



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 1, 2026 – 03:41 PM UTC

PDB ID : 6BA5 / pdb_00006ba5
Title : Potent and Selective Antitumor Activity of a T-Cell Engaging Bispecific Antibody Targeting a Membrane-Proximal Epitope of ROR1
Authors : Park, H.; Rader, C.
Deposited on : 2017-10-12
Resolution : 1.62 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:

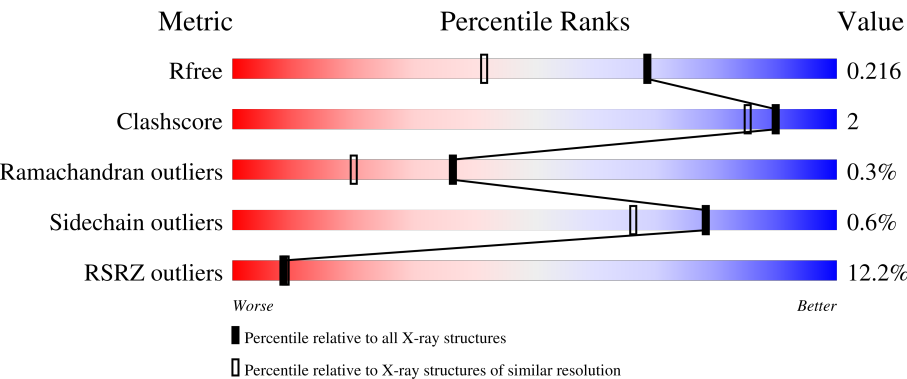
MolProbity	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 1.62 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	6728 (1.64-1.60)
Clashscore	190562	7023 (1.64-1.60)
Ramachandran outliers	187476	6898 (1.64-1.60)
Sidechain outliers	187428	6896 (1.64-1.60)
RSRZ outliers	180081	6727 (1.64-1.60)

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	114	8% 92%
1	C	114	5% 95%
1	E	114	7% 91% 6%
1	G	114	3% 96%
2	B	117	13% 91% 6%

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Mol	Chain	Length	Quality of chain
2	D	117	9% 85% 11%
2	F	117	8% 89% 8%
2	H	117	9% 90% 7%
3	M	82	15% 91% 7%
3	N	82	21% 96%
3	O	82	26% 94%
3	P	82	33% 96%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 10620 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 Variable domain of Light Chain, antibody R11.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	110	Total	C	N	O	S	0	0	0
			805	498	139	165	3			
1	C	110	Total	C	N	O	S	0	0	0
			805	498	139	165	3			
1	E	111	Total	C	N	O	S	0	0	0
			813	503	140	166	4			
1	G	111	Total	C	N	O	S	0	0	0
			813	503	140	166	4			

- Molecule 2 is a protein called Variable domain Heavy chain, antibody R11.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	113	Total	C	N	O	S	0	0	0
			865	550	139	173	3			
2	D	113	Total	C	N	O	S	0	0	0
			863	548	139	173	3			
2	F	113	Total	C	N	O	S	0	0	0
			865	550	139	173	3			
2	H	113	Total	C	N	O	S	0	0	0
			863	548	139	173	3			

- Molecule 3 is a protein called Inactive tyrosine-protein kinase transmembrane receptor ROR1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	M	81	Total	C	N	O	S	0	0	0
			646	401	117	122	6			
3	N	81	Total	C	N	O	S	0	0	0
			646	401	117	122	6			
3	O	80	Total	C	N	O	S	0	0	0
			636	395	114	121	6			
3	P	80	Total	C	N	O	S	0	0	0
			636	395	114	121	6			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
M	310	MET	-	initiating methionine	UNP Q01973
N	310	MET	-	initiating methionine	UNP Q01973
O	310	MET	-	initiating methionine	UNP Q01973
P	310	MET	-	initiating methionine	UNP Q01973

