



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 02:03 PM UTC

PDB ID : 6AA9 / pdb_00006aa9
Title : T166A mutant of D-Serine deaminase from Salmonella typhimurium
Authors : Deka, G.; Bharath, S.R.; Shavithri, H.S.; Murthy, M.R.N.
Deposited on : 2018-07-17
Resolution : 2.70 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

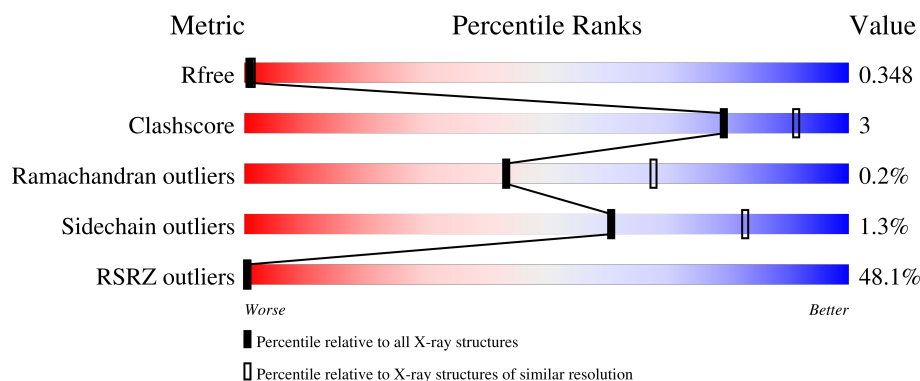
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 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	3538 (2.70-2.70)
Clashscore	190562	3843 (2.70-2.70)
Ramachandran outliers	187476	3778 (2.70-2.70)
Sidechain outliers	187428	3778 (2.70-2.70)
RSRZ outliers	180081	3538 (2.70-2.70)

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	448	45% 87% 6% 7%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 3249 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 D-serine dehydratase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	417	Total	C	N	O	P	S	0	1	0
			3101	1960	531	592	1	17			

There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	166	ALA	THR	engineered mutation	UNP Q8ZL08
A	441	LEU	-	expression tag	UNP Q8ZL08
A	442	GLU	-	expression tag	UNP Q8ZL08
A	443	HIS	-	expression tag	UNP Q8ZL08
A	444	HIS	-	expression tag	UNP Q8ZL08
A	445	HIS	-	expression tag	UNP Q8ZL08
A	446	HIS	-	expression tag	UNP Q8ZL08
A	447	HIS	-	expression tag	UNP Q8ZL08
A	448	HIS	-	expression tag	UNP Q8ZL08

- Molecule 2 is SODIUM ION (CCD ID: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Na	0	0
			1	1		

- Molecule 3 is PHOSPHATE ION (CCD ID: PO4) (formula: O₄P).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	O	P	0	0
			5	4	1		

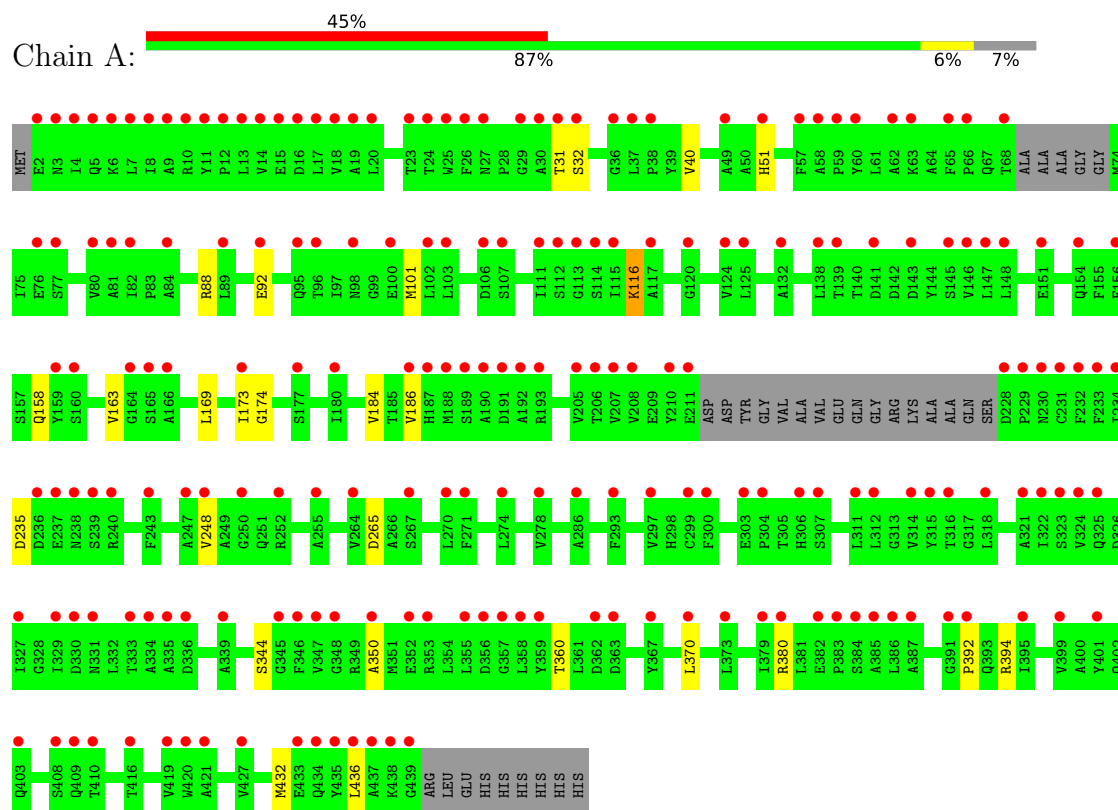
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	142	Total	O	0	0
			142	142		

