



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 27, 2026 – 05:33 PM EDT

PDB ID : 5J98 / pdb_00005j98
Title : Crystal structure of Slow Bee Paralysis Virus at 2.6Å resolution
Authors : Kalynych, S.; Levdansky, Y.; Palkova, L.; Plevka, P.
Deposited on : 2016-04-08
Resolution : 2.60 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

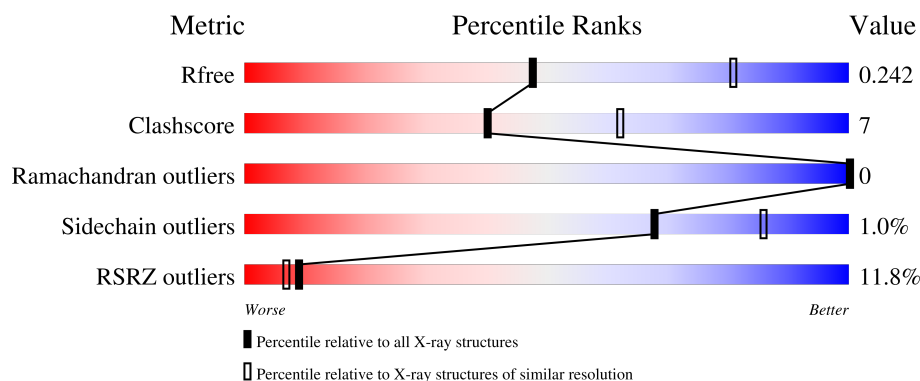
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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	4008 (2.60-2.60)
Clashscore	190562	4347 (2.60-2.60)
Ramachandran outliers	187476	4277 (2.60-2.60)
Sidechain outliers	187428	4277 (2.60-2.60)
RSRZ outliers	180081	4008 (2.60-2.60)

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	266	3% 79% 14% 5%
2	B	261	3% 82% 16% •
3	C	430	21% 82% 14% • •

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 7438 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 VP1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	252	Total	C	N	O	S	0	0	0
			2023	1293	353	368	9			

- Molecule 2 is a protein called VP2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	260	Total	C	N	O	S	0	0	0
			2086	1341	347	384	14			

- Molecule 3 is a protein called VP3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	417	Total	C	N	O	S	0	0	0
			3260	2113	538	601	8			

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	20	Total	O	0	0
			20	20		
4	B	19	Total	O	0	0
			19	19		
4	C	30	Total	O	0	0
			30	30		

4 Data and refinement statistics

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, α , β , γ	340.04Å 396.85Å 431.70Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.50 – 2.60 49.50 – 2.60	Depositor EDS
% Data completeness (in resolution range)	88.3 (49.50-2.60) 88.6 (49.50-2.60)	Depositor EDS
R_{merge}	0.20	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.42 (at 2.61Å)	Xtriage
Refinement program	CNS 1.3, PHENIX	Depositor
R, R_{free}	0.279 , (Not available) 0.243 , 0.242	Depositor DCC
R_{free} test set	38971 reflections (4.42%)	wwPDB-VP
Wilson B-factor (Å ²)	34.4	Xtriage
Anisotropy	0.509	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 28.0	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	0.34	EDS
Total number of atoms	7438	wwPDB-VP
Average B, all atoms (Å ²)	20.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.56% 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	0.31	0/2079	0.78	2/2832 (0.1%)
2	B	0.31	0/2139	0.77	3/2907 (0.1%)
3	C	0.31	0/3360	0.76	3/4600 (0.1%)
All	All	0.31	0/7578	0.77	8/10339 (0.1%)

There are no bond length outliers.

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	245	ALA	N-CA-C	7.80	121.30	111.24
3	C	70	TRP	CA-CB-CG	6.06	125.11	113.60
2	B	105	ILE	CA-C-N	-5.86	113.64	119.56
2	B	105	ILE	C-N-CA	-5.86	113.64	119.56
1	A	249	THR	CA-C-N	5.25	125.05	119.28
1	A	249	THR	C-N-CA	5.25	125.05	119.28
3	C	298	VAL	N-CA-C	-5.19	102.90	109.80
2	B	5	GLU	N-CA-C	-5.14	103.74	110.53

