



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 03:08 PM UTC

PDB ID : 4GMO / pdb_00004gmo
Title : Crystal structure of Syo1
Authors : Bange, G.; Sinning, I.
Deposited on : 2012-08-16
Resolution : 2.10 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
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

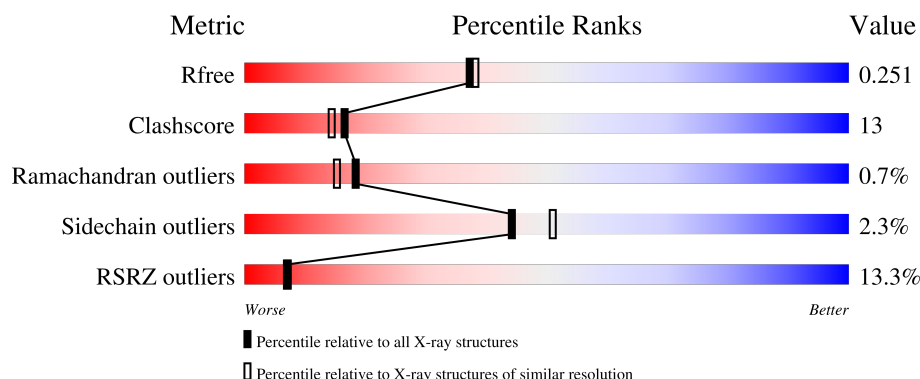
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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	6658 (2.10-2.10)
Clashscore	190562	7164 (2.10-2.10)
Ramachandran outliers	187476	7099 (2.10-2.10)
Sidechain outliers	187428	7100 (2.10-2.10)
RSRZ outliers	180081	6662 (2.10-2.10)

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	684	11% 62% 17% • 19%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 4548 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 Putative uncharacterized protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	556	Total	C	N	O	S	0	0	0
			4327	2756	745	815	11			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	677	GLY	-	expression tag	UNP G0S5S6
A	678	SER	-	expression tag	UNP G0S5S6
A	679	HIS	-	expression tag	UNP G0S5S6
A	680	HIS	-	expression tag	UNP G0S5S6
A	681	HIS	-	expression tag	UNP G0S5S6
A	682	HIS	-	expression tag	UNP G0S5S6
A	683	HIS	-	expression tag	UNP G0S5S6
A	684	HIS	-	expression tag	UNP G0S5S6

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	221	Total	O	0	0
			221	221		

- Molecule 1: Putative uncharacterized protein



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	166.43Å 59.73Å 69.55Å 90.00° 97.71° 90.00°	Depositor
Resolution (Å)	40.45 – 2.10 40.45 – 2.10	Depositor EDS
% Data completeness (in resolution range)	99.8 (40.45-2.10) 99.6 (40.45-2.10)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.39 (at 2.10Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.6.4_486)	Depositor
R, R_{free}	0.219 , 0.256 0.219 , 0.251	Depositor DCC
R_{free} test set	1994 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å ²)	34.4	Xtriage
Anisotropy	0.390	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 42.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	4548	wwPDB-VP
Average B, all atoms (Å ²)	41.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.73% 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	0.67	4/4404 (0.1%)	0.92	11/5991 (0.2%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	303	ASN	N-CA	6.80	1.54	1.46
1	A	487	PRO	C-O	-6.25	1.16	1.24
1	A	46	PRO	N-CD	5.20	1.55	1.47
1	A	45	SER	C-N	5.14	1.41	1.34

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	301	TYR	N-CA-C	-14.82	93.56	112.23
1	A	49	LYS	N-CA-C	-10.21	100.11	111.14
1	A	47	ASP	CA-C-N	6.16	132.78	121.70
1	A	47	ASP	C-N-CA	6.16	132.78	121.70
1	A	33	GLU	N-CA-C	5.97	117.87	111.36
1	A	303	ASN	CA-C-N	5.71	128.53	120.42
1	A	303	ASN	C-N-CA	5.71	128.53	120.42
1	A	50	SER	N-CA-C	-5.63	105.51	112.38
1	A	45	SER	CA-C-N	-5.53	112.92	119.05
1	A	45	SER	C-N-CA	-5.53	112.92	119.05
1	A	490	GLU	N-CA-C	-5.34	101.28	109.76

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	4327	0	4421	113	1
2	A	221	0	0	6	0
All	All	4548	0	4421	113	1

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 13.

