

Full wwPDB X-ray Structure Validation Report (i)

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:	9ISA
:	Dimeric amylosucrase from Deinococcus geothermalis
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:	2024-07-17
:	2.69 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 (i) 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 (1)) were used in the production of this report:

MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.21
EDS	:	3.0
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.004 (Gargrove)
Density-Fitness	:	1.0.11
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.40

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: $X\text{-}RAY\;DIFFRACTION$

The reported resolution of this entry is 2.69 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	$egin{array}{c} { m Whole \ archive} \ (\#{ m Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries,\ resolution\ range}({ m \AA}))$
R_{free}	164625	3333 (2.70-2.70)
Clashscore	180529	3684(2.70-2.70)
Ramachandran outliers	177936	3633 (2.70-2.70)
Sidechain outliers	177891	3633 (2.70-2.70)
RSRZ outliers	164620	3333 (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 <=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	А	645	84%	12% ••
1	В	645	6% 87%	11% •



2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 10170 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 Amylosucrase.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace	
1	А	628	Total 5030	C 3185	N 927	O 906	S 12	0	1	0
1	В	639	Total 5100	C 3234	N 934	O 920	S 12	0	0	0

• Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	А	24	Total O 24 24	0	0
2	В	16	Total O 16 16	0	0





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: Amylosucrase



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants	149.92Å 149.92Å 188.13Å	Depositor
a, b, c, α , β , γ	90.00° 90.00° 90.00°	Depositor
$\mathbf{Posolution} \left(\overset{\circ}{\mathbf{A}} \right)$	46.22 - 2.69	Depositor
Resolution (A)	46.22 - 2.69	EDS
% Data completeness	86.9 (46.22-2.69)	Depositor
(in resolution range)	86.9(46.22-2.69)	EDS
R_{merge}	0.10	Depositor
R _{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	$2.37 (at 2.69 \text{\AA})$	Xtriage
Refinement program	REFMAC 5.8.0267	Depositor
P. P.	0.176 , 0.220	Depositor
n, n_{free}	0.192 , 0.228	DCC
R_{free} test set	2940 reflections $(4.89%)$	wwPDB-VP
Wilson B-factor $(Å^2)$	51.3	Xtriage
Anisotropy	0.056	Xtriage
Bulk solvent $k_{sol}(e/Å^3), B_{sol}(Å^2)$	0.33, 39.8	EDS
L-test for twinning ²	$ < L >=0.49, < L^2>=0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	10170	wwPDB-VP
Average B, all atoms $(Å^2)$	49.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 3.09% of the height of the origin peak. No significant pseudotranslation is detected.

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.



¹Intensities estimated from amplitudes.

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).

Mal	Chain	Bond	lengths	Bond angles	
	Ullalli	RMSZ	# Z > 5	RMSZ	# Z > 5
1	А	0.47	0/5159	0.84	0/7012
1	В	0.44	0/5233	0.82	0/7117
All	All	0.46	0/10392	0.83	0/14129

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	А	5030	0	4903	74	0
1	В	5100	0	4970	63	0
2	А	24	0	0	0	0
2	В	16	0	0	0	0
All	All	10170	0	9873	136	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 (136) 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:339:GLY:HA2	1:B:343:HIS:CD2	1.44	1.50