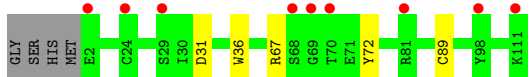
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	151	Total 151	O 151	0	0
4	B	139	Total 139	O 139	0	0
4	C	147	Total 147	O 147	0	0
4	D	136	Total 136	O 136	0	0
4	E	160	Total 160	O 160	0	0
4	F	145	Total 145	O 145	0	0
4	G	136	Total 136	O 136	0	0
4	H	136	Total 136	O 136	0	0
4	M	70	Total 70	O 70	0	0
4	N	50	Total 50	O 50	0	0
4	O	58	Total 58	O 58	0	0
4	P	36	Total 36	O 36	0	0

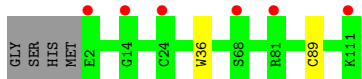
3 Residue-property plots [i](#)

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: Variable domain of Light Chain, antibody R11



- Molecule 1: Variable domain of Light Chain, antibody R11



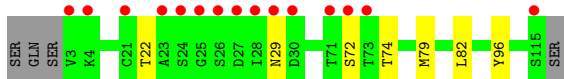
- Molecule 1: Variable domain of Light Chain, antibody R11



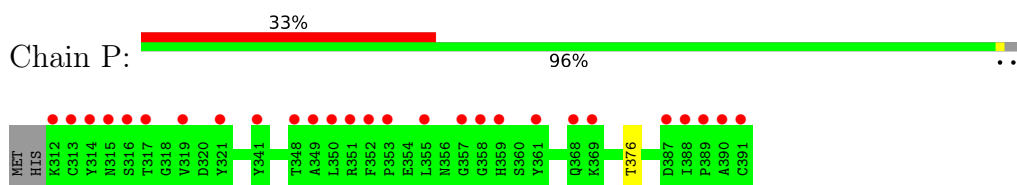
- Molecule 1: Variable domain of Light Chain, antibody R11



- Molecule 2: Variable domain Heavy chain, antibody R11



- Molecule 2: Variable domain Heavy chain, antibody R11



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	58.02Å 73.90Å 84.12Å 89.86° 71.30° 84.49°	Depositor
Resolution (Å)	39.53 – 1.62 39.53 – 1.62	Depositor EDS
% Data completeness (in resolution range)	96.1 (39.53-1.62) 96.1 (39.53-1.62)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.70 (at 1.62Å)	Xtriage
Refinement program	BUSTER 2.10.2	Depositor
R, R_{free}	0.194 , 0.214 0.198 , 0.216	Depositor DCC
R_{free} test set	3234 reflections (2.01%)	wwPDB-VP
Wilson B-factor (Å ²)	11.7	Xtriage
Anisotropy	0.735	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 45.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.000 for -h,-k,-h+l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	10620	wwPDB-VP
Average B, all atoms (Å ²)	21.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 58.64 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 1.9847e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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

5.1 Standard geometry

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	0.80	0/819	0.95	1/1114 (0.1%)
1	C	0.77	0/819	0.93	0/1114
1	E	0.80	0/827	0.97	1/1124 (0.1%)
1	G	0.77	0/827	0.94	0/1124
2	B	0.80	0/888	0.91	0/1214
2	D	0.79	0/886	0.91	0/1211
2	F	0.78	0/888	0.89	0/1214
2	H	0.79	0/886	0.93	0/1211
3	M	0.76	0/667	1.07	1/907 (0.1%)
3	N	0.75	0/667	1.04	1/907 (0.1%)
3	O	0.75	0/656	1.10	2/892 (0.2%)
3	P	0.72	0/656	1.04	0/892
All	All	0.78	0/9486	0.97	6/12924 (0.0%)

There are no bond length outliers.

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	31	ASP	CA-CB-CG	6.25	118.85	112.60
3	N	384	ASP	CA-CB-CG	5.76	118.36	112.60
3	M	384	ASP	CA-CB-CG	5.72	118.32	112.60
3	O	357	GLY	N-CA-C	5.24	120.22	114.40
1	A	31	ASP	CA-CB-CG	5.16	117.75	112.60
3	O	384	ASP	CA-CB-CG	5.10	117.70	112.60

