



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 25, 2026 – 06:36 PM EDT

PDB ID : 3ITE / pdb_00003ite
Title : The third adenylation domain of the fungal SidN non-ribosomal peptide synthetase
Authors : Lee, T.V.; Lott, J.S.; Johnson, R.D.; Johnson, L.J.; Arcus, V.L.
Deposited on : 2009-08-28
Resolution : 2.00 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 types of validation reports are described at

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

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

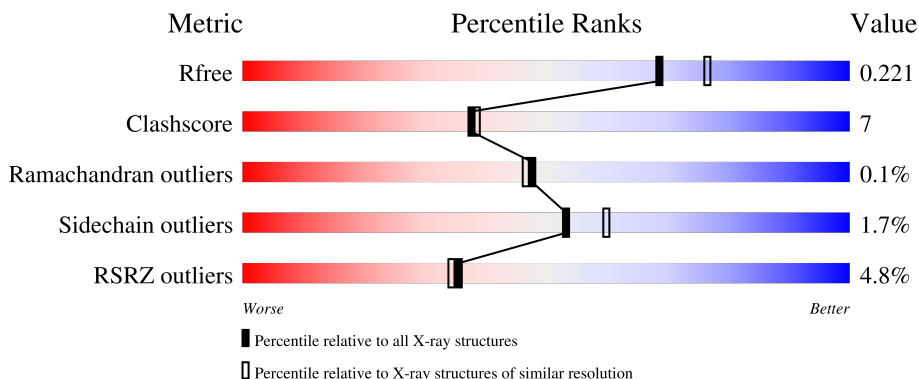
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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	10052 (2.00-2.00)
Clashscore	190562	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)
RSRZ outliers	180081	10067 (2.00-2.00)

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 $\leq 5\%$. 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	562	 2% 64% 7% 28%
1	B	562	 6% 73% 15% 10%

2 Entry composition [i](#)

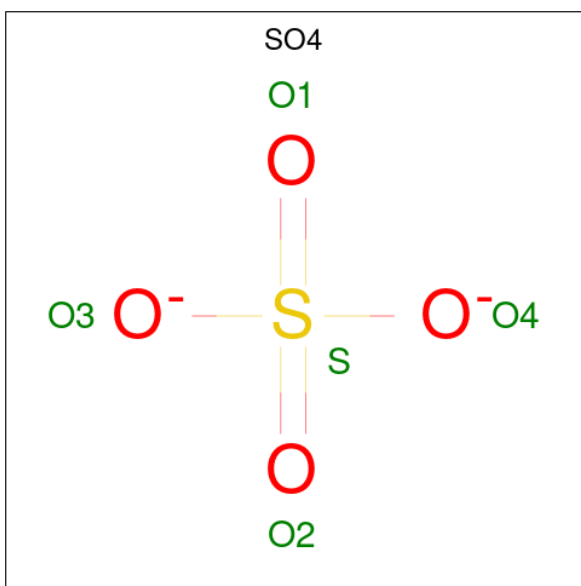
There are 4 unique types of molecules in this entry. The entry contains 7397 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 SidN siderophore synthetase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	S	Se			
1	A	402	Total 3075	C 1944	N 536	O 580	S 6	Se 9	0	1	1
1	B	503	Total 3855	C 2437	N 668	O 733	S 7	Se 10	0	0	1

- Molecule 2 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



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

- Molecule 3 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total Cl 1 1	0	0
3	B	1	Total Cl 1 1	0	0

- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	230	Total O 230 230	0	0
4	B	225	Total O 225 225	0	0

4 Data and refinement statistics i

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	50.60Å 75.28Å 84.14Å 114.85° 94.78° 90.18°	Depositor
Resolution (Å)	42.62 – 2.00 42.62 – 2.00	Depositor EDS
% Data completeness (in resolution range)	95.7 (42.62-2.00) 96.2 (42.62-2.00)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.08	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.71 (at 2.00Å)	Xtrriage
Refinement program	PHENIX (phenix.refine)	Depositor
R, R_{free}	0.194 , 0.228 0.190 , 0.221	Depositor DCC
R_{free} test set	3690 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å ²)	24.7	Xtrriage
Anisotropy	0.718	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 46.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	0.159 for -h,k,-k-l	Xtrriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	7397	wwPDB-VP
Average B, all atoms (Å ²)	37.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.23% 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: CL, 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	1.13	2/3135 (0.1%)	1.07	2/4243 (0.0%)
1	B	1.02	3/3918 (0.1%)	1.04	3/5299 (0.1%)
All	All	1.07	5/7053 (0.1%)	1.05	5/9542 (0.1%)