		Interatomic	Clash
Atom-1	Atom-2	distance (Å)	overlap (Å)
1:B:339:GLY:CA	1:B:343:HIS:CD2	2.24	1.20
1:A:39:TRP:HB3	1:A:43:ARG:HH12	1.02	1.15
1:A:36:GLU:HG2	1:A:37:ASP:H	1.11	1.14
1:A:344:HIS:CE1	1:A:383:PRO:HB3	1.86	1.09
1:A:79:ARG:HG3	1:A:320:ALA:HA	1.34	1.07
1:B:79:ARG:HG3	1:B:320:ALA:HA	1.35	1.07
1:A:39:TRP:HB3	1:A:43:ARG:NH1	1.73	1.01
1:B:49:GLN:HE21	1:B:51:ARG:HA	1.27	0.98
1:A:344:HIS:CE1	1:A:383:PRO:CB	2.46	0.97
1:B:339:GLY:HA2	1:B:343:HIS:HD2	1.12	0.92
1:A:397:ASP:OD2	1:A:449:ARG:HD3	1.71	0.91
1:B:339:GLY:CA	1:B:343:HIS:HD2	1.72	0.90
1:A:91:MET:HE1	1:A:122:TYR:HB2	1.54	0.90
1:B:339:GLY:HA2	1:B:343:HIS:NE2	1.87	0.89
1:A:36:GLU:HG2	1:A:37:ASP:N	1.89	0.86
1:B:647:GLU:HG3	1:B:648:ALA:H	1.40	0.86
1:B:49:GLN:HG3	1:B:51:ARG:H	1.41	0.85
1:A:444:VAL:HG13	1:A:445:ASN:H	1.44	0.82
1:A:39:TRP:CB	1:A:43:ARG:HH12	1.90	0.82
1:B:37:ASP:OD1	1:B:346:LYS:HD3	1.79	0.82
1:B:49:GLN:HE21	1:B:51:ARG:CA	1.93	0.81
1:B:49:GLN:NE2	1:B:51:ARG:HA	1.96	0.80
1:A:82:ARG:HD3	1:A:88:ARG:HD2	1.70	0.74
1:A:344:HIS:HE1	1:A:383:PRO:HA	1.50	0.74
1:B:558:ARG:HG2	1:B:558:ARG:O	1.88	0.72
1:B:50:VAL:HG13	1:B:52:ALA:H	1.53	0.72
1:B:292:ARG:HH11	1:B:300:GLN:HE21	1.38	0.71
1:A:130:ARG:HD2	1:A:143:GLN:HE21	1.54	0.71
1:A:444:VAL:HG13	1:A:445:ASN:N	2.06	0.70
1:A:9:GLU:HG2	1:A:10:LEU:N	2.07	0.69
1:A:344:HIS:HE1	1:A:383:PRO:CA	2.05	0.69
1:A:591:MET:HE3	1:A:642:TRP:HB3	1.75	0.68
1:A:591:MET:CE	1:A:642:TRP:HB3	2.23	0.68
1:A:36:GLU:CG	1:A:37:ASP:H	1.99	0.67
1:B:130:ARG:HD2	1:B:143:GLN:HE21	1.60	0.66
1:A:344:HIS:CE1	1:A:383:PRO:HA	2.31	0.66
1:A:344:HIS:CE1	1:A:383:PRO:CA	2.78	0.65
1:A:377:ARG:HH11	1:A:377:ARG:HG2	1.62	0.64
1:B:647:GLU:HG3	1:B:648:ALA:N	2.11	0.64
1:A:616:HIS:CE1	1:A:627:ARG:HD3	2.32	0.64
1:A:620:ARG:HH11	1:A:620:ARG:HG2	1.63	0.64