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	805	0	783	2	0
1	C	805	0	783	1	0
1	E	813	0	795	3	0
1	G	813	0	795	1	0
2	B	865	0	822	3	0
2	D	863	0	815	8	0
2	F	865	0	822	5	0
2	H	863	0	815	4	0
3	M	646	0	587	2	0
3	N	646	0	587	0	0
3	O	636	0	580	0	0
3	P	636	0	580	0	0
4	A	151	0	0	0	0
4	B	139	0	0	0	0
4	C	147	0	0	0	0
4	D	136	0	0	1	0
4	E	160	0	0	0	0
4	F	145	0	0	0	0
4	G	136	0	0	0	0
4	H	136	0	0	0	0
4	M	70	0	0	0	0
4	N	50	0	0	0	0
4	O	58	0	0	0	0
4	P	36	0	0	0	0
All	All	10620	0	8764	27	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 2.

All (27) 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)
2:H:22:THR:HG22	2:H:74:THR:HG22	1.66	0.78
2:D:22:THR:HG22	2:D:74:THR:HG22	1.67	0.76
2:F:22:THR:HG22	2:F:74:THR:HG22	1.68	0.75
2:B:22:THR:HG22	2:B:74:THR:HG22	1.69	0.74
2:D:10:LEU:HB2	2:F:20:THR:CG2	2.26	0.66
2:D:13:PRO:HD3	2:D:115:SER:HB2	1.77	0.66
3:M:313:CYS:HG	3:M:391:CYS:HG	0.65	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:29:ASN:HB3	2:B:72:SER:O	2.08	0.54
2:D:82:LEU:HB3	2:D:114:ILE:HG12	1.92	0.51
2:F:29:ASN:HB3	2:F:72:SER:O	2.13	0.48
2:H:66:PHE:CD2	2:H:79:MET:HG2	2.49	0.47
2:D:29:ASN:HB3	2:D:72:SER:O	2.15	0.47
1:E:67:ARG:HD2	1:E:72:TYR:CE2	2.50	0.47
2:H:29:ASN:HB3	2:H:72:SER:O	2.14	0.46
2:D:26:SER:HB2	4:D:291:HOH:O	2.17	0.45
2:D:79:MET:HB3	2:D:82:LEU:HD21	1.98	0.44
2:F:79:MET:HB2	2:F:82:LEU:HD21	1.99	0.44
2:D:5:GLU:HG2	2:F:92:CYS:SG	2.58	0.44
1:E:9:PRO:CG	1:E:12:THR:HG23	2.48	0.43
2:B:79:MET:HB2	2:B:82:LEU:HD21	1.99	0.43
1:A:36:TRP:CZ3	1:A:89:CYS:HB3	2.54	0.42
2:H:11:VAL:HG11	2:H:82:LEU:HD12	2.02	0.42
1:A:67:ARG:HD2	1:A:72:TYR:CE2	2.54	0.41
1:C:36:TRP:CZ3	1:C:89:CYS:HB3	2.56	0.41
1:G:9:PRO:CG	1:G:12:THR:HG23	2.51	0.41
1:E:9:PRO:HG2	1:E:12:THR:HG23	2.02	0.40
3:M:328:THR:HA	3:M:386:CYS:HA	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	Percentiles	
1	A	108/114 (95%)	102 (94%)	6 (6%)	0	100	100
1	C	108/114 (95%)	103 (95%)	5 (5%)	0	100	100
1	E	109/114 (96%)	103 (94%)	6 (6%)	0	100	100
1	G	109/114 (96%)	105 (96%)	4 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	B	111/117 (95%)	109 (98%)	1 (1%)	1 (1%)	14	3
2	D	111/117 (95%)	110 (99%)	0	1 (1%)	14	3
2	F	111/117 (95%)	110 (99%)	0	1 (1%)	14	3
2	H	111/117 (95%)	109 (98%)	2 (2%)	0	100	100
3	M	79/82 (96%)	76 (96%)	3 (4%)	0	100	100
3	N	79/82 (96%)	77 (98%)	2 (2%)	0	100	100
3	O	78/82 (95%)	77 (99%)	1 (1%)	0	100	100
3	P	78/82 (95%)	76 (97%)	2 (3%)	0	100	100
All	All	1192/1252 (95%)	1157 (97%)	32 (3%)	3 (0%)	36	20