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	288	ALA	CA-CB	7.95	1.62	1.53
1	A	247	ALA	CA-CB	5.89	1.61	1.53
1	B	172	ASP	N-CA	5.29	1.52	1.46
1	B	33	ALA	CA-CB	5.27	1.62	1.53
1	B	252	ARG	C-O	-5.23	1.18	1.24

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	298	GLY	N-CA-C	-5.92	107.65	114.69
1	A	252	ARG	NE-CZ-NH2	-5.79	113.99	119.20
1	B	113	LYS	N-CA-C	-5.30	105.50	111.28
1	B	490	GLU	N-CA-C	-5.20	106.01	112.93
1	A	138	PRO	O-C-N	5.09	123.65	121.31

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	3075	0	3059	32	0
1	B	3855	0	3851	71	0
2	A	5	0	0	0	0
2	B	5	0	0	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	230	0	0	7	0
4	B	225	0	0	4	0
All	All	7397	0	6910	97	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 7.

All (97) 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:492:ASN:OD1	1:B:496:ARG:HG3	1.77	0.84
1:A:156:SER:CB	1:B:479:GLY:HA2	2.20	0.72
1:B:425:VAL:HG13	1:B:455:LEU:HD22	1.75	0.68
1:B:432:LEU:HD13	1:B:507:MSE:HG2	1.76	0.68
1:B:491:ILE:C	1:B:491:ILE:HD12	2.22	0.64
1:B:432:LEU:HD12	1:B:507:MSE:HE2	1.81	0.63
1:B:477:VAL:HG13	1:B:517:PHE:CD2	2.36	0.60
1:A:156:SER:HB3	1:B:479:GLY:HA2	1.82	0.60
1:A:152:ILE:HG21	1:B:480:GLU:HB3	1.84	0.60
1:B:130:ASN:HB3	1:B:133:ASP:CG	2.27	0.60
1:A:28:HIS:ND1	4:A:826:HOH:O	2.33	0.57
1:B:205:LEU:HD13	1:B:348:LEU:HD21	1.86	0.57
1:B:425:VAL:HG11	1:B:455:LEU:HB2	1.86	0.57
1:A:365:LYS:HB2	1:A:368[A]:MSE:SE	2.54	0.57
1:A:27:THR:HG21	1:B:253:LEU:HD23	1.87	0.56
1:B:322:GLY:HA2	4:B:959:HOH:O	2.05	0.56
1:A:130:ASN:HB3	1:A:133:ASP:CG	2.31	0.56
1:B:358:PRO:HB3	1:B:421:LYS:HD2	1.90	0.54
1:A:39:GLY:O	1:A:40:PHE:HB2	2.07	0.54
1:B:38:THR:HG22	1:B:39:GLY:H	1.73	0.54
1:B:420:ARG:HG2	1:B:526:LYS:HG2	1.89	0.54
1:B:425:VAL:HG12	1:B:425:VAL:O	2.07	0.53
1:B:21:ILE:HD11	1:B:241:TRP:CE3	2.44	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:38:THR:HG22	1:A:39:GLY:H	1.74	0.53
1:B:112:ARG:HB3	4:B:979:HOH:O	2.09	0.53
1:A:156:SER:HB2	1:B:479:GLY:HA2	1.92	0.52
1:B:490:GLU:O	1:B:493:ASN:HB2	2.09	0.52
1:B:504:PRO:HB2	1:B:506:TYR:CE1	2.44	0.52
1:B:519:PRO:HB2	1:B:528:ASP:HB3	1.90	0.51
1:B:426:LYS:HA	1:B:430:GLN:O	2.10	0.51
1:A:21:ILE:HD11	1:A:241:TRP:CE3	2.46	0.51
1:B:425:VAL:O	1:B:432:LEU:HB3	2.10	0.51
1:B:492:ASN:ND2	1:B:512:ILE:H	2.09	0.49
1:A:202:TRP:CE2	1:A:348:LEU:HD13	2.48	0.49
1:B:469:PHE:HB3	1:B:515:ILE:HD13	1.94	0.49
1:A:322:GLY:HA2	4:A:829:HOH:O	2.12	0.49
1:A:205:LEU:HD13	1:A:348:LEU:HD21	1.95	0.48
1:B:425:VAL:CG1	1:B:455:LEU:HD22	2.43	0.48
1:B:495:LEU:O	1:B:499:CYS:CB	2.62	0.48
1:B:420:ARG:CG	1:B:526:LYS:HG2	2.43	0.48
1:A:252:ARG:NH2	4:A:909:HOH:O	2.47	0.47
