 (94%)	264 (97%)	8 (3%)	0	100	100
1	B	288/290 (99%)	284 (99%)	4 (1%)	0	100	100
All	All	560/580 (97%)	548 (98%)	12 (2%)	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	224/242 (93%)	215 (96%)	9 (4%)	28	17
1	B	242/242 (100%)	238 (98%)	4 (2%)	53	49
All	All	466/484 (96%)	453 (97%)	13 (3%)	38	30

All (13) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	4	LEU
1	A	92	GLN
1	A	93	LEU
1	A	134	ARG
1	A	153	MET
1	A	213	ASP
1	A	219	THR
1	A	254	ASP
1	A	288	ASP
1	B	9	GLN
1	B	110	SER
1	B	131	ASP
1	B	193	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	92	GLN
1	A	259	GLN
1	B	9	GLN
1	B	242	HIS
1	B	251	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 oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 8 ligands modelled in this entry, 5 are monoatomic - leaving 3 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
2	IPE	B	301	3	12,13,13	1.12	1 (8%)	16,19,19	1.20	1 (6%)
2	IPE	A	301	3	12,13,13	0.79	0	16,19,19	0.97	1 (6%)
2	IPE	B	302	-	12,13,13	0.74	0	16,19,19	1.10	0

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
2	IPE	B	301	3	-	6/13/13/13	-
2	IPE	A	301	3	-	3/13/13/13	-
2	IPE	B	302	-	-	2/13/13/13	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	301	IPE	PA-O3A	3.37	1.63	1.59

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	301	IPE	C5-C3-C2	2.36	121.43	114.96
2	A	301	IPE	O3B-PB-O1B	2.03	115.41	107.80

There are no chirality outliers.

All (11) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	301	IPE	C1-O1-PA-O1A
2	B	301	IPE	C1-O1-PA-O2A
2	B	301	IPE	C1-C2-C3-C4
2	B	301	IPE	C1-C2-C3-C5
2	B	302	IPE	C1-C2-C3-C4
2	B	302	IPE	C1-C2-C3-C5
2	A	301	IPE	PA-O3A-PB-O3B
2	B	301	IPE	C1-O1-PA-O3A
2	B	301	IPE	O1-C1-C2-C3
2	A	301	IPE	O1-C1-C2-C3
2	A	301	IPE	PB-O3A-PA-O2A

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	301	IPE	1	0
2	B	302	IPE	1	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<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	274/290 (94%)	1.94	96 (35%) <b>1</b> <b>0</b>	21, 36, 72, 111	2 (0%)
1	B	288/290 (99%)	1.60	78 (27%) <b>1</b> <b>1</b>	22, 32, 55, 80	2 (0%)
All	All	562/580 (96%)	1.77	174 (30%) <b>1</b> <b>1</b>	21, 33, 64, 111	4 (0%)

All (174) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	220	ALA	8.6
1	A	91	GLY	7.9
1	A	155	ALA	7.5
1	A	157	GLY	6.8
1	A	154	ALA	6.2
1	A	218	ILE	6.2
1	A	159	LYS	5.2
1	A	35	ALA	5.1
1	A	158	LYS	5.1
1	A	90	ARG	4.9
1	A	156	GLU	4.8
1	B	269	ASP	4.6
1	A	160	LEU	4.6
1	B	234	MET	4.6
1	B	289	ALA	4.5
1	A	287	LEU	4.4
1	B	40	ILE	4.4
1	A	0	SER	4.3
1	A	162	LEU	4.3
1	A	216	LEU	4.2
1	A	289	ALA	4.2
1	B	2	ASP	4.2
1	A	153	MET	4.1
1	A	12	HIS	4.1

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	A	40	ILE	4.0
1	A	282	ILE	4.0
1	A	219	THR	4.0
1	A	250	TYR	4.0
1	A	193	ASN	3.9
1	B	5	LYS	3.8
1	A	246	LEU	3.8
1	A	237	LYS	3.7
1	A	242	HIS	3.7
1	A	209	PHE	3.7
1	A	247	ASN	3.6
1	A	163	LYS	3.6
1	A	21	ILE	3.6
1	A	215	ILE	3.6
1	B	20	VAL	3.5
1	A	16	CYS	3.5
1	A	217	ASP	3.4
1	A	17	GLU	3.4
1	B	281	LEU	3.4
1	B	24	LYS	3.4
1	A	288	ASP	3.3
1	A	4	LEU	3.3
1	A	167	LEU	3.3
1	B	160	LEU	3.3
1	B	225	ILE	3.3
1	B	271	ILE	3.3
1	B	246	LEU	3.3
1	B	143	PHE	3.3
1	B	19	ALA	3.2
1	A	238	MET	3.2
1	B	144	GLY	3.2
1	A	1	MET	3.2
1	A	18	LYS	3.2
1	A	266	LYS	3.2
1	A	92	GLN	3.2
1	A	36	GLY	3.1
1	B	4	LEU	3.1
1	A	281	LEU	3.1
1	A	207	LEU	3.0
1	B	245	GLY	3.0
1	A	284	ARG	3.0
1	A	213	ASP	3.0

