



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 10, 2026 – 01:06 PM UTC

PDB ID : 6LRF / pdb_00006lrf
Title : Crystal structure of unliganded AgrE
Authors : Lee, H.; Rhee, S.
Deposited on : 2020-01-16
Resolution : 2.05 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

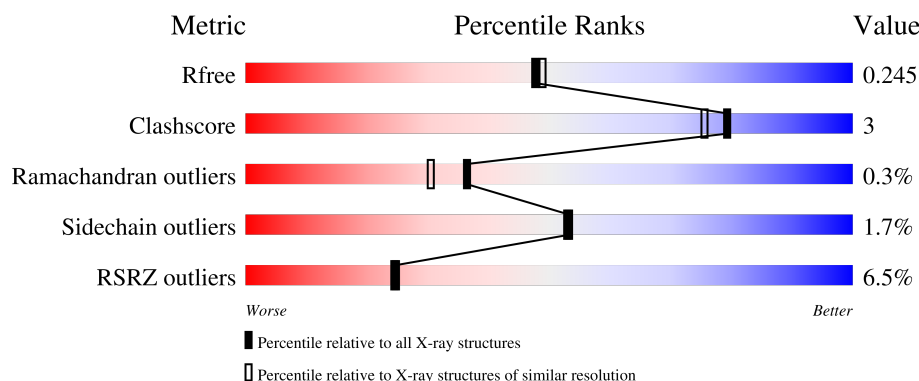
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.05 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	3774 (2.08-2.04)
Clashscore	190562	3883 (2.08-2.04)
Ramachandran outliers	187476	3860 (2.08-2.04)
Sidechain outliers	187428	3860 (2.08-2.04)
RSRZ outliers	180081	3775 (2.08-2.04)

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	703	6% 87% 7% 5%
1	B	703	7% 89% 8%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 10993 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 Alr4995 protein.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	671	Total	C	N	O	S	Se	0	0	0
			5238	3315	915	983	8	17			
1	B	681	Total	C	N	O	S	Se	0	0	0
			5314	3360	930	999	8	17			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MSE	-	initiating methionine	UNP Q8YMD9
B	1	MSE	-	initiating methionine	UNP Q8YMD9

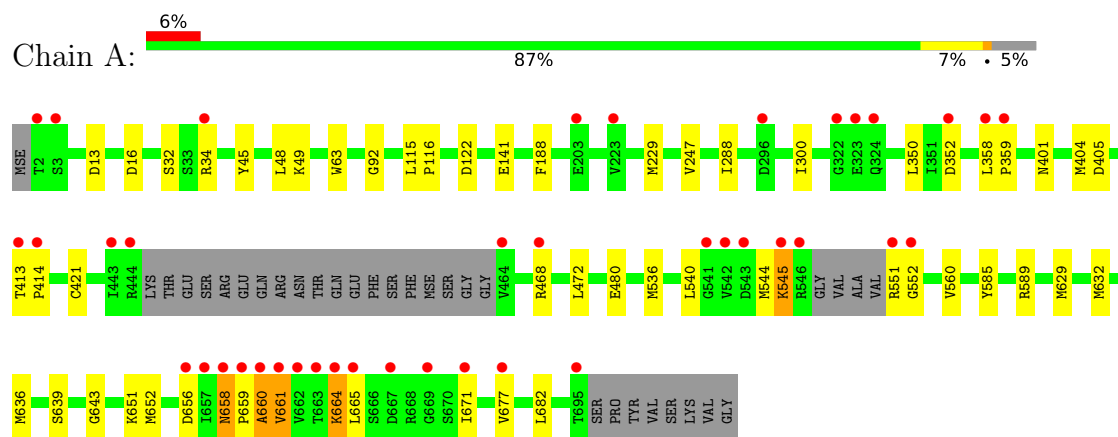
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	254	Total	O	0	0
			254	254		
2	B	187	Total	O	0	0
			187	187		