1:A:76:ALA:HB1	1:A:102:VAL:HG21	1.96	0.47
1:B:504:PRO:HB2	1:B:506:TYR:CD1	2.50	0.47
1:A:408:ARG:NH1	4:A:843:HOH:O	2.48	0.46
1:B:412:ASP:O	1:B:413:SER:HB2	2.16	0.46
1:A:148:ASN:OD1	1:A:150:SER:HB3	2.16	0.46
1:A:40:PHE:HA	1:A:261:ARG:NH1	2.30	0.46
1:B:350:ASP:OD1	1:B:350:ASP:C	2.58	0.46
1:B:39:GLY:O	1:B:40:PHE:HB2	2.15	0.46
1:A:130:ASN:HA	4:A:928:HOH:O	2.16	0.45
1:B:355:VAL:HG12	1:B:370:GLY:HA3	1.97	0.45
1:B:492:ASN:OD1	1:B:492:ASN:C	2.59	0.45
1:B:148:ASN:OD1	1:B:150:SER:HB3	2.17	0.45
1:B:503:LEU:HD23	1:B:504:PRO:HD2	1.98	0.45
1:B:154:ASN:O	1:B:157:THR:HB	2.17	0.45
1:B:465:PHE:HB3	1:B:510:ASP:OD2	2.17	0.45
1:B:228:ARG:NH2	4:B:750:HOH:O	2.50	0.44
1:B:40:PHE:HA	1:B:261:ARG:NH1	2.33	0.44
1:B:76:ALA:HB1	1:B:102:VAL:HG21	1.99	0.44
1:B:488:TYR:HB3	1:B:491:ILE:HG23	1.99	0.44
1:B:476:ALA:C	1:B:478:ARG:H	2.25	0.44
1:A:34:VAL:HG23	1:A:85:LEU:HD22	2.00	0.43
1:B:432:LEU:CD1	1:B:507:MSE:HG2	2.46	0.43
1:B:455:LEU:HD12	1:B:465:PHE:O	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:506:TYR:OH	1:B:507:MSE:HE3	2.19	0.43
1:B:495:LEU:O	1:B:499:CYS:HB2	2.19	0.43
1:A:300:LYS:HE2	1:A:342:ARG:HG2	2.01	0.43
1:B:495:LEU:O	1:B:499:CYS:HB3	2.18	0.43
1:B:336:LEU:HB3	1:B:337:PRO:HD2	2.01	0.43
1:B:500:GLU:HG3	1:B:508:VAL:HG11	2.00	0.43
1:B:456:LEU:HD21	1:B:533:GLU:HG2	2.01	0.43
1:A:40:PHE:C	1:A:261:ARG:HH12	2.26	0.42
1:B:264:ARG:HD3	4:B:951:HOH:O	2.18	0.42
1:A:157:THR:HA	1:B:478:ARG:HD3	2.00	0.42
1:A:350:ASP:C	1:A:350:ASP:OD1	2.61	0.42
1:A:410:ASP:HB3	1:A:412:ASP:OD1	2.20	0.42
1:A:73:HIS:CE1	4:A:732:HOH:O	2.73	0.42
1:B:401:TYR:CE2	1:B:403:THR:HA	2.55	0.42
1:B:477:VAL:HG13	1:B:517:PHE:CE2	2.54	0.42
1:A:412:ASP:O	1:A:413:SER:HB2	2.19	0.41
1:B:78:ALA:O	1:B:125:ALA:HA	2.20	0.41
1:A:224:CYS:HB2	1:A:249:THR:HB	2.03	0.41
1:B:500:GLU:HG3	1:B:508:VAL:HG21	2.03	0.41
1:B:127:VAL:HG11	1:B:132:PHE:CD2	2.55	0.41
1:B:490:GLU:O	1:B:493:ASN:N	2.54	0.41
1:B:530:LYS:O	1:B:531:ALA:C	2.63	0.41
1:A:202:TRP:CZ2	1:A:348:LEU:CD1	3.03	0.41
1:B:40:PHE:C	1:B:261:ARG:HH12	2.28	0.41
1:B:279:ASP:OD1	1:B:305:THR:OG1	2.36	0.41
1:B:456:LEU:CD2	1:B:533:GLU:HG2	2.50	0.41
1:B:410:ASP:HB3	1:B:412:ASP:OD1	2.20	0.41
1:B:535:MSE:HE2	1:B:535:MSE:HB3	2.03	0.41
1:B:202:TRP:CE2	1:B:348:LEU:HD13	2.56	0.40
1:A:132:PHE:HA	1:A:135:VAL:HG21	2.04	0.40
1:B:194:ASN:OD1	1:B:380:ALA:HA	2.22	0.40
1:A:112:ARG:HB3	4:A:907:HOH:O	2.21	0.40
1:B:29:PRO:O	1:B:52:THR:HB	2.22	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	397/562 (71%)	388 (98%)	9 (2%)	0	100	100
1	B	491/562 (87%)	464 (94%)	26 (5%)	1 (0%)	43	42
All	All	888/1124 (79%)	852 (96%)	35 (4%)	1 (0%)	48	46