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: D-serine dehydratase



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	108.31Å 46.14Å 99.28Å 90.00° 100.80° 90.00°	Depositor
Resolution (Å)	53.20 – 2.70 53.20 – 2.70	Depositor EDS
% Data completeness (in resolution range)	99.8 (53.20-2.70) 99.8 (53.20-2.70)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.92 (at 2.69Å)	Xtriage
Refinement program	REFMAC 5.8.0069	Depositor
R, R_{free}	0.289 , 0.349 0.291 , 0.348	Depositor DCC
R_{free} test set	673 reflections (4.97%)	wwPDB-VP
Wilson B-factor (Å ²)	24.7	Xtriage
Anisotropy	0.578	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 36.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.75	EDS
Total number of atoms	3249	wwPDB-VP
Average B, all atoms (Å ²)	19.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.66% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: NA, PO4, LLP

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	0.40	0/3144	0.70	0/4266

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	3101	0	2931	16	0
2	A	1	0	0	0	0
3	A	5	0	0	0	0
4	A	142	0	0	0	0
All	All	3249	0	2931	16	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 (16) 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:116:LLP:HE3	1:A:116:LLP:O3	2.01	0.60
1:A:116:LLP:OP4	1:A:116:LLP:H4'1	2.03	0.58
1:A:116:LLP:H4'1	1:A:116:LLP:P	2.52	0.50
1:A:380:ARG:HB2	1:A:432:MET:HE2	1.94	0.49
1:A:88:ARG:NH1	1:A:92:GLU:OE2	2.47	0.48
1:A:370:LEU:HD21	1:A:432:MET:HE1	1.96	0.48
1:A:51[B]:HIS:CD2	1:A:248:VAL:HG13	2.49	0.47
1:A:163:VAL:HG13	1:A:186:VAL:HG13	1.96	0.47
1:A:360:THR:O	1:A:394:ARG:NH1	2.50	0.44
1:A:101:MET:HE3	1:A:392:PRO:HG2	2.00	0.43
1:A:370:LEU:HD23	1:A:370:LEU:C	2.44	0.41
1:A:40:VAL:HA	1:A:350:ALA:HB1	2.02	0.41
1:A:174:GLY:HA2	1:A:184:VAL:HG11	2.01	0.41
1:A:116:LLP:HG3	1:A:169:LEU:HA	2.03	0.41
1:A:31:THR:OG1	1:A:32:SER:N	2.53	0.41
1:A:432:MET:HE3	1:A:436:LEU:HG	2.03	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	411/448 (92%)	395 (96%)	15 (4%)	1 (0%)	43 68

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	235	ASP

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	300/346 (87%)	296 (99%)	4 (1%)	61 83

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	158	GLN
1	A	173	ILE
1	A	265	ASP
1	A	344	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	203	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

1 non-standard protein/DNA/RNA residue is 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
1	LLP	A	116	1	23,24,25	2.43	3 (13%)	25,32,34	2.07	7 (28%)

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
1	LLP	A	116	1	-	7/16/17/19	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	116	LLP	C3-C2	7.74	1.49	1.41
1	A	116	LLP	C4-C5	6.05	1.50	1.42
1	A	116	LLP	C4-C3	5.35	1.49	1.41

