



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 06:06 AM UTC

PDB ID : 4BK4 / pdb_00004bk4
Title : crystal structure of the human EphA4 ectodomain
Authors : Seiradake, E.; Schaupp, A.; del Toro Ruiz, D.; Kaufmann, R.; Mitakidis, N.; Harlos, K.; Aricescu, A.R.; Klein, R.; Jones, E.Y.
Deposited on : 2013-04-22
Resolution : 3.65 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

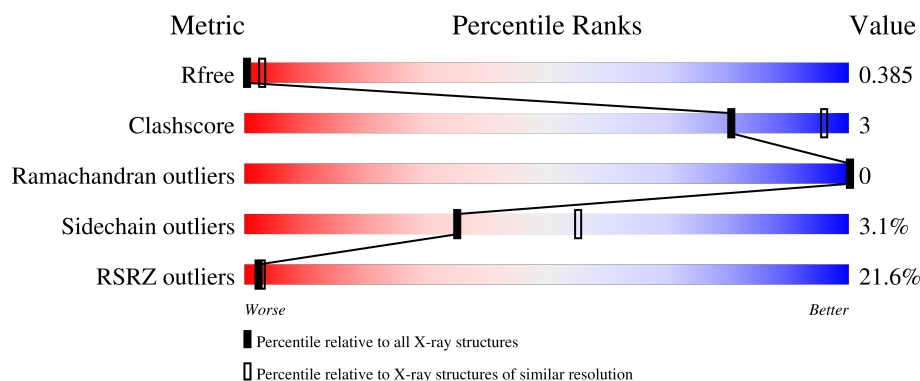
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.65 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	1062 (3.78-3.54)
Clashscore	190562	1009 (3.76-3.56)
Ramachandran outliers	187476	1054 (3.78-3.54)
Sidechain outliers	187428	1052 (3.78-3.54)
RSRZ outliers	180081	1061 (3.78-3.54)

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	568	17% 83% 7% 10%
1	B	568	14% 46% 6% 47%

2 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 6344 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 EPHRIN TYPE-A RECEPTOR 4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	514	Total	C	N	O	S	0	0	0
			4002	2496	692	788	26			
1	B	300	Total	C	N	O	S	0	0	0
			2342	1460	398	462	22			

There are 80 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-11	MET	-	expression tag	UNP P54764
A	-10	GLY	-	expression tag	UNP P54764
A	-9	ILE	-	expression tag	UNP P54764
A	-8	LEU	-	expression tag	UNP P54764
A	-7	PRO	-	expression tag	UNP P54764
A	-6	SER	-	expression tag	UNP P54764
A	-5	PRO	-	expression tag	UNP P54764
A	-4	GLY	-	expression tag	UNP P54764
A	-3	MET	-	expression tag	UNP P54764
A	-2	PRO	-	expression tag	UNP P54764
A	-1	ALA	-	expression tag	UNP P54764
A	0	LEU	-	expression tag	UNP P54764
A	1	LEU	-	expression tag	UNP P54764
A	2	SER	-	expression tag	UNP P54764
A	3	LEU	-	expression tag	UNP P54764
A	4	VAL	-	expression tag	UNP P54764
A	5	SER	-	expression tag	UNP P54764
A	6	LEU	-	expression tag	UNP P54764
A	7	LEU	-	expression tag	UNP P54764
A	8	SER	-	expression tag	UNP P54764
A	9	VAL	-	expression tag	UNP P54764
A	10	LEU	-	expression tag	UNP P54764
A	11	LEU	-	expression tag	UNP P54764
A	12	MET	-	expression tag	UNP P54764
A	13	GLY	-	expression tag	UNP P54764