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	477	VAL

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	335/463 (72%)	329 (98%)	6 (2%)	51	58
1	B	423/463 (91%)	416 (98%)	7 (2%)	53	60
All	All	758/926 (82%)	745 (98%)	13 (2%)	53	60

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

Mol	Chain	Res	Type
1	A	38	THR
1	A	150	SER
1	A	153	GLU
1	A	157	THR
1	A	176	LEU

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Mol	Chain	Res	Type
1	A	408	ARG
1	B	38	THR
1	B	150	SER
1	B	153	GLU
1	B	157	THR
1	B	176	LEU
1	B	491	ILE
1	B	500	GLU

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

Mol	Chain	Res	Type
1	A	73	HIS
1	A	290	HIS
1	A	346	HIS
1	A	361	ASN
1	B	19	HIS
1	B	73	HIS
1	B	346	HIS

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 4 ligands modelled in this entry, 2 are 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	$\# Z > 2$
2	SO4	B	558	-	4,4,4	0.34	0	6,6,6	0.77	0
2	SO4	A	558	-	4,4,4	0.26	0	6,6,6	0.71	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, 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	394/562 (70%)	-0.22	10 (2%) 58 58	14, 26, 60, 83	0
1	B	493/562 (87%)	0.17	33 (6%) 24 22	15, 33, 92, 126	0
All	All	887/1124 (78%)	-0.00	43 (4%) 35 34	14, 29, 81, 126	0

All (43) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	180	GLY	4.7
1	B	536	PHE	4.5
1	B	140	GLU	3.6
1	B	425	VAL	3.5
1	B	164	LEU	3.5
1	B	499	CYS	3.3
1	B	12	THR	3.3
1	A	39	GLY	3.3
1	A	164	LEU	3.2
1	B	491	ILE	3.1
1	A	179	SER	3.1
1	B	502	THR	2.9
1	B	166	ASN	2.9
1	B	150	SER	2.9
1	B	465	PHE	2.9
1	B	498	ALA	2.8
1	B	479	GLY	2.7
1	A	38	THR	2.7
1	B	478	ARG	2.6
1	B	511	PHE	2.6
1	B	488	TYR	2.6
1	B	482	ARG	2.5
1	A	14	THR	2.5
1	B	426	LYS	2.4

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Mol	Chain	Res	Type	RSRZ
1	B	505	ALA	2.4
1	B	432	LEU	2.4
1	A	40	PHE	2.4
1	B	534	HIS	2.4
1	A	183	GLY	2.3
1	B	138	PRO	2.3
1	B	136	GLU	2.3
1	B	149	GLN	2.3
1	B	509	PRO	2.3
1	A	150	SER	2.3
1	A	165	ASN	2.3
1	B	183	GLY	2.2
1	B	137	LEU	2.2
1	B	395	ILE	2.2
1	B	411	ALA	2.2
1	B	480	GLU	2.1
1	A	166	ASN	2.1
1	B	506	TYR	2.1
1	B	153	GLU	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, 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(Å ²)	Q<0.9
2	SO4	B	558	5/5	0.93	0.09	30,46,48,54	0
2	SO4	A	558	5/5	0.98	0.05	27,40,46,46	0
3	CL	A	559	1/1	0.99	0.03	24,24,24,24	0
3	CL	B	559	1/1	0.99	0.04	22,22,22,22	0

6.5 Other polymers [i](#)

There are no such residues in this entry.