All (113) 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:62:VAL:HG11	1:A:102:VAL:HG12	1.25	1.10
1:A:108:GLU:HG3	1:A:110:ASP:OD1	1.52	1.09
1:A:261:GLN:HG3	1:A:263:MET:HE2	1.39	1.04
1:A:89:ASN:HD21	1:A:91:ASP:HB2	1.18	1.02
1:A:62:VAL:CG1	1:A:102:VAL:HG12	1.93	0.98
1:A:62:VAL:HG11	1:A:102:VAL:CG1	1.98	0.93
1:A:300:ARG:O	1:A:303:ASN:HB2	1.68	0.91
1:A:57:ALA:O	1:A:61:ILE:HG13	1.74	0.88
1:A:617:ASP:HB3	2:A:784:HOH:O	1.75	0.85
1:A:141:PRO:HG2	1:A:144:LYS:HD3	1.59	0.84
1:A:261:GLN:HG3	1:A:263:MET:CE	2.10	0.81
1:A:89:ASN:ND2	1:A:91:ASP:HB2	1.95	0.80
1:A:58:ILE:O	1:A:62:VAL:HB	1.81	0.78
1:A:551:PRO:N	2:A:862:HOH:O	2.15	0.78
1:A:47:ASP:HA	1:A:48:ALA:CB	2.17	0.75
1:A:206:ILE:HG21	1:A:248:MET:HB3	1.70	0.72
1:A:263:MET:HE3	1:A:265:HIS:CE1	2.24	0.71
1:A:563:VAL:HG13	1:A:579:VAL:HG13	1.71	0.71
1:A:301:TYR:C	1:A:303:ASN:N	2.48	0.71
1:A:301:TYR:C	1:A:303:ASN:H	2.00	0.70
1:A:62:VAL:CG1	1:A:102:VAL:CG1	2.63	0.70
1:A:263:MET:HE3	1:A:265:HIS:HE1	1.57	0.70
1:A:50:SER:HA	1:A:53:THR:OG1	1.92	0.69
1:A:47:ASP:HA	1:A:48:ALA:HB2	1.73	0.69
1:A:108:GLU:HG2	2:A:911:HOH:O	1.91	0.69
1:A:485:ILE:O	1:A:489:LEU:HG	1.94	0.67
1:A:121:LEU:HB3	1:A:181:LYS:HZ2	1.61	0.65
1:A:282:THR:HG21	1:A:420:THR:HG22	1.77	0.65
1:A:65:ALA:O	1:A:69:LYS:HG2	1.96	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:433:ILE:HD12	1:A:439:LEU:HD13	1.80	0.64
1:A:44:LYS:O	1:A:45:SER:HB3	1.97	0.64
1:A:481:TRP:HA	1:A:485:ILE:HD12	1.81	0.63
1:A:141:PRO:HG2	1:A:144:LYS:CD	2.26	0.62
1:A:52:THR:HA	1:A:95:ALA:HB2	1.80	0.62
1:A:145:LEU:HD11	2:A:732:HOH:O	2.00	0.61
1:A:657:ASP:OD1	1:A:658:GLU:N	2.33	0.61
1:A:300:ARG:C	1:A:303:ASN:H	2.09	0.60
1:A:29:ALA:O	1:A:33:GLU:HG3	2.01	0.59
1:A:61:ILE:HG22	1:A:67:CYS:HB3	1.84	0.59
1:A:71:LEU:O	1:A:76:VAL:HG23	2.03	0.59
1:A:490:GLU:O	1:A:491:ALA:CB	2.51	0.58
1:A:487:PRO:O	1:A:490:GLU:O	2.21	0.58
1:A:254:HIS:HE1	1:A:314:SER:OG	1.85	0.58
1:A:654:THR:O	1:A:657:ASP:OD1	2.21	0.58
1:A:264:ASP:CG	1:A:412:PRO:HD2	2.27	0.58
1:A:57:ALA:C	1:A:61:ILE:HG13	2.30	0.57
1:A:71:LEU:HD22	1:A:76:VAL:HG21	1.86	0.57
1:A:479:LYS:HE3	1:A:483:LYS:HG3	1.87	0.57
1:A:524:HIS:HE1	1:A:578:GLU:OE1	1.89	0.56
1:A:47:ASP:CA	1:A:48:ALA:CB	2.84	0.55
1:A:57:ALA:O	1:A:61:ILE:CG1	2.53	0.55
1:A:54:ALA:O	1:A:58:ILE:HG13	2.07	0.55
1:A:121:LEU:HB3	1:A:181:LYS:NZ	2.21	0.54
1:A:300:ARG:HD3	1:A:303:ASN:ND2	2.22	0.54
1:A:474:TYR:HB3	1:A:475:PRO:HD3	1.89	0.54
1:A:254:HIS:HD2	1:A:274:ASP:OD1	1.91	0.53
1:A:196:ILE:C	1:A:196:ILE:HD12	2.33	0.53
