Full wwPDB X-ray Structure Validation Report (i)

Jan 30, 2021 – 08:56 PM EST

PDB ID	:	3N3D
Title	:	Crystal structure of geranylgeranyl pyrophosphate synthase from lactobacillus brevis atcc 367
Authors	:	Patskovsky, Y.; Toro, R.; Rutter, M.; Chang, S.; Sauder, J.M.; Burley, S.K.; Almo, S.C.; New York Structural GenomiX Research Consortium (NYSGXRC); New York SGX Research Center for Structural Genomics (NYSGXRC)
Deposited on	:	2010-05-19
Resolution	:	2.40 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 (i) symbol.

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

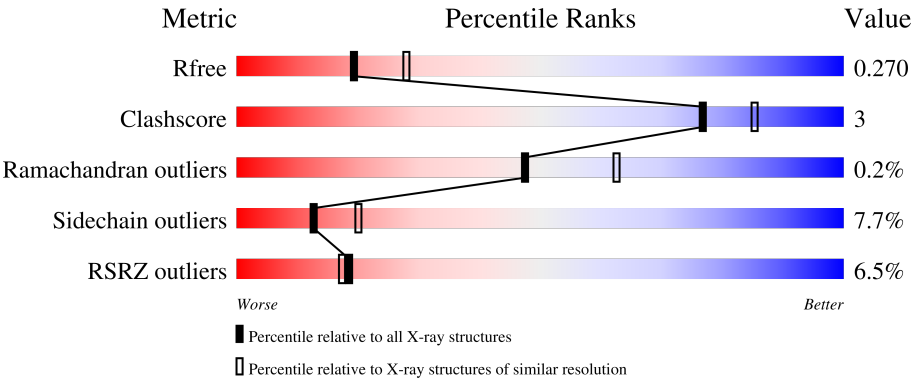
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.16
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.16

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 2.40 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	3907 (2.40-2.40)
Clashscore	141614	4398 (2.40-2.40)
Ramachandran outliers	138981	4318 (2.40-2.40)
Sidechain outliers	138945	4319 (2.40-2.40)
RSRZ outliers	127900	3811 (2.40-2.40)

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 >=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 <=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	335	4% 84% 11%
1	B	335	8% 82% 10% 7%

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 5110 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 pyrophosphate synthase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	322	Total	C	N	O	S	0	1	0
			2554	1618	453	475	8			
1	B	313	Total	C	N	O	S	0	0	0
			2478	1574	434	462	8			

There are 36 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	SER	-	expression tag	UNP Q03Q08
A	1	LEU	-	expression tag	UNP Q03Q08
A	64	ALA	THR	conflict	UNP Q03Q08
A	128	LYS	GLN	conflict	UNP Q03Q08
A	144	HIS	ARG	conflict	UNP Q03Q08
A	199	ARG	HIS	conflict	UNP Q03Q08
A	202	ASP	GLU	conflict	UNP Q03Q08
A	226	ARG	LYS	conflict	UNP Q03Q08
A	291	GLN	ARG	conflict	UNP Q03Q08
A	306	VAL	ALA	conflict	UNP Q03Q08
A	326	GLU	-	expression tag	UNP Q03Q08
A	327	GLY	-	expression tag	UNP Q03Q08
A	328	HIS	-	expression tag	UNP Q03Q08
A	329	HIS	-	expression tag	UNP Q03Q08
A	330	HIS	-	expression tag	UNP Q03Q08
A	331	HIS	-	expression tag	UNP Q03Q08
A	332	HIS	-	expression tag	UNP Q03Q08
A	333	HIS	-	expression tag	UNP Q03Q08
B	0	SER	-	expression tag	UNP Q03Q08
B	1	LEU	-	expression tag	UNP Q03Q08
B	64	ALA	THR	conflict	UNP Q03Q08
B	128	LYS	GLN	conflict	UNP Q03Q08
B	144	HIS	ARG	conflict	UNP Q03Q08
B	199	ARG	HIS	conflict	UNP Q03Q08
B	202	ASP	GLU	conflict	UNP Q03Q08

