



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 12:49 AM UTC

PDB ID : 2FTS / pdb_00002fts
Title : Crystal structure of the glycine receptor-gephyrin complex
Authors : Kim, E.Y.; Schindelin, H.
Deposited on : 2006-01-24
Resolution : 2.41 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

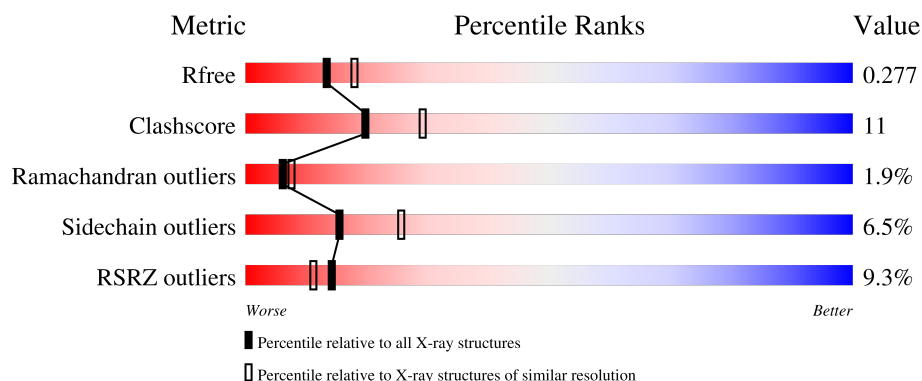
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.41 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	6062 (2.44-2.40)
Clashscore	190562	6562 (2.44-2.40)
Ramachandran outliers	187476	6481 (2.44-2.40)
Sidechain outliers	187428	6482 (2.44-2.40)
RSRZ outliers	180081	6066 (2.44-2.40)

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	419	
2	P	13	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 3448 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 gephyrin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	419	Total	C	N	O	S	0	0	0
			3194	2012	554	607	21			

- Molecule 2 is a protein called Glycine receptor beta chain precursor.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	P	13	Total	C	N	O	0	0	0
			104	69	16	19			

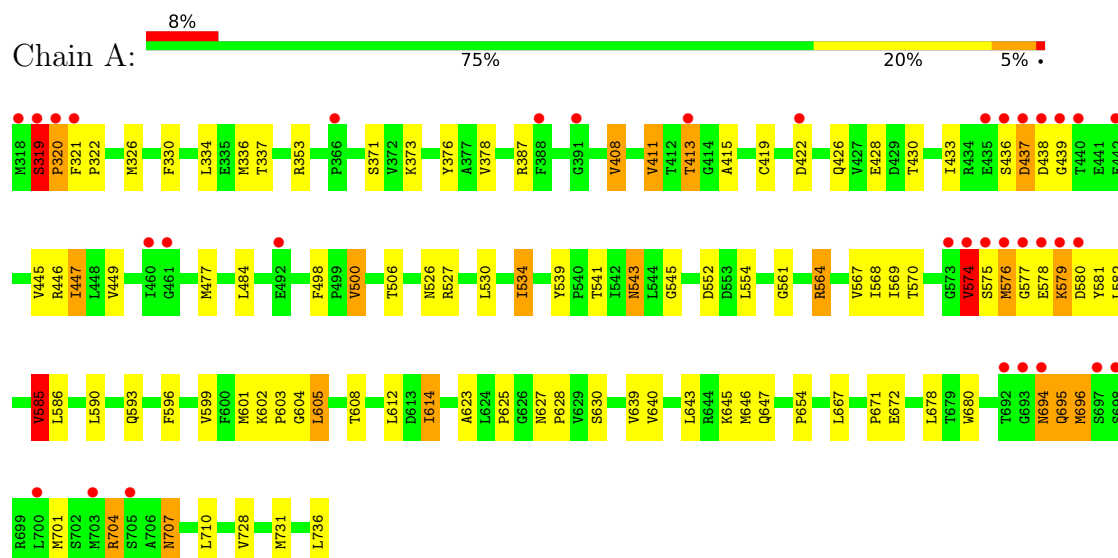
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	149	Total	O	0	0
			149	149		
3	P	1	Total	O	0	0
			1	1		

