



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 10, 2026 – 12:45 PM UTC

PDB ID : 7MO6 / pdb_00007mo6
Title : Guanosine Monophosphate Synthase from *Aspergillus fumigatus* Af293
Authors : Nguyen, S.; Bruning, J.B.
Deposited on : 2021-05-01
Resolution : 2.30 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
Xtrriage (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

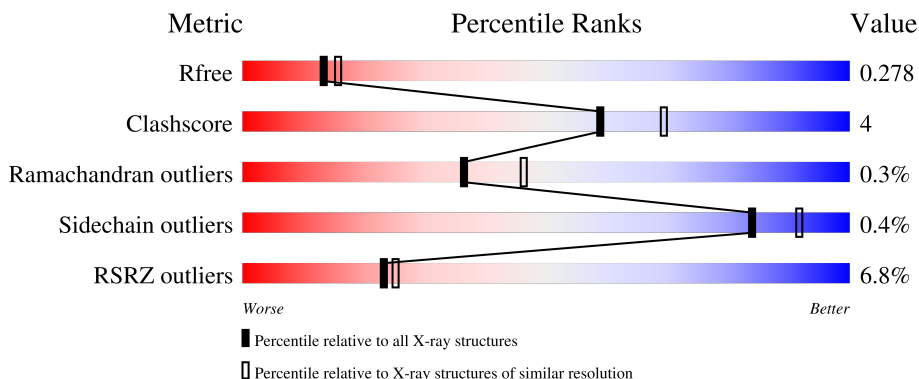
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION


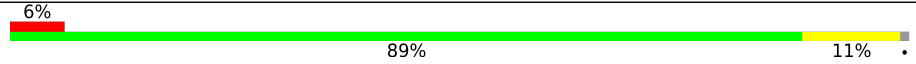
The reported resolution of this entry is 2.30 Å.

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	6319 (2.30-2.30)
Clashscore	190562	6919 (2.30-2.30)
Ramachandran outliers	187476	6854 (2.30-2.30)
Sidechain outliers	187428	6854 (2.30-2.30)
RSRZ outliers	180081	6325 (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 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	540	
1	B	540	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 8209 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 GMP synthase [glutamine-hydrolyzing].

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	518	3861	2462	666	716	17	0	0	0
1	B	535	3983	2529	684	751	19	0	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	GLY	-	expression tag	UNP A0A229XUE6
B	1	GLY	-	expression tag	UNP A0A229XUE6

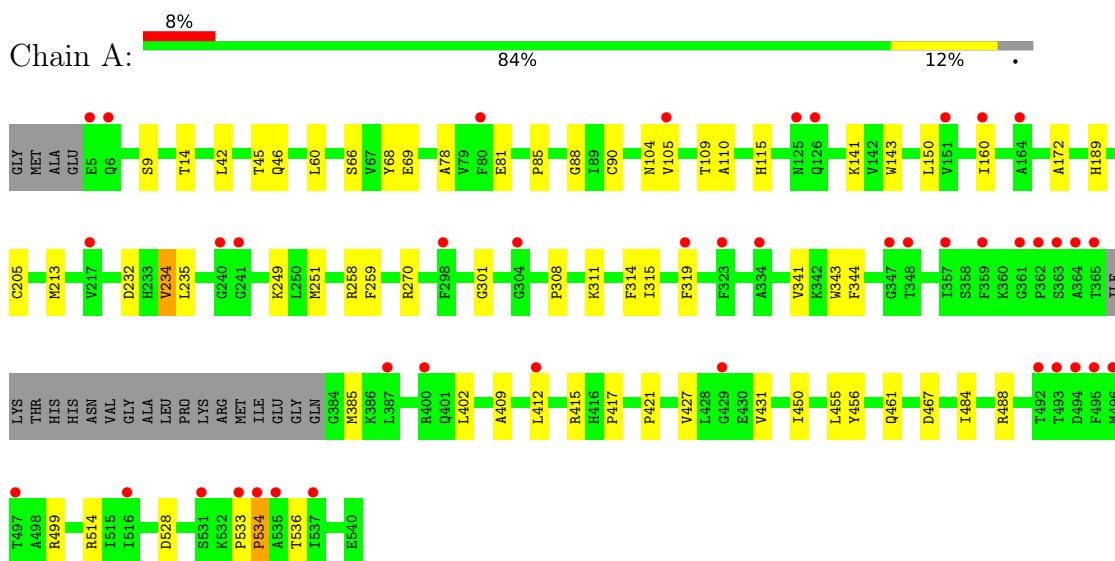
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	187	Total	O	0	0
			187	187		
2	B	178	Total	O	0	0
			178	178		