	lo us page	Interatomic	Clash
Atom-1	Atom-2	distance (Å)	overlap (Å)
1:B:423:ASP:OD1	1:B:428:GLN:HB2	2.01	0.61
1:A:558:ARG:HG2	1:A:558:ARG:O	1.99	0.61
1:A:344:HIS:CE1	1:A:383:PRO:CG	2.84	0.60
1:A:344:HIS:ND1	1:A:383:PRO:HG3	2.17	0.59
1:A:620:ARG:HG2	1:A:620:ARG:NH1	2.17	0.59
1:A:344:HIS:CE1	1:A:383:PRO:HG3	2.37	0.59
1:A:79:ARG:HG3	1:A:320:ALA:CA	2.22	0.58
1:B:292:ARG:HH11	1:B:300:GLN:NE2	2.01	0.58
1:B:339:GLY:HA3	1:B:343:HIS:CD2	2.32	0.58
1:B:222:PHE:HE2	1:B:248:PHE:HA	1.68	0.58
1:B:173:VAL:HG22	1:B:280:VAL:HB	1.85	0.57
1:A:377:ARG:HG2	1:A:377:ARG:NH1	2.19	0.57
1:B:292:ARG:NH1	1:B:300:GLN:HE21	2.03	0.56
1:A:39:TRP:CB	1:A:43:ARG:NH1	2.58	0.56
1:A:131:PRO:HD2	1:A:149:ARG:HG3	1.87	0.56
1:A:173:VAL:HG22	1:A:280:VAL:HB	1.86	0.56
1:B:6:LEU:O	1:B:6:LEU:HD23	2.07	0.54
1:B:75:LEU:O	1:B:79:ARG:HG2	2.07	0.54
1:B:339:GLY:HA3	1:B:343:HIS:HD2	1.67	0.53
1:B:49:GLN:HG3	1:B:51:ARG:N	2.16	0.53
1:A:627:ARG:HE	1:A:629:ASP:HB2	1.75	0.52
1:B:130:ARG:HD2	1:B:143:GLN:NE2	2.25	0.51
1:A:75:LEU:O	1:A:79:ARG:HG2	2.09	0.50
1:A:86:LEU:HD13	1:A:350:MET:SD	2.52	0.50
1:A:203:HIS:HB2	1:A:245:TRP:HB2	1.93	0.50
1:A:307:THR:HG21	1:A:347:VAL:O	2.12	0.49
1:B:433:PHE:O	1:B:459:GLY:HA2	2.12	0.49
1:A:36:GLU:CG	1:A:37:ASP:N	2.63	0.49
1:B:79:ARG:HG3	1:B:320:ALA:CA	2.25	0.48
1:B:199:ARG:HH12	1:B:236:ILE:HG23	1.78	0.48
1:B:533:GLU:HG3	1:B:536:ARG:HH21	1.78	0.48
1:B:360:LEU:HD21	1:B:485:VAL:HG11	1.95	0.47
1:A:349:ASP:O	1:A:350:MET:HG3	2.14	0.47
1:B:131:PRO:HD2	1:B:149:ARG:HG3	1.97	0.47
1:A:444:VAL:CG1	1:A:445:ASN:N	2.77	0.47
1:B:267:VAL:O	1:B:271:LEU:HG	2.15	0.46
1:A:350:MET:HA	1:A:387:THR:O	2.16	0.46
1:A:433:PHE:O	1:A:459:GLY:HA2	2.14	0.46
1:A:124:HIS:HA	1:A:173:VAL:HB	1.99	0.45
1:A:9:GLU:HG2	1:A:10:LEU:H	1.81	0.45
1:B:234:GLU:O	1:B:241:GLY:HA2	2.16	0.45