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	116	LLP	C3-C4-C5	-4.61	114.57	118.28
1	A	116	LLP	C3-C4-C4'	4.35	128.25	120.40
1	A	116	LLP	CE-NZ-C4'	3.76	130.75	118.72
1	A	116	LLP	CD-CE-NZ	-3.36	101.94	110.83
1	A	116	LLP	C5-C4-C4'	-2.78	117.18	121.47
1	A	116	LLP	C4-C3-C2	-2.57	118.69	120.14
1	A	116	LLP	OP4-C5'-C5	2.23	113.54	109.36

There are no chirality outliers.

All (7) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	116	LLP	C4-C4'-NZ-CE
1	A	116	LLP	C4-C5-C5'-OP4
1	A	116	LLP	C6-C5-C5'-OP4
1	A	116	LLP	C-CA-CB-CG
1	A	116	LLP	CG-CD-CE-NZ
1	A	116	LLP	CE-CD-CG-CB

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Mol	Chain	Res	Type	Atoms
1	A	116	LLP	CD-CE-NZ-C4'

There are no ring outliers.

1 monomer is involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	116	LLP	4	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 2 ligands modelled in this entry, 1 is monoatomic - leaving 1 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	PO4	A	502	-	4,4,4	0.95	0	6,6,6	0.47	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 ⓘ

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	416/448 (92%)	2.07	200 (48%) 0 0	7, 18, 31, 55	1 (0%)

All (200) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	439	GLY	6.3
1	A	3	ASN	6.1
1	A	2	GLU	5.5
1	A	11	TYR	4.9
1	A	10	ARG	4.8
1	A	385	ALA	4.8
1	A	318	LEU	4.7
1	A	335	ALA	4.6
1	A	345	GLY	4.6
1	A	12	PRO	4.6
1	A	323	SER	4.6
1	A	362	ASP	4.5
1	A	395	ILE	4.4
1	A	18	VAL	4.4
1	A	4	ILE	4.2
1	A	5	GLN	4.1
1	A	9	ALA	4.0
1	A	333	THR	3.9
1	A	437	ALA	3.9
1	A	145	SER	3.9
1	A	346	PHE	3.8
1	A	350	ALA	3.8
1	A	36	GLY	3.8
1	A	228	ASP	3.8
1	A	231	CYS	3.8
1	A	188	MET	3.8
1	A	6	LYS	3.7

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Mol	Chain	Res	Type	RSRZ
1	A	367	TYR	3.7
1	A	336	ASP	3.7
1	A	8	ILE	3.7
1	A	19	ALA	3.6
1	A	327	ILE	3.5
1	A	165	SER	3.5
1	A	24	THR	3.5
1	A	62	ALA	3.4
1	A	7	LEU	3.4
1	A	236	ASP	3.4
1	A	322	ILE	3.3
1	A	421	ALA	3.3
1	A	347	VAL	3.3
1	A	234	ILE	3.3
1	A	143	ASP	3.3
1	A	438	LYS	3.2
1	A	348	GLY	3.2
1	A	409	GLN	3.2
1	A	207	VAL	3.2
1	A	239	SER	3.2
1	A	250	GLY	3.2
1	A	410	THR	3.2
1	A	358	LEU	3.1
1	A	187	HIS	3.1
1	A	233	PHE	3.1
1	A	324	VAL	3.1
1	A	208	VAL	3.1
1	A	58	ALA	3.1
1	A	148	LEU	3.0
1	A	15	GLU	3.0
1	A	59	PRO	3.0
1	A	160	SER	3.0
1	A	356	ASP	3.0
1	A	434	GLN	3.0
1	A	180	ILE	3.0
1	A	314	VAL	3.0
1	A	427	VAL	3.0
1	A	274	LEU	2.9
1	A	339	ALA	2.9
1	A	124	VAL	2.9
1	A	17	LEU	2.9
1	A	16	ASP	2.9