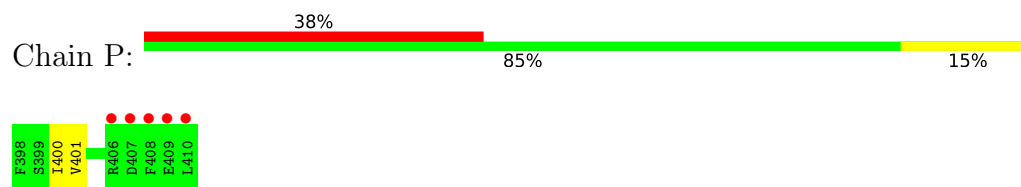
3 Residue-property plots

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: gephyrin



• Molecule 2: Glycine receptor beta chain precursor



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	51.30Å 123.54Å 155.05Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.41 20.00 – 2.41	Depositor EDS
% Data completeness (in resolution range)	93.2 (20.00-2.41) 93.2 (20.00-2.41)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.08 (at 2.42Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.192 , 0.272 (Not available) , 0.277	Depositor DCC
R_{free} test set	936 reflections (4.78%)	wwPDB-VP
Wilson B-factor (Å ²)	37.2	Xtriage
Anisotropy	0.585	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 53.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	3448	wwPDB-VP
Average B, all atoms (Å ²)	46.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.15% 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	1.17	6/3255 (0.2%)	1.00	13/4427 (0.3%)
2	P	1.04	0/106	0.69	0/142
All	All	1.17	6/3361 (0.2%)	0.99	13/4569 (0.3%)

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	640	VAL	CA-CB	12.04	1.60	1.54
1	A	574	VAL	CA-CB	7.74	1.62	1.54
1	A	614	ILE	CA-CB	6.43	1.62	1.54
1	A	585	VAL	CA-CB	5.92	1.62	1.54
1	A	422	ASP	CB-CG	5.71	1.66	1.52
1	A	411	VAL	CA-CB	5.41	1.62	1.54

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	415	ALA	N-CA-C	9.67	120.72	109.60
1	A	694	ASN	N-CA-C	-7.69	102.41	112.41
1	A	387	ARG	N-CA-C	5.88	119.12	109.72
1	A	319	SER	CA-C-N	-5.58	112.87	119.84
1	A	319	SER	C-N-CA	-5.58	112.87	119.84
1	A	447	ILE	CB-CA-C	5.54	117.67	110.96
1	A	439	GLY	N-CA-C	-5.54	100.06	113.18
1	A	477	MET	N-CA-C	5.53	119.25	109.96
1	A	500	VAL	CB-CA-C	5.30	117.48	110.91
1	A	419	CYS	N-CA-C	5.27	119.19	112.34
1	A	576	MET	N-CA-C	-5.25	105.00	111.40
1	A	701	MET	N-CA-C	5.24	118.07	110.42
1	A	577	GLY	N-CA-C	-5.20	101.99	111.15

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	3194	0	3235	76	0
2	P	104	0	102	4	0
3	A	149	0	0	2	1
3	P	1	0	0	0	0
All	All	3448	0	3337	76	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 11.