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	2023	0	1972	29	0
2	B	2086	0	2072	32	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	C	3260	0	3208	45	0
4	A	20	0	0	0	0
4	B	19	0	0	0	0
4	C	30	0	0	0	0
All	All	7438	0	7252	97	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 (97) 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)
3:C:124:TYR:HB2	3:C:245:ALA:HB3	1.61	0.81
3:C:82:HIS:HB3	3:C:216:ILE:HD12	1.63	0.81
2:B:127:ASP:OD2	3:C:140:ARG:NH2	2.15	0.80
1:A:17:PRO:O	3:C:126:ARG:NH2	2.15	0.79
3:C:188:THR:HG22	3:C:190:THR:H	1.47	0.77
3:C:11:PHE:O	3:C:12:PHE:HD1	1.73	0.71
3:C:140:ARG:HG3	3:C:226:VAL:HG21	1.72	0.71
1:A:102:ARG:HD2	3:C:48:ILE:HD13	1.73	0.70
2:B:132:TRP:HE1	2:B:163:LEU:HB3	1.57	0.69
1:A:103:GLY:HA3	1:A:227:PHE:HA	1.77	0.67
1:A:190:ASP:OD1	2:B:182:ARG:NH2	2.29	0.64
1:A:127:PRO:HG2	1:A:192:LEU:O	1.99	0.63
3:C:294:ARG:NH1	3:C:296:GLY:O	2.31	0.63
1:A:6:THR:O	1:A:6:THR:OG1	2.16	0.61
3:C:285:PHE:CG	3:C:292:ILE:HD11	2.37	0.60
2:B:114:ARG:HG3	2:B:178:TYR:CD2	2.37	0.59
1:A:223:ILE:HG23	1:A:227:PHE:HB3	1.86	0.58
3:C:294:ARG:HH22	3:C:299:SER:HA	1.70	0.57
3:C:63:GLY:HA3	3:C:113:PRO:HB3	1.86	0.57
2:B:125:PRO:HB3	2:B:229:LEU:HD21	1.87	0.56
2:B:148:LYS:HA	2:B:151:ARG:HD2	1.87	0.56
2:B:115:ALA:O	2:B:178:TYR:HB2	2.05	0.56
3:C:123:ALA:N	3:C:246:VAL:O	2.36	0.56
3:C:65:LEU:HD21	3:C:93:VAL:HG21	1.87	0.56
3:C:70:TRP:HB3	3:C:230:VAL:O	2.05	0.56
2:B:151:ARG:HH22	2:B:260:PRO:C	2.14	0.56
2:B:105:ILE:HG22	2:B:106:PRO:HD3	1.89	0.55
1:A:244:THR:OG1	1:A:245:TYR:N	2.39	0.54
3:C:103:THR:HB	3:C:106:LYS:HB2	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:366:PRO:HB2	3:C:368:THR:HG22	1.91	0.52
3:C:368:THR:HG23	3:C:371:GLY:H	1.74	0.52
2:B:114:ARG:HG3	2:B:178:TYR:CE2	2.45	0.52
1:A:50:GLU:HG2	1:A:210:ILE:HB	1.90	0.52
3:C:285:PHE:CD2	3:C:292:ILE:HD11	2.45	0.51
2:B:116:ASP:HB2	2:B:238:THR:HB	1.93	0.51
2:B:15:SER:HB3	2:B:56:ARG:HG3	1.94	0.50
2:B:114:ARG:HD3	2:B:183:PRO:O	2.11	0.50
3:C:139:PRO:HB2	3:C:140:ARG:NH1	2.26	0.50
2:B:115:ALA:HB2	2:B:240:ALA:HA	1.93	0.49
3:C:272:SER:HA	3:C:275:PHE:HE1	1.77	0.49
3:C:281:SER:HB2	3:C:288:SER:HB2	1.94	0.49
3:C:269:SER:HB3	3:C:410:LEU:HD23	1.95	0.48
2:B:82:PRO:HG3	2:B:117:PHE:CZ	2.49	0.48
1:A:28:GLU:HG3	1:A:30:PHE:CZ	2.48	0.48
1:A:228:SER:OG	3:C:44:ARG:NH2	2.46	0.48
2:B:65:TRP:CH2	2:B:217:PHE:HB2	2.49	0.48
3:C:298:VAL:O	3:C:301:HIS:HB2	2.14	0.48