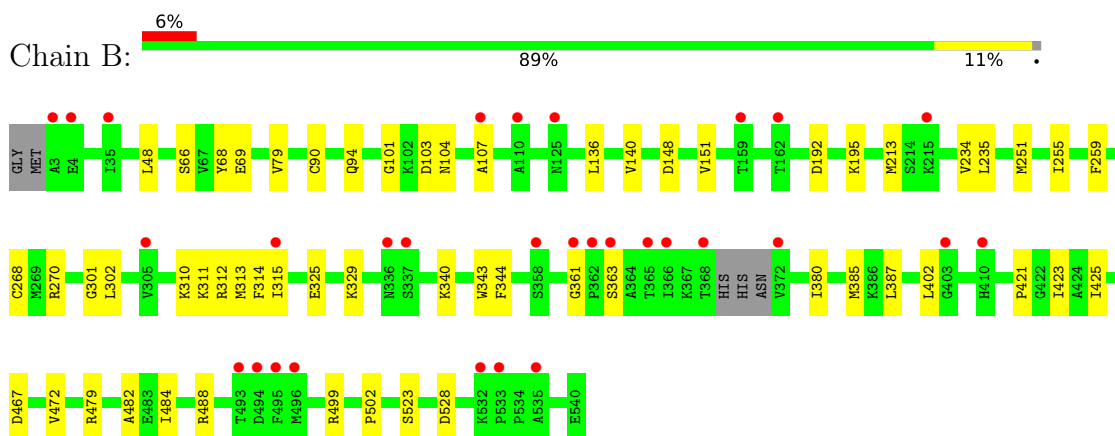
3 Residue-property plots [i](#)

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: GMP synthase [glutamine-hydrolyzing]



- Molecule 1: GMP synthase [glutamine-hydrolyzing]



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	47.30Å 159.76Å 76.17Å 90.00° 108.00° 90.00°	Depositor
Resolution (Å)	39.94 – 2.30 39.94 – 2.30	Depositor EDS
% Data completeness (in resolution range)	99.0 (39.94-2.30) 98.9 (39.94-2.30)	Depositor EDS
R_{merge}	0.21	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.43 (at 2.29Å)	Xtrriage
Refinement program	PHENIX 1.16-3549	Depositor
R, R_{free}	0.230 , 0.277 0.231 , 0.278	Depositor DCC
R_{free} test set	2015 reflections (4.23%)	wwPDB-VP
Wilson B-factor (Å ²)	44.7	Xtrriage
Anisotropy	0.583	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 37.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtrriage
Estimated twinning fraction	0.086 for h,-k,-h-l	Xtrriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	8209	wwPDB-VP
Average B, all atoms (Å ²)	59.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.45% 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](#)

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	0.09	0/3943	0.26	0/5363
1	B	0.09	0/4065	0.26	0/5533
All	All	0.09	0/8008	0.26	0/10896

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 [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	3861	0	3708	35	0
1	B	3983	0	3801	33	0
2	A	187	0	0	4	0
2	B	178	0	0	2	0
All	All	8209	0	7509	68	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 4.