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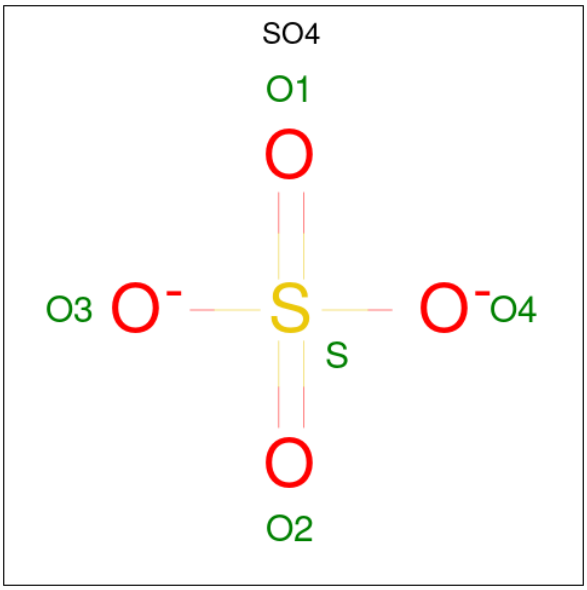
Chain	Residue	Modelled	Actual	Comment	Reference
B	226	ARG	LYS	conflict	UNP Q03Q08
B	291	GLN	ARG	conflict	UNP Q03Q08
B	306	VAL	ALA	conflict	UNP Q03Q08
B	326	GLU	-	expression tag	UNP Q03Q08
B	327	GLY	-	expression tag	UNP Q03Q08
B	328	HIS	-	expression tag	UNP Q03Q08
B	329	HIS	-	expression tag	UNP Q03Q08
B	330	HIS	-	expression tag	UNP Q03Q08
B	331	HIS	-	expression tag	UNP Q03Q08
B	332	HIS	-	expression tag	UNP Q03Q08
B	333	HIS	-	expression tag	UNP Q03Q08

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O_4S).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total O S 5 4 1	0	0
2	A	1	Total O S 5 4 1	0	0
2	A	1	Total O S 5 4 1	0	0
2	A	1	Total O S 5 4 1	0	0
2	B	1	Total O S 5 4 1	0	0

- Molecule 3 is water.

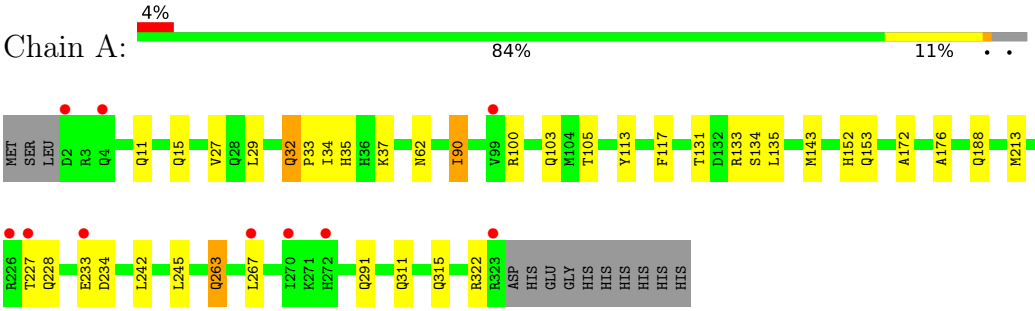
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	34	Total O 34 34	0	0
3	B	19	Total O 19 19	0	0

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.

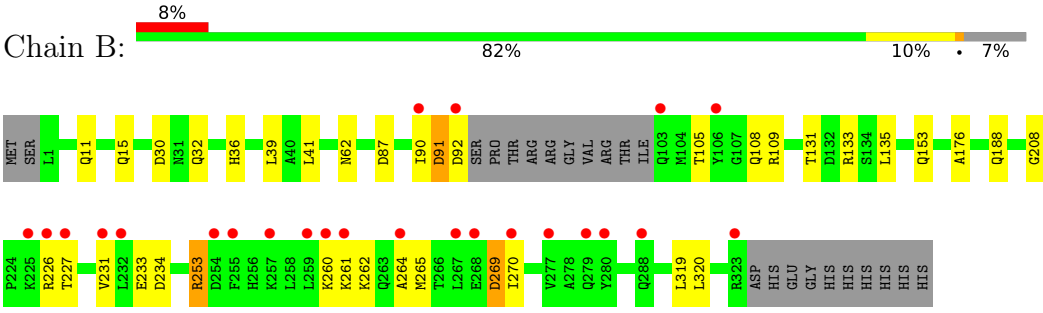
• Molecule 1: Geranylgeranyl pyrophosphate synthase