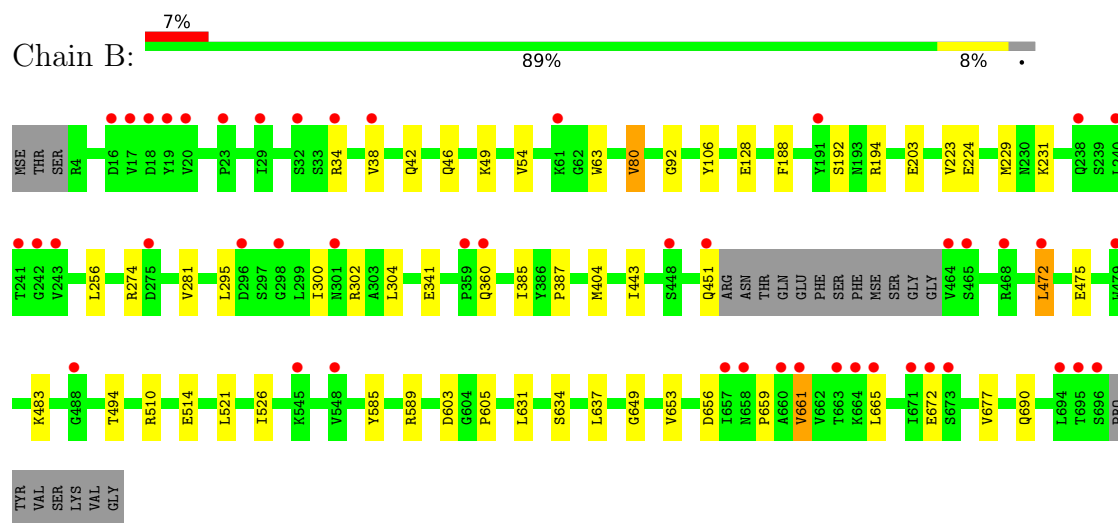
3 Residue-property plots [i](#)

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: Alr4995 protein



• Molecule 1: Alr4995 protein



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	187.65Å 201.73Å 99.59Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	26.59 – 2.05 26.59 – 2.06	Depositor EDS
% Data completeness (in resolution range)	97.7 (26.59-2.05) 97.7 (26.59-2.06)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.41 (at 2.06Å)	Xtriage
Refinement program	PHENIX 1.9_1692	Depositor
R, R_{free}	0.208 , 0.246 0.211 , 0.245	Depositor DCC
R_{free} test set	1999 reflections (1.70%)	wwPDB-VP
Wilson B-factor (Å ²)	26.0	Xtriage
Anisotropy	0.204	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 39.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.35$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	10993	wwPDB-VP
Average B, all atoms (Å ²)	31.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.21% 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	0.58	0/5317	0.84	3/7178 (0.0%)
1	B	0.51	0/5394	0.77	0/7282
All	All	0.54	0/10711	0.80	3/14460 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	661	VAL	N-CA-C	-14.91	98.05	112.96
1	A	115	LEU	CA-C-N	5.08	124.84	119.76
1	A	115	LEU	C-N-CA	5.08	124.84	119.76