All (76) 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:678:LEU:H	1:A:707:ASN:HD21	1.15	0.94
1:A:527:ARG:HH11	1:A:543:ASN:HD21	1.28	0.79
1:A:608:THR:HB	1:A:623:ALA:HB3	1.69	0.74
1:A:433:ILE:HD11	1:A:446:ARG:HG2	1.71	0.72
1:A:564:ARG:HH11	1:A:564:ARG:HG2	1.56	0.71
1:A:319:SER:O	1:A:320:PRO:C	2.35	0.70
1:A:581:TYR:O	1:A:585:VAL:HG12	1.92	0.69
1:A:321:PHE:HB3	1:A:322:PRO:HD2	1.74	0.68
1:A:436:SER:O	1:A:437:ASP:C	2.40	0.64
1:A:602:LYS:O	1:A:672:GLU:HA	1.98	0.64
1:A:696:MET:HA	1:A:696:MET:HE2	1.79	0.63
1:A:534:ILE:HD11	1:A:541:THR:CG2	2.29	0.62
1:A:707:ASN:HD22	1:A:707:ASN:H	1.47	0.62
1:A:371:SER:O	1:A:413:THR:O	2.18	0.61
1:A:426:GLN:HE21	1:A:428:GLU:HB2	1.67	0.60
1:A:437:ASP:OD2	1:A:438:ASP:N	2.34	0.60
1:A:543:ASN:HD22	1:A:545:GLY:H	1.50	0.59
1:A:601:MET:HE2	1:A:603:PRO:O	2.04	0.58
1:A:336:MET:HA	1:A:336:MET:HE2	1.84	0.58
1:A:530:LEU:O	1:A:534:ILE:HG23	2.04	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:319:SER:HB3	1:A:320:PRO:HD2	1.87	0.56
1:A:704:ARG:HG2	1:A:704:ARG:HH11	1.71	0.56
1:A:671:PRO:HB3	2:P:401:VAL:HG13	1.87	0.55
1:A:526:ASN:HD21	1:A:628:PRO:HA	1.70	0.55
1:A:604:GLY:HA2	1:A:625:PRO:HG2	1.89	0.54
1:A:543:ASN:ND2	1:A:545:GLY:H	2.05	0.54
1:A:321:PHE:HB3	1:A:322:PRO:CD	2.39	0.53
1:A:643:LEU:HD23	1:A:646:MET:HE3	1.89	0.53
1:A:353:ARG:HD2	1:A:498:PHE:CE1	2.44	0.53
1:A:543:ASN:HD22	1:A:543:ASN:C	2.19	0.51
1:A:554:LEU:HD12	1:A:582:LEU:HD13	1.91	0.51
1:A:643:LEU:HD23	1:A:646:MET:CE	2.41	0.51
1:A:704:ARG:HH11	1:A:704:ARG:CG	2.23	0.51
1:A:581:TYR:O	1:A:585:VAL:CG1	2.60	0.50
1:A:373:LYS:HD3	1:A:426:GLN:HB3	1.94	0.49
1:A:643:LEU:HA	1:A:646:MET:HE3	1.94	0.49
1:A:678:LEU:N	1:A:707:ASN:HD21	1.98	0.48
1:A:695:GLN:O	1:A:696:MET:HB2	2.13	0.48
1:A:627:ASN:HD22	1:A:630:SER:H	1.60	0.48
1:A:446:ARG:HG3	3:A:79:HOH:O	2.12	0.47
1:A:534:ILE:HD11	1:A:541:THR:HG23	1.95	0.47
1:A:710:LEU:HD11	1:A:728:VAL:HG21	1.95	0.47
1:A:534:ILE:HD11	1:A:541:THR:HG22	1.96	0.47
1:A:578:GLU:O	1:A:579:LYS:HB3	2.15	0.47
1:A:654:PRO:CB	1:A:731:MET:HE3	2.44	0.47
1:A:322:PRO:HG2	1:A:596:PHE:HA	1.96	0.47
1:A:567:VAL:CG2	1:A:646:MET:HE1	2.45	0.46
1:A:326:MET:CE	2:P:400:ILE:HD12	2.46	0.45
1:A:334:LEU:O	1:A:645:LYS:HE3	2.17	0.45
1:A:695:GLN:O	1:A:696:MET:CB	2.65	0.44
1:A:569:ILE:HD11	1:A:639:VAL:HG11	1.99	0.44
1:A:654:PRO:HB2	1:A:731:MET:HE3	1.99	0.44
1:A:567:VAL:HG21	1:A:646:MET:HE1	1.99	0.43
1:A:576:MET:HE1	1:A:605:LEU:HD12	2.01	0.43
1:A:570:THR:HG21	1:A:582:LEU:CD2	2.48	0.43
1:A:376:TYR:CE1	1:A:430:THR:HG21	2.54	0.43
1:A:603:PRO:HB2	1:A:630:SER:OG	2.18	0.42
1:A:561:GLY:HA3	1:A:568:ILE:HD11	2.01	0.42
1:A:570:THR:HG21	1:A:582:LEU:HD21	2.00	0.42
1:A:353:ARG:HD3	3:A:35:HOH:O	2.20	0.42
1:A:437:ASP:CG	1:A:438:ASP:N	2.76	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:330:PHE:HB2	2:P:400:ILE:HD11	2.00	0.42
1:A:408:VAL:HG21	1:A:447:ILE:HD11	2.01	0.42
1:A:680:TRP:CH2	1:A:736:LEU:HD13	2.55	0.42
1:A:319:SER:O	1:A:321:PHE:N	2.52	0.41
1:A:337:THR:O	1:A:645:LYS:HE3	2.20	0.41
1:A:534:ILE:HD12	1:A:539:TYR:HB2	2.01	0.41
1:A:576:MET:SD	1:A:576:MET:N	2.93	0.41
1:A:506:THR:HG21	1:A:554:LEU:HD11	2.01	0.41
1:A:707:ASN:HD22	1:A:707:ASN:N	2.09	0.41
1:A:330:PHE:HB2	2:P:400:ILE:CD1	2.51	0.41
1:A:574:VAL:HG12	1:A:579:LYS:HA	2.03	0.41
1:A:376:TYR:HB3	1:A:408:VAL:HG13	2.02	0.40
1:A:408:VAL:HG21	1:A:447:ILE:CD1	2.51	0.40
1:A:586:LEU:HD23	1:A:590:LEU:HD12	2.03	0.40
1:A:707:ASN:H	1:A:707:ASN:ND2	2.16	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)
3:A:125:HOH:O	3:A:126:HOH:O 3_554	1.92	0.28