Interatomic			Clash
Atom-1	Atom-2	distance $(Å)$	overlap (Å)
1:B:647:GLU:CG	1:B:648:ALA:H	2.21	0.45
1:B:598:SER:OG	1:B:600:GLU:HG3	2.16	0.44
1:A:444:VAL:CG1	1:A:445:ASN:H	2.22	0.44
1:A:586:HIS:CG	1:A:587:PRO:HD2	2.53	0.44
1:A:175:ASP:HB3	1:A:284:ASP:OD2	2.18	0.44
1:B:100:ARG:HD2	1:B:521:TRP:HZ3	1.81	0.44
1:A:617:VAL:HG23	1:A:626:PHE:HB2	1.99	0.44
1:B:58:LEU:HD12	1:B:61:MET:HE2	1.98	0.44
1:B:203:HIS:HB2	1:B:245:TRP:HB2	1.99	0.44
1:A:131:PRO:CD	1:A:149:ARG:HG3	2.47	0.44
1:B:335:ILE:HD12	1:B:335:ILE:HA	1.85	0.43
1:A:236:ILE:HD12	1:A:236:ILE:HA	1.71	0.43
1:B:131:PRO:CD	1:B:149:ARG:HG3	2.48	0.43
1:B:124:HIS:HA	1:B:173:VAL:HB	2.01	0.43
1:A:282:ARG:NH2	1:A:326:GLU:HG3	2.34	0.43
1:A:292:ARG:HG2	1:A:295:THR:HG23	2.00	0.43
1:B:51:ARG:O	1:B:51:ARG:HG3	2.19	0.43
1:B:647:GLU:OE2	1:B:647:GLU:HA	2.19	0.43
1:B:222:PHE:CE2	1:B:248:PHE:HA	2.52	0.42
1:B:58:LEU:HD12	1:B:61:MET:CE	2.49	0.42
1:B:423:ASP:OD1	1:B:428:GLN:CB	2.67	0.42
1:B:613:LEU:HD23	1:B:613:LEU:HA	1.90	0.42
1:A:413:ASN:HB3	1:A:416:ALA:HB3	2.02	0.42
1:B:36:GLU:H	1:B:36:GLU:HG2	1.56	0.42
1:A:311:ARG:NH2	1:A:315:ARG:CZ	2.83	0.42
1:A:391:TYR:N	1:A:391:TYR:CD1	2.88	0.41
1:B:400:TRP:O	1:B:418:ARG:HD2	2.20	0.41
1:B:586:HIS:CG	1:B:587:PRO:HD2	2.55	0.41
1:A:100:ARG:HD2	1:A:521:TRP:HZ3	1.85	0.41
1:B:282:ARG:NH2	1:B:326:GLU:HG3	2.35	0.41
1:A:247:THR:HG23	1:A:254:ASP:OD2	2.20	0.41
1:B:175:ASP:HB3	1:B:284:ASP:OD2	2.19	0.41
1:A:360:LEU:HB3	1:A:482:LEU:HD22	2.02	0.41
1:B:616:HIS:CE1	1:B:648:ALA:HB2	2.56	0.41
1:A:552:HIS:O	1:A:556:VAL:HG23	2.21	0.41
1:A:605:PRO:O	1:A:608:VAL:HG13	2.20	0.41
1:A:616:HIS:HE1	1:A:627:ARG:HD3	1.82	0.41
1:B:509:PHE:CE2	1:B:519:ASN:HA	2.56	0.41
1:A:413:ASN:O	1:A:414:GLY:C	2.59	0.41
1:A:53:LEU:HB3	1:A:54:PRO:HD3	2.03	0.41
1:A:617:VAL:CG2	1:A:626:PHE:HB2	2.51	0.41



Atom-1	Atom-2	Interatomic	Clash
Atom-1	Atom-2	distance (Å)	overlap (Å)
1:A:360:LEU:HD21	1:A:485:VAL:HG11	2.02	0.41
1:A:440:GLN:HB2	1:A:449:ARG:HG3	2.03	0.41
1:A:518:ASP:OD2	1:A:520:ARG:NH2	2.54	0.41
1:B:49:GLN:HE21	1:B:51:ARG:N	2.18	0.41
1:B:118:LEU:HD23	1:B:118:LEU:HA	1.91	0.41
1:B:405:GLU:OE1	1:B:405:GLU:N	2.53	0.41
1:A:91:MET:HE2	1:A:91:MET:HB3	1.95	0.40
1:A:349:ASP:C	1:A:350:MET:HG3	2.41	0.40
1:B:31:LEU:HD21	1:B:58:LEU:HD11	2.02	0.40
1:A:10:LEU:H	1:A:10:LEU:HG	1.72	0.40
1:A:74:ARG:HD3	1:B:25:GLU:HG3	2.03	0.40
1:B:50:VAL:HG13	1:B:52:ALA:HB3	2.04	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	Perce	entiles
1	А	623/645~(97%)	597~(96%)	25~(4%)	1 (0%)	44	68
1	В	633/645~(98%)	609~(96%)	23~(4%)	1 (0%)	44	68
All	All	1256/1290~(97%)	1206 (96%)	48 (4%)	2~(0%)	44	68