All (68) 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:467:ASP:HB3	1:A:484:ILE:HB	1.72	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:234:VAL:HG21	1:A:251:MET:HE2	1.72	0.70
1:A:417:PRO:O	1:A:461:GLN:NE2	2.30	0.65
1:B:234:VAL:HG22	1:B:343:TRP:HB2	1.80	0.63
1:B:467:ASP:HB3	1:B:484:ILE:HB	1.83	0.60
1:B:421:PRO:HB2	1:B:425:ILE:HG12	1.84	0.59
1:A:160:ILE:HD13	1:A:172:ALA:HB2	1.86	0.58
1:A:143:TRP:HB2	1:A:189:HIS:HB2	1.85	0.57
1:B:312:ARG:HD3	1:B:425:ILE:HD11	1.87	0.57
1:A:514:ARG:NH1	2:A:603:HOH:O	2.37	0.57
1:B:48:LEU:HD11	1:B:79:VAL:HG22	1.86	0.57
1:B:66:SER:HB3	1:B:69:GLU:HG3	1.85	0.57
1:A:213:MET:HE2	1:A:402:LEU:HB2	1.89	0.55
1:A:9:SER:HA	1:A:14:THR:HG21	1.87	0.55
1:B:302:LEU:HD21	1:B:315:ILE:HD11	1.88	0.55
1:B:310:LYS:HA	1:B:313:MET:HE2	1.88	0.55
1:A:249:LYS:NZ	2:A:605:HOH:O	2.38	0.55
1:B:344:PHE:HB2	1:B:385:MET:HE2	1.90	0.54
1:A:409:ALA:HB3	1:A:412:LEU:HG	1.90	0.54
1:A:344:PHE:HB2	1:A:385:MET:HE3	1.88	0.54
1:A:115:HIS:HB3	1:A:141:LYS:HE3	1.91	0.53
1:A:235:LEU:HB2	1:A:341:VAL:HG11	1.91	0.53
1:A:488:ARG:NH2	1:A:536:THR:O	2.40	0.52
1:B:380:ILE:HD11	1:B:387:LEU:HG	1.91	0.52
1:A:270:ARG:NH2	2:A:611:HOH:O	2.42	0.52
1:B:255:ILE:HD11	1:B:259:PHE:HB2	1.92	0.51
1:A:66:SER:HB3	1:A:69:GLU:HG3	1.92	0.51
1:B:270:ARG:NH1	2:B:609:HOH:O	2.43	0.51
1:B:213:MET:HE2	1:B:402:LEU:HB2	1.91	0.50
1:B:107:ALA:HB2	1:B:151:VAL:HG13	1.94	0.49
1:A:234:VAL:HG23	1:A:259:PHE:HD1	1.78	0.49
1:A:427:VAL:HB	1:A:431:VAL:HG22	1.96	0.47
1:B:361:GLY:O	1:B:363:SER:N	2.44	0.47
1:A:78:ALA:HA	1:A:81:GLU:HG2	1.95	0.47
1:A:232:ASP:O	1:A:258:ARG:NH1	2.46	0.47
1:B:325:GLU:O	1:B:329:LYS:HD3	2.15	0.47
1:A:109:THR:OG1	1:A:110:ALA:N	2.48	0.46
1:A:308:PRO:HA	1:A:311:LYS:HD3	1.98	0.46
1:A:533:PRO:HB2	1:A:534:PRO:HD3	1.97	0.46
1:B:235:LEU:HB3	1:B:385:MET:HE1	1.96	0.46
1:B:94:GLN:NE2	1:B:148:ASP:OD1	2.49	0.46
1:A:234:VAL:HG12	1:A:343:TRP:HB2	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:488:ARG:HD3	1:A:528:ASP:HB3	1.98	0.46
1:B:311:LYS:O	1:B:315:ILE:HG12	2.16	0.46
1:B:315:ILE:HG21	1:B:421:PRO:HG3	1.97	0.46
1:B:340:LYS:HD2	2:B:645:HOH:O	2.17	0.45
1:B:234:VAL:HG11	1:B:251:MET:HE2	1.97	0.45
1:A:499:ARG:NH2	2:A:615:HOH:O	2.50	0.44
1:A:105:VAL:HG23	1:A:150:LEU:HD22	1.99	0.44
1:B:301:GLY:HA3	1:B:314:PHE:CZ	2.53	0.44
1:B:472:VAL:HG21	1:B:479:ARG:NH1	2.33	0.44
1:A:450:ILE:HG23	1:A:455:LEU:HB2	2.00	0.44
1:B:488:ARG:HD3	1:B:528:ASP:HB3	1.99	0.43
1:B:136:LEU:HB3	1:B:140:VAL:HG21	2.00	0.43
1:A:415:ARG:HA	1:A:456:TYR:HE2	1.84	0.42
1:A:301:GLY:HA3	1:A:314:PHE:CZ	2.55	0.42
1:B:482:ALA:HB3	1:B:523:SER:HB3	2.02	0.42
1:B:136:LEU:HD22	1:B:192:ASP:HB3	2.02	0.41
1:A:42:LEU:HB3	1:A:46:GLN:HG3	2.03	0.41
1:B:499:ARG:HH12	1:B:502:PRO:HB3	1.85	0.41
1:A:68:TYR:CE2	1:A:104:ASN:HA	2.55	0.41
1:B:268:CYS:O	1:B:423:ILE:HG12	2.21	0.41
1:B:101:GLY:C	1:B:103:ASP:H	2.29	0.41
1:B:136:LEU:HD21	1:B:195:LYS:HB2	2.02	0.40
1:B:68:TYR:CE2	1:B:104:ASN:HA	2.57	0.40
1:A:60:LEU:HB2	1:A:88:GLY:HA2	2.04	0.40
1:A:85:PRO:HG2	1:A:205:CYS:HA	2.04	0.40
1:A:315:ILE:HD13	1:A:421:PRO:HB3	2.02	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	514/540 (95%)	498 (97%)	14 (3%)	2 (0%)	30	38
1	B	531/540 (98%)	512 (96%)	18 (3%)	1 (0%)	43	55
All	All	1045/1080 (97%)	1010 (97%)	32 (3%)	3 (0%)	36	46