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	B	159	LYS	3.0
1	B	16	CYS	3.0
1	A	285	LEU	2.9
1	A	161	ASN	2.9
1	B	17	GLU	2.9
1	B	21	ILE	2.9
1	A	257	LEU	2.9
1	A	97	LYS	2.8
1	B	244	LEU	2.8
1	A	89	ARG	2.8
1	B	255	GLU	2.8
1	A	131	ASP	2.8
1	B	33	ILE	2.8
1	A	251	GLN	2.7
1	B	134	ARG	2.7
1	A	248	GLU	2.7
1	A	243	LEU	2.7
1	B	195	LEU	2.7
1	B	268	SER	2.7
1	B	8	ASP	2.7
1	B	191	ASP	2.7
1	B	168	ILE	2.7
1	B	205	ILE	2.7
1	B	272	ALA	2.6
1	B	82	ALA	2.6
1	A	240	TYR	2.6
1	A	165	LEU	2.6
1	A	252	ILE	2.6
1	B	43	ILE	2.6
1	A	245	GLY	2.6
1	B	12	HIS	2.5
1	A	88	TYR	2.5
1	B	267	LEU	2.5
1	B	288	ASP	2.5
1	A	38	LYS	2.5
1	B	163	LYS	2.5
1	A	267	LEU	2.5
1	A	164	ASN	2.5
1	B	247	ASN	2.5
1	A	170	ARG	2.5
1	B	51	ALA	2.5
1	B	102	ALA	2.5

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	A	23	GLU	2.5
1	A	99	PHE	2.5
1	B	193	ASN	2.5
1	A	82	ALA	2.5
1	A	20	VAL	2.5
1	A	143	PHE	2.4
1	A	168	ILE	2.4
1	B	158	LYS	2.4
1	B	277	LYS	2.4
1	B	23	GLU	2.4
1	B	167	LEU	2.4
1	B	216	LEU	2.4
1	B	11	ILE	2.4
1	B	44	LEU	2.4
1	B	260	ALA	2.4
1	B	192	GLU	2.4
1	B	131	ASP	2.3
1	B	67	LEU	2.3
1	B	250	TYR	2.3
1	A	13	ALA	2.3
1	A	81	PRO	2.3
1	B	162	LEU	2.3
1	B	177	LEU	2.3
1	B	103	THR	2.3
1	B	206	GLY	2.3
1	A	86[A]	ASP	2.3
1	A	34	ASN	2.3
1	B	14	PHE	2.3
1	A	33	ILE	2.3
1	B	70	ILE	2.3
1	A	123	ASP	2.3
1	A	177	LEU	2.3
1	A	244	LEU	2.3
1	B	120	ALA	2.2
1	A	70	ILE	2.2
1	A	271	ILE	2.2
1	B	164	ASN	2.2
1	B	203	MET	2.2
1	A	139	ALA	2.2
1	A	152	ASP	2.2
1	B	218	ILE	2.2
1	A	203	MET	2.2

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Mol	Chain	Res	Type	RSRZ
1	B	284[A]	ARG	2.2
1	A	44	LEU	2.2
1	A	151	LEU	2.2
1	B	194	LEU	2.2
1	A	58	GLU	2.2
1	A	128	VAL	2.2
1	A	211	VAL	2.2
1	B	127	ASP	2.2
1	B	207	LEU	2.2
1	A	150[A]	MET	2.1
1	A	192	GLU	2.1
1	B	276	GLN	2.1
1	B	197	THR	2.1
1	B	125	PRO	2.1
1	A	175	GLN	2.1
1	B	150	MET	2.1
1	A	263	ILE	2.0
1	B	282	ILE	2.0
1	A	37	GLY	2.0
1	A	194	LEU	2.0
1	B	7	ILE	2.0
1	B	112	PHE	2.0
1	B	181	PHE	2.0
1	B	9	GLN	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 oligosaccharides 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, 95<sup>th</sup> 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( $\text{\AA}^2$ )	Q<0.9
3	MG	B	305	1/1	0.86	0.08	24,24,24,24	0
3	MG	A	302	1/1	0.87	0.10	32,32,32,32	0
3	MG	A	303	1/1	0.92	0.07	36,36,36,36	0
2	IPE	A	301	14/14	0.94	0.11	32,42,51,52	0
3	MG	B	304	1/1	0.95	0.05	28,28,28,28	0
3	MG	B	303	1/1	0.96	0.04	28,28,28,28	0
2	IPE	B	301	14/14	0.96	0.09	21,26,36,39	0
2	IPE	B	302	14/14	0.96	0.09	22,27,35,38	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.