1:A:118:LEU:O	1:A:119:ASP:HB3	2.08	0.53
1:A:262:TRP:CD2	1:A:268:GLY:HA3	2.43	0.53
1:A:295:PHE:HB2	1:A:298:ASP:CB	2.40	0.52
1:A:300:ARG:O	1:A:303:ASN:CB	2.51	0.52
1:A:264:ASP:OD2	1:A:412:PRO:HD2	2.11	0.51
1:A:301:TYR:O	1:A:302:ALA:C	2.49	0.51
1:A:644:ILE:HD13	1:A:652:LEU:HG	1.93	0.51
1:A:490:GLU:O	1:A:491:ALA:HB3	2.10	0.50
1:A:640:LEU:C	1:A:640:LEU:HD12	2.37	0.50
1:A:273:CYS:O	1:A:276:ILE:HG12	2.12	0.50
1:A:37:LEU:N	1:A:38:PRO:CD	2.74	0.49
1:A:301:TYR:O	1:A:303:ASN:N	2.44	0.49
1:A:194:ALA:O	1:A:196:ILE:HG23	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:32:ARG:O	1:A:37:LEU:HG	2.13	0.48
1:A:289:VAL:HB	1:A:290:PRO:HD2	1.94	0.48
1:A:628:LYS:O	1:A:632:GLU:HG3	2.13	0.48
1:A:664:GLY:O	1:A:668:GLN:HG2	2.13	0.48
1:A:657:ASP:OD1	2:A:824:HOH:O	2.19	0.48
1:A:486:LEU:HD12	1:A:489:LEU:HD12	1.96	0.47
1:A:36:ILE:O	1:A:40:LEU:HG	2.15	0.47
1:A:300:ARG:HB3	1:A:303:ASN:HB2	1.95	0.47
1:A:500:THR:HA	1:A:555:LEU:HD13	1.97	0.47
1:A:577:ARG:O	1:A:581:VAL:HG23	2.15	0.47
1:A:170:ALA:C	1:A:171:ARG:HG2	2.40	0.47
1:A:247:VAL:HG21	1:A:304:ILE:HG23	1.97	0.47
1:A:108:GLU:CG	1:A:110:ASP:OD1	2.43	0.46
1:A:50:SER:CA	1:A:53:THR:OG1	2.62	0.46
1:A:622:TRP:CE2	1:A:675:PRO:HD3	2.51	0.46
1:A:64:ASP:HB3	1:A:67:CYS:HB2	1.99	0.45
1:A:646:LYS:HG2	1:A:653:ARG:HG2	1.99	0.44
1:A:461:PHE:CD1	1:A:470:HIS:HB2	2.53	0.44
1:A:233:ASP:O	1:A:237:LYS:HG3	2.18	0.44
1:A:637:MET:SD	1:A:640:LEU:HD21	2.58	0.43
1:A:37:LEU:HB2	1:A:38:PRO:HD3	2.00	0.43
1:A:47:ASP:CA	1:A:48:ALA:HB3	2.49	0.43
1:A:190:ARG:HE	1:A:190:ARG:HB2	1.71	0.43
1:A:190:ARG:HD2	2:A:857:HOH:O	2.19	0.42
1:A:52:THR:HA	1:A:95:ALA:CB	2.47	0.42
1:A:528:ILE:O	1:A:531:TYR:HB3	2.20	0.42
1:A:137:THR:O	1:A:141:PRO:HA	2.19	0.42
1:A:486:LEU:HA	1:A:489:LEU:HD12	2.01	0.42
1:A:47:ASP:CB	1:A:48:ALA:HB3	2.51	0.41
1:A:474:TYR:HB3	1:A:475:PRO:CD	2.50	0.41
1:A:486:LEU:N	1:A:487:PRO:CD	2.83	0.41
1:A:559:CYS:O	1:A:563:VAL:HB	2.20	0.41
1:A:48:ALA:HA	1:A:51:ARG:HG3	2.02	0.41
1:A:49:LYS:O	1:A:51:ARG:N	2.54	0.41
1:A:417:LEU:O	1:A:422:VAL:HG23	2.20	0.41
1:A:300:ARG:HH11	1:A:303:ASN:CG	2.27	0.41
1:A:252:VAL:O	1:A:256:VAL:HG13	2.21	0.41
1:A:319:PHE:CE1	1:A:455:THR:HG21	2.55	0.41
1:A:666:PHE:O	1:A:670:LYS:HG2	2.20	0.41
1:A:287:HIS:CD2	1:A:301:TYR:OH	2.74	0.40
1:A:62:VAL:HG12	1:A:102:VAL:CG1	2.50	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:267:PRO:HB3	1:A:271:GLY:HA2	2.04	0.40
1:A:261:GLN:HG2	1:A:261:GLN:O	2.22	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:32:ARG:NH2	1:A:325:LYS:NZ[4_556]	1.36	0.84