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	660	ALA	Peptide

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	5238	0	5254	29	0
1	B	5314	0	5332	28	0
2	A	254	0	0	0	0
2	B	187	0	0	1	0
All	All	10993	0	10586	57	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 (57) 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:480:GLU:HB3	1:A:629:MSE:HE1	1.73	0.69
1:B:649:GLY:N	1:B:672:GLU:OE2	2.20	0.67
1:B:387:PRO:HB2	1:B:443:ILE:HG13	1.78	0.66
1:A:288:ILE:HD13	1:A:350:LEU:HD13	1.84	0.60
1:A:229:MSE:HE3	1:A:247:VAL:HG13	1.85	0.59
1:A:629:MSE:HE2	1:A:651:LYS:HG2	1.84	0.57
1:A:658:ASN:O	1:A:660:ALA:N	2.38	0.56
1:A:13:ASP:O	1:A:34:ARG:NH1	2.43	0.52
1:B:300:ILE:O	1:B:304:LEU:HG	2.09	0.52
1:A:63:TRP:CH2	1:A:92:GLY:HA3	2.45	0.51
1:A:404:MSE:HE3	1:A:405:ASP:OD2	2.11	0.50
1:A:658:ASN:C	1:A:660:ALA:H	2.22	0.48
1:B:631:LEU:HD12	1:B:653:VAL:HB	1.96	0.48
1:A:551:ARG:HB3	1:A:552:GLY:H	1.56	0.47
1:B:34:ARG:O	1:B:38:VAL:HG23	2.15	0.46
1:B:510:ARG:NE	1:B:514:GLU:OE2	2.45	0.46
1:B:659:PRO:HB3	1:B:677:VAL:HG21	1.96	0.46
1:B:63:TRP:CH2	1:B:92:GLY:HA3	2.51	0.46
1:B:661:VAL:HG13	1:B:665:LEU:HD12	1.97	0.46
1:A:116:PRO:HD2	1:A:141:GLU:HG3	1.98	0.45
1:A:632:MSE:SE	1:A:665:LEU:HD23	2.66	0.45
1:B:637:LEU:HD23	2:B:979:HOH:O	2.16	0.45
1:B:475:GLU:HG3	1:B:690:GLN:HE21	1.82	0.45
1:A:656:ASP:O	1:A:677:VAL:HA	2.17	0.45
1:B:188:PHE:HB3	1:B:192:SER:HB2	1.98	0.44
1:B:637:LEU:HD12	1:B:637:LEU:HA	1.86	0.44
1:A:639:SER:HB3	1:A:665:LEU:HD21	2.00	0.44
1:A:116:PRO:HD2	1:A:141:GLU:CG	2.48	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:475:GLU:HG3	1:B:690:GLN:NE2	2.33	0.44
1:B:656:ASP:O	1:B:677:VAL:HA	2.18	0.43
1:A:540:LEU:HD23	1:A:540:LEU:HA	1.70	0.43
1:B:42:GLN:O	1:B:46:GLN:HG2	2.19	0.43
1:B:585:TYR:CZ	1:B:589:ARG:HG3	2.54	0.43
1:B:80:VAL:HG12	1:B:106:TYR:HB3	2.01	0.43
1:B:302:ARG:HH22	1:B:451:GLN:HB3	1.83	0.43
1:B:49:LYS:HE2	1:B:54:VAL:HB	2.01	0.43
1:B:603:ASP:O	1:B:605:PRO:HA	2.19	0.42
1:A:48:LEU:HD23	1:A:48:LEU:HA	1.87	0.42
1:B:494:THR:HA	1:B:521:LEU:O	2.20	0.42
1:B:194:ARG:NH1	1:B:341:GLU:OE2	2.51	0.42
1:A:401:ASN:O	1:A:421:CYS:HB3	2.20	0.42
1:A:585:TYR:CZ	1:A:589:ARG:HG3	2.55	0.42
1:B:229:MSE:HE3	1:B:229:MSE:HB2	1.93	0.42
1:A:45:TYR:CZ	1:A:49:LYS:HD2	2.55	0.41
1:A:660:ALA:O	1:A:664:LYS:HG3	2.19	0.41
1:B:385:ILE:HG23	1:B:404:MSE:HE3	2.02	0.41
1:A:636:MSE:HA	1:A:661:VAL:HG21	2.02	0.41
1:B:295:LEU:HA	1:B:295:LEU:HD23	1.77	0.41
1:A:643:GLY:HA2	1:A:652:MSE:HE1	2.02	0.41
1:A:536:MSE:HE1	1:A:560:VAL:HG23	2.02	0.41
1:B:472:LEU:HD13	1:B:472:LEU:HA	1.90	0.41
1:A:413:THR:HB	1:A:414:PRO:HD2	2.02	0.41
1:A:544:MSE:HE2	1:A:544:MSE:HA	2.03	0.41
1:B:128:GLU:O	1:B:274:ARG:HD2	2.20	0.40
1:A:188:PHE:O	1:A:545:LYS:HG2	2.20	0.40
1:A:16:ASP:OD1	1:A:32:SER:HB3	2.21	0.40
1:A:358:LEU:HA	1:A:359:PRO:HD2	1.82	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	665/703 (95%)	643 (97%)	20 (3%)	2 (0%)	36	30
1	B	677/703 (96%)	653 (96%)	22 (3%)	2 (0%)	36	30
All	All	1342/1406 (95%)	1296 (97%)	42 (3%)	4 (0%)	36	30

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	658	ASN
1	B	224	GLU
1	B	634	SER
1	A	659	PRO

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	568/576 (99%)	559 (98%)	9 (2%)	55	55
1	B	576/576 (100%)	565 (98%)	11 (2%)	50	49
All	All	1144/1152 (99%)	1124 (98%)	20 (2%)	53	53