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	534	PRO
1	A	90	CYS
1	B	90	CYS

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	382/446 (86%)	379 (99%)	3 (1%)	73	86
1	B	395/446 (89%)	395 (100%)	0	100	100
All	All	777/892 (87%)	774 (100%)	3 (0%)	84	92

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	45	THR
1	A	234	VAL
1	A	319	PHE

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	128	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](#)

There are no ligands in this entry.

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	518/540 (95%)	0.85	42 (8%) 18 19	40, 58, 88, 129	0
1	B	535/540 (99%)	0.76	30 (5%) 30 32	33, 56, 89, 128	0
All	All	1053/1080 (97%)	0.80	72 (6%) 23 25	33, 57, 88, 129	0

All (72) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	494	ASP	4.8
1	A	363	SER	4.7
1	A	533	PRO	4.1
1	B	363	SER	4.1
1	B	336	ASN	3.8
1	A	365	THR	3.7
1	A	497	THR	3.6
1	B	532	LYS	3.4
1	A	125	ASN	3.4
1	B	494	ASP	3.4
1	A	364	ALA	3.2
1	A	319	PHE	3.2
1	A	496	MET	3.2
1	A	516	ILE	3.1
1	B	125	ASN	3.1
1	B	372	VAL	3.1
1	A	298	PHE	3.0
1	B	533	PRO	3.0
1	B	368	THR	2.9
1	B	361	GLY	2.8
1	A	164	ALA	2.8
1	B	496	MET	2.8
1	B	107	ALA	2.8
1	B	535	ALA	2.8

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Mol	Chain	Res	Type	RSRZ
1	A	429	GLY	2.8
1	A	334	ALA	2.8
1	B	3	ALA	2.8
1	A	323	PHE	2.8
1	A	362	PRO	2.7
1	A	387	LEU	2.7
1	A	6	GLN	2.7
1	B	493	THR	2.7
1	B	362	PRO	2.6
1	A	495	PHE	2.6
1	A	240	GLY	2.6
1	A	537	ILE	2.6
1	A	531	SER	2.5
1	A	5	GLU	2.5
1	A	126	GLN	2.5
1	A	359	PHE	2.5
1	B	315	ILE	2.5
1	B	110	ALA	2.5
1	A	493	THR	2.4
1	A	347	GLY	2.4
1	B	366	ILE	2.4
1	A	412	LEU	2.4
1	A	534	PRO	2.4
1	B	365	THR	2.4
1	B	162	THR	2.4
1	B	4	GLU	2.4
1	A	304	GLY	2.3
1	A	357	ILE	2.3
1	A	217	VAL	2.3
1	A	361	GLY	2.2
1	A	535	ALA	2.2
1	B	358	SER	2.2
1	A	160	ILE	2.2
1	B	305	VAL	2.2
1	A	80	PHE	2.2
1	A	241	GLY	2.2
1	A	492	THR	2.2
1	A	105	VAL	2.1
1	B	410	HIS	2.1
1	B	495	PHE	2.1
1	B	403	GLY	2.1
1	B	337	SER	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	348	THR	2.0
1	B	35	ILE	2.0
1	A	151	VAL	2.0
1	B	215	LYS	2.0
1	B	159	THR	2.0
1	A	400	ARG	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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.