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	В	347	VAL
1	А	206	PRO



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 side chain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	А	513/524~(98%)	503~(98%)	10~(2%)	52 79
1	В	520/524~(99%)	511 (98%)	9(2%)	56 81
All	All	1033/1048 (99%)	1014 (98%)	19 (2%)	54 80

All (19) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	А	8	SER
1	А	124	HIS
1	А	135	GLU
1	А	236	ILE
1	А	254	ASP
1	А	349	ASP
1	А	372	PHE
1	А	409	ARG
1	А	445	ASN
1	А	627	ARG
1	В	8	SER
1	В	254	ASP
1	В	344	HIS
1	В	372	PHE
1	В	409	ARG
1	В	511	ASP
1	В	600	GLU
1	В	610	ARG
1	В	612	VAL

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

Mol	Chain	Res	Type
1	А	143	GLN
1	А	547	ASN
1	А	616	HIS



Continued from previous page...

Mol	Chain	Res	Type
1	В	49	GLN
1	В	143	GLN
1	В	300	GLN
1	В	547	ASN

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 (i)

6.1 Protein, DNA and RNA chains (i)

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, 95^{th} 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	А	628/645~(97%)	-0.30	29 (4%) 38 36	11, 43, 84, 128	1 (0%)
1	В	639/645~(99%)	-0.30	36 (5%) 31 29	26, 47, 92, 147	0
All	All	1267/1290~(98%)	-0.30	65 (5%) 34 32	11, 45, 87, 147	1 (0%)

All (65) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	А	347	VAL	9.1
1	А	348	SER	7.6
1	В	343	HIS	7.3
1	В	223	PRO	6.3
1	В	344	HIS	5.5
1	В	351	ALA	4.9
1	В	345	GLY	4.8
1	В	650	ALA	4.5
1	В	649	PRO	4.5
1	А	346	LYS	4.4
1	В	50	VAL	4.3
1	В	226	ALA	4.2
1	А	442	ASN	4.2
1	А	219	PRO	3.9
1	В	248	PHE	3.8
1	В	209	ARG	3.8
1	А	8	SER	3.7
1	А	646	GLY	3.7
1	А	7	THR	3.7
1	A	12	ALA	3.6
1	A	9	GLU	3.5
1	В	342	ALA	3.5
1	A	616	HIS	3.4
1	В	618	GLN	3.4



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Mol	Chain	Res	Type	RSRZ
1	А	43	ARG	3.3
1	В	227	PRO	3.2
1	А	443	PRO	3.2
1	А	444	VAL	3.1
1	А	344	HIS	3.1
1	А	600	GLU	3.1
1	В	509	PHE	3.0
1	А	10	LEU	3.0
1	А	250	SER	2.9
1	В	444	VAL	2.9
1	В	349	ASP	2.9
1	В	207	ASP	2.8
1	В	6	LEU	2.8
1	А	248	PHE	2.8
1	А	634	ARG	2.8
1	В	348	SER	2.8
1	В	440	GLN	2.7
1	А	445	ASN	2.7
1	В	648	ALA	2.7
1	А	249	ASN	2.7
1	В	232	TRP	2.7
1	А	236	ILE	2.6
1	В	507	TYR	2.6
1	В	510	GLU	2.5
1	В	241	GLY	2.5
1	В	206	PRO	2.5
1	А	507	TYR	2.5
1	В	51	ARG	2.4
1	А	49	GLN	2.4
1	В	514	GLU	2.4
1	А	350	MET	2.3
1	В	250	SER	2.3
1	А	625	ALA	2.3
1	А	626	PHE	2.2
1	А	627	ARG	2.2
1	В	140	TYR	2.2
1	В	428	GLN	2.2
1	В	346	LYS	2.1
1	В	219	PRO	2.1
1	В	222	PHE	2.1
1	В	341	ARG	2.0

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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 monosaccharides 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.