Chain A:



• Molecule 1: Geranylgeranyl pyrophosphate synthase

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α, β, γ	111.56Å 111.56Å 198.50Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.40 39.84 – 2.40	Depositor EDS
% Data completeness (in resolution range)	97.0 (20.00-2.40) 97.0 (39.84-2.40)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.09	Depositor
$< I/\sigma(I) >$ [1]	1.58 (at 2.39Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.234 , 0.267 0.234 , 0.270	Depositor DCC
R_{free} test set	1494 reflections (3.11%)	wwPDB-VP
Wilson B-factor (Å^2)	57.9	Xtriage
Anisotropy	0.267	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.32 , 44.8	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	5110	wwPDB-VP
Average B, all atoms (Å^2)	76.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.51% 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, 0.333 respectively for untwinned datasets, and 0.375, 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: SO4

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	0.41	0/2603	0.56	0/3528
1	B	0.39	0/2522	0.55	0/3417
All	All	0.40	0/5125	0.56	0/6945

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	2554	0	2579	16	0
1	B	2478	0	2498	16	0
2	A	20	0	0	0	0
2	B	5	0	0	0	0
3	A	34	0	0	0	0
3	B	19	0	0	0	0
All	All	5110	0	5077	30	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 3.

All (30) 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:135:LEU:HD21	1:A:188:GLN:HG2	1.51	0.93
1:B:265:MET:HE2	1:B:270:ILE:HG22	1.54	0.90
1:B:265:MET:CE	1:B:270:ILE:HG22	2.20	0.70
1:A:223:ASP:N	1:A:223:ASP:OD1	2.30	0.65
1:B:90:ILE:HG12	1:B:108:GLN:HE22	1.61	0.65
1:B:261:LYS:NZ	1:B:269:ASP:OD2	2.29	0.64
1:B:91:ASP:O	1:B:92:ASP:CG	2.41	0.59
1:A:172:ALA:HA	1:A:176:ALA:HB3	1.88	0.53
1:B:91:ASP:O	1:B:92:ASP:CB	2.55	0.53
1:B:135:LEU:HD21	1:B:188:GLN:HG2	1.90	0.52
1:B:262:LYS:O	1:B:265:MET:HG3	2.10	0.51
1:A:90:ILE:HG23	1:B:109:ARG:HD2	1.92	0.51
1:B:91:ASP:O	1:B:92:ASP:OD2	2.30	0.50
1:A:291:GLN:HG3	1:A:322:ARG:HH22	1.77	0.49
1:A:227:THR:CG2	1:A:228:GLN:N	2.74	0.49
1:B:261:LYS:O	1:B:264:ALA:HB3	2.15	0.47
1:A:213:MET:HG2	1:A:242:LEU:HD22	1.97	0.46
1:A:27:VAL:HG13	1:A:117:PHE:HE2	1.81	0.44
1:A:32:GLN:HG3	1:A:33:PRO:HD3	2.00	0.44
1:B:176:ALA:HA	1:B:208:GLY:HA3	2.01	0.42
1:A:135:LEU:HD23	1:A:135:LEU:HA	1.84	0.42
1:B:260:LYS:O	1:B:262:LYS:HG3	2.20	0.42
1:B:253:ARG:H	1:B:253:ARG:HE	1.68	0.42
1:A:311:GLN:HG3	1:A:315:GLN:HE21	1.84	0.42
1:A:113:TYR:OH	1:B:87:ASP:OD2	2.31	0.42
1:A:263:GLN:H	1:A:263:GLN:HG2	1.21	0.41
1:A:29:LEU:HB3	1:A:35:HIS:HB2	2.03	0.41
1:B:226:ARG:HB3	1:B:227:THR:H	1.77	0.41
1:A:223:ASP:HA	1:A:224:PRO:HD3	1.68	0.40

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	321/335 (96%)	316 (98%)	5 (2%)	0	100	100
1	B	309/335 (92%)	303 (98%)	5 (2%)	1 (0%)	41	55
All	All	630/670 (94%)	619 (98%)	10 (2%)	1 (0%)	47	62

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	222	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	272/283 (96%)	251 (92%)	21 (8%)	13	20
1	B	263/283 (93%)	243 (92%)	20 (8%)	13	20
All	All	535/566 (94%)	494 (92%)	41 (8%)	13	20