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	96	TYR
2	D	96	TYR
2	F	96	TYR

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	89/92 (97%)	89 (100%)	0	100	100
1	C	89/92 (97%)	89 (100%)	0	100	100
1	E	90/92 (98%)	88 (98%)	2 (2%)	45	21
1	G	90/92 (98%)	90 (100%)	0	100	100
2	B	94/98 (96%)	94 (100%)	0	100	100
2	D	93/98 (95%)	93 (100%)	0	100	100
2	F	94/98 (96%)	94 (100%)	0	100	100
2	H	93/98 (95%)	93 (100%)	0	100	100
3	M	72/73 (99%)	71 (99%)	1 (1%)	59	37

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	N	72/73 (99%)	71 (99%)	1 (1%)	59	37
3	O	71/73 (97%)	70 (99%)	1 (1%)	59	37
3	P	71/73 (97%)	70 (99%)	1 (1%)	59	37
All	All	1018/1052 (97%)	1012 (99%)	6 (1%)	78	66

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	49	ILE
1	E	71	GLU
3	M	376	THR
3	N	376	THR
3	O	376	THR
3	P	376	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (16) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	38	GLN
1	C	25	GLN
1	C	38	GLN
1	C	39	GLN
2	D	38	GLN
1	E	33	ASN
1	E	38	GLN
1	E	39	GLN
2	F	38	GLN
1	G	25	GLN
1	G	38	GLN
1	G	39	GLN
2	H	16	ASN
2	H	38	GLN
3	M	333	GLN
3	N	359	HIS

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	110/114 (96%)	0.05	9 (8%) 17 18	8, 13, 28, 59	0
1	C	110/114 (96%)	0.05	6 (5%) 30 33	8, 15, 31, 68	0
1	E	111/114 (97%)	0.14	8 (7%) 21 23	8, 13, 30, 52	0
1	G	111/114 (97%)	0.09	3 (2%) 56 60	9, 15, 30, 70	0
2	B	113/117 (96%)	0.37	15 (13%) 7 7	7, 12, 43, 59	0
2	D	113/117 (96%)	0.19	11 (9%) 13 14	7, 12, 35, 48	0
2	F	113/117 (96%)	0.02	9 (7%) 18 19	7, 11, 33, 47	0
2	H	113/117 (96%)	0.19	10 (8%) 15 16	8, 14, 32, 51	0
3	M	81/82 (98%)	0.85	12 (14%) 5 5	9, 26, 52, 69	0
3	N	81/82 (98%)	0.99	17 (20%) 2 2	10, 31, 52, 79	0
3	O	80/82 (97%)	1.29	21 (26%) 1 1	9, 33, 67, 92	0
3	P	80/82 (97%)	1.61	27 (33%) 1 1	14, 40, 73, 106	0
All	All	1216/1252 (97%)	0.42	148 (12%) 8 9	7, 16, 51, 106	0

All (148) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	N	391	CYS	7.8
2	B	25	GLY	7.3
2	B	3	VAL	7.3
2	H	3	VAL	7.0
2	D	25	GLY	6.7
2	B	26	SER	6.4
3	O	312	LYS	6.1
3	O	350	LEU	5.9
3	O	391	CYS	5.9
3	P	391	CYS	5.4
2	B	29	ASN	5.3

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Mol	Chain	Res	Type	RSRZ
3	O	348	THR	5.2
2	B	28	ILE	5.1
2	D	3	VAL	5.1
3	P	312	LYS	5.1
2	B	27	ASP	5.0
2	D	28	ILE	5.0
2	F	3	VAL	4.8
2	F	26	SER	4.6
3	P	319	VAL	4.6
3	P	350	LEU	4.4
3	P	313	CYS	4.2
2	B	24	SER	4.2
3	O	351	ARG	4.1
1	C	111	LYS	4.0
3	P	389	PRO	4.0
2	D	26	SER	3.9
1	G	111	LYS	3.8
3	P	348	THR	3.8
2	H	4	LYS	3.7
3	N	311	HIS	3.7
3	P	388	ILE	3.7
3	O	352	PHE	3.7
3	N	312	LYS	3.6
3	M	350	LEU	3.6
3	O	357	GLY	3.6
3	P	368	GLN	3.6
2	B	115	SER	3.5
2	B	23	ALA	3.5
2	H	25	GLY	3.5
2	D	24	SER	3.5
3	O	349	ALA	3.5
3	M	311	HIS	3.4
2	F	24	SER	3.4
3	P	317	THR	3.3
2	B	21	CYS	3.3
3	O	319	VAL	3.3
2	D	29	ASN	3.3
2	D	27	ASP	3.3
2	B	72	SER	3.2
3	M	391	CYS	3.2
3	P	357	GLY	3.2
2	F	25	GLY	3.2