1:A:127:PRO:HB3	1:A:198:GLY:HA2	1.95	0.47
3:C:318:TRP:CZ3	3:C:413:PRO:HG3	2.50	0.47
3:C:223:MET:HE2	3:C:225:SER:H	1.79	0.46
1:A:49:LEU:HD23	1:A:214:GLY:HA3	1.96	0.46
3:C:269:SER:HB2	3:C:408:ASN:ND2	2.30	0.46
1:A:210:ILE:HG23	1:A:215:ILE:HG23	1.98	0.46
1:A:169:PHE:CZ	1:A:171:GLN:HB2	2.51	0.45
2:B:36:PRO:HG3	2:B:114:ARG:HH22	1.82	0.45
3:C:143:ALA:HB2	3:C:220:LEU:HA	1.99	0.45
3:C:246:VAL:HA	3:C:247:PRO:HD3	1.86	0.45
1:A:119:TRP:CE2	1:A:203:GLY:HA3	2.52	0.45
2:B:3:ARG:HD2	2:B:7:SER:HA	1.98	0.45
3:C:198:GLY:O	3:C:251:ALA:HA	2.16	0.45
1:A:143:ASP:O	1:A:201:LEU:HD22	2.17	0.45
3:C:18:HIS:CE1	3:C:29:PRO:HB2	2.52	0.44
1:A:54:ARG:NH2	1:A:139:ILE:O	2.50	0.44
3:C:272:SER:HA	3:C:275:PHE:CE1	2.52	0.44
1:A:123:HIS:CE1	1:A:201:LEU:HD13	2.52	0.44
1:A:87:ARG:HH12	1:A:244:THR:HG22	1.82	0.44
1:A:181:SER:HB2	2:B:145:PHE:HA	1.99	0.44
2:B:36:PRO:HG3	2:B:114:ARG:HH12	1.82	0.44
3:C:289:THR:HG21	3:C:392:ARG:NH2	2.32	0.44
2:B:28:ASP:OD1	2:B:29:ILE:N	2.49	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:181:SER:HA	2:B:145:PHE:HB3	1.99	0.43
2:B:3:ARG:HB2	2:B:5:GLU:O	2.17	0.43
2:B:80:LYS:NZ	2:B:202:GLU:OE2	2.41	0.43
1:A:102:ARG:CD	3:C:48:ILE:HD13	2.45	0.43
2:B:36:PRO:CG	2:B:114:ARG:HH22	2.32	0.43
2:B:85:TRP:CE2	2:B:235:VAL:HB	2.53	0.43
3:C:191:MET:H	3:C:191:MET:HG3	1.61	0.43
3:C:198:GLY:N	3:C:205:GLU:HG2	2.34	0.43
1:A:116:SER:OG	1:A:117:CYS:N	2.50	0.43
3:C:149:TYR:CD1	3:C:184:VAL:HB	2.54	0.43
2:B:14:THR:OG1	2:B:55:ASP:O	2.29	0.42
2:B:101:ILE:HA	2:B:102:PRO:HD2	1.86	0.42
1:A:19:THR:HG23	3:C:126:ARG:NH2	2.35	0.42
2:B:86:VAL:HA	2:B:104:PHE:CZ	2.54	0.42
3:C:223:MET:HE3	3:C:223:MET:HB2	1.78	0.42
1:A:102:ARG:NH1	1:A:174:LEU:O	2.51	0.42
3:C:333:LYS:HA	3:C:339:TRP:O	2.20	0.42
1:A:64:GLN:HG3	1:A:201:LEU:HD21	2.02	0.41
1:A:132:ARG:HD2	1:A:132:ARG:HA	1.88	0.41
1:A:91:ILE:HB	1:A:92:PRO:HD3	2.02	0.41
3:C:70:TRP:CD1	3:C:232:ILE:HD11	2.55	0.41
3:C:292:ILE:HG22	3:C:293:LEU:N	2.36	0.41
2:B:111:GLN:HG3	2:B:190:ILE:HD13	2.03	0.41
2:B:193:GLY:HA3	2:B:197:ILE:O	2.20	0.41
2:B:60:TRP:HB3	2:B:233:LEU:HB2	2.03	0.41
3:C:198:GLY:H	3:C:205:GLU:HG2	1.86	0.40
3:C:86:SER:HB2	3:C:211:TYR:CE2	2.56	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	250/266 (94%)	239 (96%)	11 (4%)	0	100	100
2	B	258/261 (99%)	245 (95%)	13 (5%)	0	100	100
3	C	415/430 (96%)	404 (97%)	11 (3%)	0	100	100
All	All	923/957 (96%)	888 (96%)	35 (4%)	0	100	100