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	417/419 (100%)	396 (95%)	13 (3%)	8 (2%)	6	7
2	P	11/13 (85%)	11 (100%)	0	0	100	100
All	All	428/432 (99%)	407 (95%)	13 (3%)	8 (2%)	6	7

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	575	SER
1	A	580	ASP
1	A	696	MET
1	A	579	LYS
1	A	695	GLN
1	A	319	SER
1	A	320	PRO
1	A	437	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	356/356 (100%)	332 (93%)	24 (7%)	15	24
2	P	12/12 (100%)	12 (100%)	0	100	100
All	All	368/368 (100%)	344 (94%)	24 (6%)	15	25

All (24) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	378	VAL
1	A	408	VAL
1	A	411	VAL
1	A	413	THR
1	A	445	VAL
1	A	449	VAL
1	A	484	LEU
1	A	500	VAL
1	A	534	ILE
1	A	543	ASN
1	A	552	ASP
1	A	564	ARG
1	A	574	VAL
1	A	585	VAL
1	A	593	GLN
1	A	599	VAL

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Mol	Chain	Res	Type
1	A	605	LEU
1	A	612	LEU
1	A	614	ILE
1	A	647	GLN
1	A	667	LEU
1	A	694	ASN
1	A	704	ARG
1	A	707	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	426	GLN
1	A	462	HIS
1	A	508	ASN
1	A	526	ASN
1	A	537	HIS
1	A	543	ASN
1	A	584	GLN
1	A	627	ASN
1	A	647	GLN
1	A	694	ASN
1	A	707	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

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	419/419 (100%)	0.76	35 (8%) 17 13	39, 46, 52, 71	0
2	P	13/13 (100%)	2.11	5 (38%) 1 0	52, 56, 80, 81	0
All	All	432/432 (100%)	0.80	40 (9%) 14 11	39, 46, 53, 81	0

All (40) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	575	SER	7.5
1	A	577	GLY	7.3
1	A	440	THR	6.7
1	A	693	GLY	6.1
2	P	410	LEU	5.3
1	A	574	VAL	5.2
1	A	576	MET	5.0
1	A	436	SER	4.9
1	A	578	GLU	4.9
1	A	321	PHE	3.7
1	A	318	MET	3.7
1	A	573	GLY	3.5
1	A	694	ASN	3.5
2	P	407	ASP	3.4
2	P	408	PHE	3.4
1	A	437	ASP	3.4
2	P	409	GLU	3.4
1	A	461	GLY	3.4
1	A	319	SER	3.3
1	A	320	PRO	3.3
1	A	439	GLY	3.2
1	A	579	LYS	3.1
1	A	422	ASP	3.1
1	A	460	ILE	2.7

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Mol	Chain	Res	Type	RSRZ
1	A	698	SER	2.7
1	A	700	LEU	2.6
1	A	413	THR	2.6
1	A	435	GLU	2.6
1	A	692	THR	2.6
1	A	366	PRO	2.5
1	A	705	SER	2.5
1	A	697	SER	2.5
1	A	580	ASP	2.4
1	A	442	GLU	2.3
1	A	492	GLU	2.3
1	A	438	ASP	2.3
2	P	406	ARG	2.3
1	A	388	PHE	2.2
1	A	391	GLY	2.1
1	A	703	MET	2.1

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.