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Mol	Chain	Res	Type	RSRZ
1	A	331	ASN	2.9
1	A	141	ASP	2.9
1	A	173	ILE	2.9
1	A	193	ARG	2.8
1	A	330	ASP	2.8
1	A	166	ALA	2.8
1	A	297	VAL	2.8
1	A	300	PHE	2.8
1	A	359	TYR	2.8
1	A	26	PHE	2.8
1	A	186	VAL	2.8
1	A	103	LEU	2.7
1	A	312	LEU	2.7
1	A	29	GLY	2.7
1	A	81	ALA	2.7
1	A	66	PRO	2.7
1	A	25	TRP	2.7
1	A	107	SER	2.7
1	A	303	GLU	2.7
1	A	264	VAL	2.7
1	A	435	TYR	2.7
1	A	211	GLU	2.7
1	A	325	GLN	2.7
1	A	30	ALA	2.7
1	A	84	ALA	2.7
1	A	146	VAL	2.7
1	A	370	LEU	2.6
1	A	384	SER	2.6
1	A	387	ALA	2.6
1	A	210	TYR	2.6
1	A	382	GLU	2.6
1	A	403	GLN	2.6
1	A	205	VAL	2.6
1	A	307	SER	2.6
1	A	82	ILE	2.5
1	A	237	GLU	2.5
1	A	286	ALA	2.5
1	A	299	CYS	2.5
1	A	206	THR	2.5
1	A	60	TYR	2.5
1	A	401	TYR	2.5
1	A	229	PRO	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	68	THR	2.5
1	A	111	ILE	2.5
1	A	51[A]	HIS	2.5
1	A	248	VAL	2.5
1	A	156	PHE	2.5
1	A	102	LEU	2.5
1	A	379	ILE	2.5
1	A	192	ALA	2.5
1	A	321	ALA	2.4
1	A	23	THR	2.4
1	A	96	THR	2.4
1	A	306	HIS	2.4
1	A	304	PRO	2.4
1	A	267	SER	2.4
1	A	278	VAL	2.4
1	A	138	LEU	2.4
1	A	139	THR	2.4
1	A	77	SER	2.4
1	A	399	VAL	2.4
1	A	419	VAL	2.4
1	A	132	ALA	2.4
1	A	355	LEU	2.3
1	A	386	LEU	2.3
1	A	436	LEU	2.3
1	A	98	ASN	2.3
1	A	191	ASP	2.3
1	A	120	GLY	2.3
1	A	232	PHE	2.3
1	A	315	TYR	2.3
1	A	95	GLN	2.3
1	A	92	GLU	2.3
1	A	32	SER	2.3
1	A	408	SER	2.3
1	A	38	PRO	2.3
1	A	106	ASP	2.3
1	A	113	GLY	2.3
1	A	255	ALA	2.3
1	A	189	SER	2.3
1	A	311	LEU	2.3
1	A	243	PHE	2.3
1	A	117	ALA	2.2
1	A	63	LYS	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	100	GLU	2.2
1	A	27	ASN	2.2
1	A	363	ASP	2.2
1	A	20	LEU	2.2
1	A	240	ARG	2.2
1	A	357	GLY	2.2
1	A	391	GLY	2.2
1	A	420	TRP	2.2
1	A	57	PHE	2.2
1	A	230	ASN	2.2
1	A	13	LEU	2.2
1	A	334	ALA	2.2
1	A	352	GLU	2.2
1	A	31	THR	2.2
1	A	316	THR	2.2
1	A	252	ARG	2.2
1	A	380	ARG	2.2
1	A	159	TYR	2.2
1	A	114	SER	2.2
1	A	49	ALA	2.1
1	A	190	ALA	2.1
1	A	270	LEU	2.1
1	A	14	VAL	2.1
1	A	177	SER	2.1
1	A	89	LEU	2.1
1	A	164	GLY	2.1
1	A	247	ALA	2.1
1	A	76	GLU	2.1
1	A	151	GLU	2.1
1	A	383	PRO	2.1
1	A	154	GLN	2.1
1	A	37	LEU	2.1
1	A	147	LEU	2.1
1	A	115	ILE	2.1
1	A	329	ILE	2.1
1	A	65	PHE	2.1
1	A	271	PHE	2.1
1	A	112	SER	2.1
1	A	373	LEU	2.1
1	A	293	PHE	2.1
1	A	353	ARG	2.0
1	A	433	GLU	2.0

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Mol	Chain	Res	Type	RSRZ
1	A	392	PRO	2.0
1	A	125	LEU	2.0
1	A	416	THR	2.0
1	A	238	ASN	2.0
1	A	80	VAL	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [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
1	LLP	A	116	24/25	0.82	0.21	18,20,21,21	0

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
3	PO4	A	502	5/5	0.66	0.20	47,47,47,48	0
2	NA	A	501	1/1	0.92	0.16	18,18,18,18	0

6.5 Other polymers [i](#)

There are no such residues in this entry.