There are no Ramachandran outliers to report.

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	218/230 (95%)	214 (98%)	4 (2%)	51	76
2	B	233/234 (100%)	231 (99%)	2 (1%)	70	87
3	C	355/366 (97%)	353 (99%)	2 (1%)	78	91
All	All	806/830 (97%)	798 (99%)	8 (1%)	68	86

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	6	THR
1	A	201	LEU
1	A	223	ILE
1	A	252	LEU
2	B	60	TRP
2	B	132	TRP
3	C	70	TRP
3	C	226	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	80	ASN
2	B	27	GLN

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Mol	Chain	Res	Type
2	B	68	ASN
2	B	110	HIS
3	C	82	HIS
3	C	97	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	252/266 (94%)	0.57	9 (3%)	46	40	9, 14, 29, 56	0
2	B	260/261 (99%)	0.57	9 (3%)	47	41	8, 15, 30, 36	0
3	C	417/430 (96%)	1.12	92 (22%)	2	2	9, 18, 56, 66	0
All	All	929/957 (97%)	0.82	110 (11%)	9	7	8, 15, 52, 66	0

All (110) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	252	LEU	5.9
3	C	295	TYR	4.9
3	C	280	GLY	4.8
3	C	355	ARG	4.8
3	C	274	TYR	4.7
3	C	359	TYR	4.7
3	C	298	VAL	4.6
3	C	285	PHE	4.5
3	C	296	GLY	4.3
3	C	284	SER	4.2
3	C	286	PHE	4.1
3	C	304	GLN	4.1
3	C	358	ALA	4.1
3	C	356	ASP	4.1
3	C	289	THR	4.1
3	C	406	LYS	4.0
3	C	310	ALA	4.0
3	C	281	SER	4.0
3	C	360	ALA	3.9
3	C	314	ARG	3.8
3	C	282	TRP	3.7
3	C	299	SER	3.7
3	C	327	PHE	3.6

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Mol	Chain	Res	Type	RSRZ
3	C	303	ALA	3.6
3	C	332	ASP	3.5
3	C	386	THR	3.5
3	C	305	LEU	3.5
3	C	307	ASN	3.5
3	C	389	SER	3.4
3	C	325	ILE	3.4
3	C	398	TYR	3.4
3	C	341	ILE	3.3
3	C	330	LYS	3.3
3	C	277	VAL	3.3
3	C	346	TYR	3.3
3	C	329	THR	3.3
3	C	302	ILE	3.3
3	C	279	VAL	3.2
3	C	328	LYS	3.1
2	B	251	ALA	3.1
1	A	251	ASP	3.1
3	C	344	GLY	3.1
3	C	357	GLY	3.1
2	B	48	ASP	3.1
1	A	249	THR	3.1
3	C	339	TRP	3.1
3	C	283	HIS	3.0
3	C	301	HIS	3.0
3	C	393	PRO	3.0
3	C	388	ILE	3.0
3	C	311	ASN	3.0
3	C	390	GLN	3.0
3	C	334	ILE	3.0
3	C	336	GLY	2.9
3	C	394	TYR	2.9
3	C	399	ILE	2.9
3	C	287	ASP	2.9
3	C	312	VAL	2.8
3	C	313	ASN	2.8
3	C	294	ARG	2.8
3	C	338	GLU	2.7
3	C	343	GLU	2.7
3	C	397	ASP	2.7
2	B	70	SER	2.7
3	C	405	SER	2.7

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Mol	Chain	Res	Type	RSRZ
3	C	333	LYS	2.7
3	C	326	LYS	2.7
1	A	250	PRO	2.7
3	C	352	VAL	2.6
3	C	354	TRP	2.6
3	C	404	ALA	2.6
3	C	400	VAL	2.6
3	C	395	ILE	2.6
3	C	27	SER	2.5
3	C	306	GLY	2.5
2	B	49	GLU	2.5
3	C	377	TYR	2.5
3	C	297	ALA	2.5
3	C	353	VAL	2.5
3	C	401	ASP	2.4
3	C	387	ALA	2.4
3	C	288	SER	2.4
3	C	265	ASP	2.4
3	C	300	ASP	2.4
1	A	247	ALA	2.4
3	C	384	SER	2.4
2	B	50	TYR	2.3
3	C	266	SER	2.3
1	A	56	ILE	2.3
2	B	92	VAL	2.3
3	C	392	ARG	2.3
3	C	278	TYR	2.2
3	C	396	PRO	2.2
1	A	248	ALA	2.2
2	B	258	ALA	2.2
3	C	292	ILE	2.2
3	C	361	TYR	2.2
3	C	403	ALA	2.1
3	C	331	LEU	2.1
3	C	275	PHE	2.1
3	C	342	PRO	2.1
2	B	196	LEU	2.1
3	C	385	ASN	2.1
3	C	264	LYS	2.0
3	C	272	SER	2.0
3	C	368	THR	2.0
1	A	114	LEU	2.0

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Mol	Chain	Res	Type	RSRZ
3	C	239	GLY	2.0
1	A	118	VAL	2.0
2	B	40	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.