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	550/684 (80%)	531 (96%)	15 (3%)	4 (1%)	18	15

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	48	ALA
1	A	302	ALA
1	A	491	ALA
1	A	45	SER

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	473/583 (81%)	462 (98%)	11 (2%)	44 51

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	44	LYS
1	A	49	LYS
1	A	61	ILE
1	A	62	VAL
1	A	229	THR
1	A	240	THR
1	A	256	VAL
1	A	486	LEU
1	A	563	VAL
1	A	592	ASN
1	A	618	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (14) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	63	GLN
1	A	89	ASN
1	A	150	GLN
1	A	182	GLN
1	A	254	HIS
1	A	265	HIS
1	A	287	HIS
1	A	450	ASN
1	A	466	ASN
1	A	470	HIS
1	A	501	GLN
1	A	524	HIS
1	A	576	ASN
1	A	649	GLN

5.3.3 RNA ⓘ

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	556/684 (81%)	0.70	74 (13%) 7 7	22, 38, 67, 90	0

All (74) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	293	ALA	7.1
1	A	296	ASN	7.0
1	A	299	ALA	5.8
1	A	298	ASP	5.7
1	A	301	TYR	5.7
1	A	48	ALA	5.5
1	A	295	PHE	5.4
1	A	60	ASN	5.1
1	A	52	THR	4.9
1	A	297	GLY	4.3
1	A	49	LYS	4.2
1	A	40	LEU	4.0
1	A	50	SER	4.0
1	A	552	PHE	3.8
1	A	62	VAL	3.7
1	A	59	ALA	3.7
1	A	494	ALA	3.6
1	A	287	HIS	3.6
1	A	292	GLY	3.6
1	A	46	PRO	3.5
1	A	657	ASP	3.5
1	A	33	GLU	3.5
1	A	55	ALA	3.4
1	A	433	ILE	3.4
1	A	58	ILE	3.3
1	A	303	ASN	3.3
1	A	291	GLY	3.1

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Mol	Chain	Res	Type	RSRZ
1	A	304	ILE	3.1
1	A	300	ARG	3.0
1	A	57	ALA	3.0
1	A	38	PRO	2.9
1	A	45	SER	2.9
1	A	56	GLY	2.9
1	A	47	ASP	2.8
1	A	437	GLU	2.8
1	A	551	PRO	2.8
1	A	37	LEU	2.8
1	A	290	PRO	2.8
1	A	35	LYS	2.8
1	A	431	LEU	2.6
1	A	462	ALA	2.6
1	A	43	LEU	2.6
1	A	490	GLU	2.5
1	A	51	ARG	2.5
1	A	28	LEU	2.5
1	A	39	VAL	2.5
1	A	294	LYS	2.5
1	A	42	ASP	2.5
1	A	409	GLU	2.4
1	A	31	LEU	2.4
1	A	496	LEU	2.3
1	A	537	GLN	2.3
1	A	492	ASP	2.3
1	A	53	THR	2.3
1	A	27	GLU	2.3
1	A	29	ALA	2.3
1	A	54	ALA	2.3
1	A	674	ALA	2.3
1	A	34	ASP	2.3
1	A	618	LYS	2.3
1	A	89	ASN	2.2
1	A	464	GLY	2.2
1	A	44	LYS	2.2
1	A	324	VAL	2.2
1	A	651	GLU	2.1
1	A	61	ILE	2.1
1	A	146	LEU	2.1
1	A	91	ASP	2.1
1	A	434	ASP	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	76	VAL	2.1
1	A	302	ALA	2.1
1	A	108	GLU	2.1
1	A	26	PRO	2.0
1	A	227	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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.