All (41) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	11	GLN
1	A	15	GLN
1	A	32	GLN
1	A	34	ILE
1	A	37	LYS
1	A	90	ILE
1	A	100	ARG
1	A	103	GLN
1	A	105	THR
1	A	131	THR
1	A	133	ARG
1	A	134	SER

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Mol	Chain	Res	Type
1	A	143	MET
1	A	152	HIS
1	A	153	GLN
1	A	223	ASP
1	A	233	GLU
1	A	234	ASP
1	A	245	LEU
1	A	263	GLN
1	A	267	LEU
1	B	11	GLN
1	B	15	GLN
1	B	30	ASP
1	B	32	GLN
1	B	36	HIS
1	B	39	LEU
1	B	41	LEU
1	B	62	ASN
1	B	91	ASP
1	B	105	THR
1	B	131	THR
1	B	133	ARG
1	B	153	GLN
1	B	231	VAL
1	B	233	GLU
1	B	234	ASP
1	B	253	ARG
1	B	269	ASP
1	B	319	LEU
1	B	320	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	138	ASN
1	A	157	ASN
1	A	185	GLN
1	A	274	GLN
1	A	310	GLN
1	A	315	GLN
1	B	15	GLN
1	B	28	GLN
1	B	32	GLN

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Mol	Chain	Res	Type
1	B	35	HIS
1	B	62	ASN
1	B	108	GLN
1	B	138	ASN
1	B	153	GLN
1	B	185	GLN
1	B	194	GLN
1	B	274	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 monosaccharides in this entry.

5.6 Ligand geometry (i)

5 ligands are modelled in this entry.

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	SO4	A	337	-	4,4,4	0.09	0	6,6,6	0.30	0
2	SO4	A	336	-	4,4,4	0.12	0	6,6,6	0.11	0
2	SO4	A	334	-	4,4,4	0.14	0	6,6,6	0.17	0
2	SO4	B	334	-	4,4,4	0.17	0	6,6,6	0.12	0
2	SO4	A	335	-	4,4,4	0.15	0	6,6,6	0.06	0

There are no bond length outliers.

There are no bond angle outliers.

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

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	322/335 (96%)	0.20	14 (4%) 35 33	39, 67, 117, 146	0
1	B	313/335 (93%)	0.43	27 (8%) 10 9	39, 74, 130, 157	0
All	All	635/670 (94%)	0.32	41 (6%) 18 17	39, 71, 127, 157	0

All (41) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	323	ARG	5.5
1	B	255	PHE	5.2
1	B	90	ILE	4.8
1	A	323	ARG	4.7
1	A	225	LYS	4.4
1	A	226	ARG	4.4
1	B	226	ARG	4.3
1	B	257	LYS	4.1
1	B	221	ALA	4.1
1	B	222	GLY	4.0
1	A	222	GLY	4.0
1	B	232	LEU	3.8
1	A	267	LEU	3.8
1	B	264	ALA	3.5
1	B	270	ILE	3.5
1	B	277	VAL	3.4
1	B	254	ASP	3.2
1	A	272	HIS	3.2
1	A	223	ASP	3.2
1	A	4	GLN	3.1
1	B	261	LYS	3.0
1	B	260	LYS	2.9
1	A	233	GLU	2.9
1	A	224	PRO	2.9

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Mol	Chain	Res	Type	RSRZ
1	B	267	LEU	2.9
1	B	280	TYR	2.8
1	A	227	THR	2.6
1	B	92	ASP	2.6
1	B	223	ASP	2.6
1	A	99	VAL	2.6
1	B	106	TYR	2.5
1	B	279	GLN	2.5
1	B	227	THR	2.4
1	B	225	LYS	2.4
1	A	2	ASP	2.4
1	B	268	GLU	2.4
1	A	270	ILE	2.4
1	B	231	VAL	2.3
1	B	103	GLN	2.3
1	B	288	GLN	2.2
1	B	259	LEU	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, 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	B-factors(Å^2)	Q<0.9
2	SO4	A	334	5/5	0.84	0.19	94,110,116,116	0
2	SO4	A	335	5/5	0.85	0.17	154,156,156,156	0
2	SO4	A	336	5/5	0.88	0.12	149,151,153,153	0
2	SO4	A	337	5/5	0.90	0.22	71,84,98,101	0
2	SO4	B	334	5/5	0.91	0.16	95,101,105,110	0

6.5 Other polymers (i)

There are no such residues in this entry.