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Mol	Chain	Res	Type	RSRZ
2	H	24	SER	3.1
3	N	353	PRO	3.1
1	A	68	SER	3.1
3	O	316	SER	3.1
1	E	1	MET	3.1
3	P	315	ASN	3.1
2	D	21	CYS	3.1
3	O	358	GLY	3.0
3	P	314	TYR	3.0
3	M	351	ARG	3.0
3	O	356	ASN	3.0
2	B	73	THR	3.0
2	F	21	CYS	3.0
2	D	115	SER	3.0
2	H	26	SER	3.0
3	P	387	ASP	3.0
3	P	353	PRO	3.0
3	P	355	LEU	3.0
3	P	316	SER	3.0
2	H	28	ILE	3.0
1	A	2	GLU	2.9
2	D	4	LYS	2.9
3	O	353	PRO	2.9
1	C	68	SER	2.8
2	H	115	SER	2.8
3	N	350	LEU	2.8
1	G	1	MET	2.8
3	N	387	ASP	2.8
3	M	357	GLY	2.8
3	O	389	PRO	2.7
1	E	24	CYS	2.7
3	N	313	CYS	2.7
3	P	358	GLY	2.7
3	P	390	ALA	2.7
1	E	111	LYS	2.7
2	F	4	LYS	2.7
3	M	370	GLU	2.6
3	M	312	LYS	2.6
2	H	21	CYS	2.6
3	N	351	ARG	2.6
3	N	389	PRO	2.6
3	O	341	TYR	2.6

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Mol	Chain	Res	Type	RSRZ
3	P	349	ALA	2.6
3	N	315	ASN	2.6
3	O	315	ASN	2.6
1	A	69	GLY	2.6
1	A	98	TYR	2.6
3	M	341	TYR	2.6
1	E	68	SER	2.6
3	N	354	GLU	2.5
3	M	368	GLN	2.5
2	F	115	SER	2.5
3	M	316	SER	2.5
3	N	370	GLU	2.5
3	P	359	HIS	2.5
1	C	14	GLY	2.4
2	F	23	ALA	2.4
3	N	390	ALA	2.4
1	G	24	CYS	2.4
3	N	368	GLN	2.4
1	A	111	LYS	2.4
2	B	4	LYS	2.4
3	N	359	HIS	2.4
1	E	81	ARG	2.3
3	P	369	LYS	2.3
3	P	341	TYR	2.3
3	O	355	LEU	2.3
3	N	357	GLY	2.3
1	A	81	ARG	2.2
2	F	27	ASP	2.2
2	H	23	ALA	2.2
3	O	313	CYS	2.2
3	P	352	PHE	2.2
3	N	388	ILE	2.2
2	B	71	THR	2.2
1	C	81	ARG	2.2
3	O	388	ILE	2.2
1	A	24	CYS	2.1
1	E	12	THR	2.1
3	P	361	TYR	2.1
3	P	351	ARG	2.1
3	M	356	ASN	2.1
1	C	2	GLU	2.1
2	D	5	GLU	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	70	THR	2.1
3	M	352	PHE	2.1
1	E	98	TYR	2.1
1	A	29	SER	2.1
1	E	13	SER	2.1
3	O	346	THR	2.1
3	O	314	TYR	2.1
3	P	321	TYR	2.1
2	B	30	ASP	2.0
2	H	27	ASP	2.0
1	C	24	CYS	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.