All (20) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	122	ASP
1	A	300	ILE
1	A	352	ASP
1	A	468	ARG
1	A	472	LEU
1	A	545	LYS
1	A	664	LYS
1	A	671	ILE
1	A	682	LEU
1	B	80	VAL
1	B	203	GLU
1	B	223	VAL

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Mol	Chain	Res	Type
1	B	231	LYS
1	B	256	LEU
1	B	281	VAL
1	B	360	GLN
1	B	472	LEU
1	B	483	LYS
1	B	526	ILE
1	B	661	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	14	HIS
1	A	87	HIS
1	A	278	HIS
1	A	301	ASN
1	A	623	HIS
1	B	401	ASN
1	B	689	GLN
1	B	690	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 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	654/703 (93%)	0.06	40 (6%) 27 27	13, 24, 51, 73	0
1	B	664/703 (94%)	0.46	46 (6%) 23 22	18, 33, 58, 76	0
All	All	1318/1406 (93%)	0.26	86 (6%) 25 24	13, 28, 56, 76	0

All (86) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	657	ILE	6.0
1	A	658	ASN	5.9
1	B	464	VAL	5.0
1	A	661	VAL	4.3
1	A	671	ILE	4.1
1	A	665	LEU	3.7
1	A	541	GLY	3.7
1	A	660	ALA	3.7
1	B	671	ILE	3.6
1	A	2	THR	3.6
1	A	352	ASP	3.5
1	A	464	VAL	3.5
1	B	661	VAL	3.5
1	B	359	PRO	3.5
1	B	696	SER	3.4
1	A	414	PRO	3.2
1	B	658	ASN	3.2
1	A	659	PRO	3.2
1	B	695	THR	3.2
1	A	664	LYS	3.1
1	A	695	THR	3.1
1	B	545	LYS	3.1
1	B	451	GLN	3.1
1	B	275	ASP	3.1

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Mol	Chain	Res	Type	RSRZ
1	A	663	THR	3.0
1	B	19	TYR	2.9
1	B	16	ASP	2.9
1	B	657	ILE	2.9
1	A	322	GLY	2.8
1	A	669	GLY	2.8
1	A	677	VAL	2.8
1	B	694	LEU	2.8
1	B	548	VAL	2.8
1	B	468	ARG	2.7
1	B	663	THR	2.7
1	A	546	ARG	2.7
1	B	38	VAL	2.7
1	A	443	ILE	2.7
1	A	552	GLY	2.7
1	B	17	VAL	2.7
1	B	61	LYS	2.7
1	A	667	ASP	2.7
1	A	34	ARG	2.7
1	A	551	ARG	2.7
1	A	542	VAL	2.6
1	B	665	LEU	2.6
1	A	656	ASP	2.6
1	B	32	SER	2.6
1	B	672	GLU	2.6
1	B	241	THR	2.6
1	B	23	PRO	2.6
1	B	360	GLN	2.5
1	A	444	ARG	2.5
1	A	545	LYS	2.5
1	A	543	ASP	2.5
1	A	296	ASP	2.5
1	B	448	SER	2.5
1	B	242	GLY	2.5
1	B	479	TRP	2.5
1	A	323	GLU	2.4
1	A	223	VAL	2.4
1	B	18	ASP	2.4
1	A	468	ARG	2.4
1	B	664	LYS	2.4
1	A	324	GLN	2.4
1	A	3	SER	2.3

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Mol	Chain	Res	Type	RSRZ
1	B	29	ILE	2.3
1	A	203	GLU	2.3
1	B	301	ASN	2.3
1	B	238	GLN	2.2
1	A	662	VAL	2.2
1	B	240	LEU	2.2
1	B	191	TYR	2.2
1	B	298	GLY	2.2
1	B	34	ARG	2.2
1	B	465	SER	2.1
1	A	359	PRO	2.1
1	B	472	LEU	2.1
1	B	673	SER	2.1
1	B	20	VAL	2.1
1	B	243	VAL	2.1
1	B	488	GLY	2.0
1	B	660	ALA	2.0
1	A	358	LEU	2.0
1	B	296	ASP	2.0
1	A	413	THR	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.