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Chain	Residue	Modelled	Actual	Comment	Reference
A	14	CYS	-	expression tag	UNP P54764
A	15	VAL	-	expression tag	UNP P54764
A	16	ALA	-	expression tag	UNP P54764
A	17	GLU	-	expression tag	UNP P54764
A	18	THR	-	expression tag	UNP P54764
A	19	GLY	-	expression tag	UNP P54764
A	548	GLY	-	expression tag	UNP P54764
A	549	THR	-	expression tag	UNP P54764
A	550	LYS	-	expression tag	UNP P54764
A	551	HIS	-	expression tag	UNP P54764
A	552	HIS	-	expression tag	UNP P54764
A	553	HIS	-	expression tag	UNP P54764
A	554	HIS	-	expression tag	UNP P54764
A	555	HIS	-	expression tag	UNP P54764
A	556	HIS	-	expression tag	UNP P54764
B	-11	MET	-	expression tag	UNP P54764
B	-10	GLY	-	expression tag	UNP P54764
B	-9	ILE	-	expression tag	UNP P54764
B	-8	LEU	-	expression tag	UNP P54764
B	-7	PRO	-	expression tag	UNP P54764
B	-6	SER	-	expression tag	UNP P54764
B	-5	PRO	-	expression tag	UNP P54764
B	-4	GLY	-	expression tag	UNP P54764
B	-3	MET	-	expression tag	UNP P54764
B	-2	PRO	-	expression tag	UNP P54764
B	-1	ALA	-	expression tag	UNP P54764
B	0	LEU	-	expression tag	UNP P54764
B	1	LEU	-	expression tag	UNP P54764
B	2	SER	-	expression tag	UNP P54764
B	3	LEU	-	expression tag	UNP P54764
B	4	VAL	-	expression tag	UNP P54764
B	5	SER	-	expression tag	UNP P54764
B	6	LEU	-	expression tag	UNP P54764
B	7	LEU	-	expression tag	UNP P54764
B	8	SER	-	expression tag	UNP P54764
B	9	VAL	-	expression tag	UNP P54764
B	10	LEU	-	expression tag	UNP P54764
B	11	LEU	-	expression tag	UNP P54764
B	12	MET	-	expression tag	UNP P54764
B	13	GLY	-	expression tag	UNP P54764
B	14	CYS	-	expression tag	UNP P54764
B	15	VAL	-	expression tag	UNP P54764

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Chain	Residue	Modelled	Actual	Comment	Reference
B	16	ALA	-	expression tag	UNP P54764
B	17	GLU	-	expression tag	UNP P54764
B	18	THR	-	expression tag	UNP P54764
B	19	GLY	-	expression tag	UNP P54764
B	548	GLY	-	expression tag	UNP P54764
B	549	THR	-	expression tag	UNP P54764
B	550	LYS	-	expression tag	UNP P54764
B	551	HIS	-	expression tag	UNP P54764
B	552	HIS	-	expression tag	UNP P54764
B	553	HIS	-	expression tag	UNP P54764
B	554	HIS	-	expression tag	UNP P54764
B	555	HIS	-	expression tag	UNP P54764
B	556	HIS	-	expression tag	UNP P54764

LYS	GLN	TYR	GLY
CYS	SER	ARG	THR
ALA	VAL	ILE	LYS
GLY	SER	VAL	HIS
ASP	VAL	ARG	HIS
PRO	THR	THR	HIS
SER	VAL	ALA	HIS
LYS	THR	ALA	HIS
CYS	ASN	ARG	HIS
ARG	GLN	THR	HIS
PRO	ALA	ASP	HIS
CYS	ALA	ILE	HIS
GLY	PRO	LYS	HIS
GLY	SER	GLY	HIS
ILE	SER	LEU	HIS
HIS	VAL	ASN	HIS
TYR	ALA	PRO	HIS
THR	LEU	LEU	HIS
THR	VAL	THR	HIS
PRO	GLN	SER	HIS
GLN	ALA	TYR	HIS
LYS	LYS	VAL	HIS
ASN	GLU	PHE	HIS
GLY	VAL	HIS	HIS
LEU	THR	VAL	HIS
LYS	ARG	VAL	HIS
THR	TYR	ALA	HIS
THR	SER	ARG	HIS
LYS	VAL	THR	HIS
VAL	ALA	ALA	HIS
SER	LEU	ALA	HIS
ILE	ALA	GLY	HIS
THR	TRP	TYR	HIS
ASP	LEU	GLY	HIS
LEU	LEU	ASP	HIS
ALA	PRO	PHE	HIS
HIS	ASP	SER	HIS
THR	ALA	GLU	HIS
PRO	ARG	PRO	HIS
ASN	THR	LEU	HIS
TYR	ASN	GLY	HIS
THR	GLY	VAL	HIS
PHE	THR	THR	HIS
ILE	ILE	THR	HIS
GLU	GLU	ASN	HIS
ILE	TRP	THR	HIS
ALA	GLU	VAL	HIS
VAL	VAL	PRO	HIS
ASN	ASN	SER	HIS
GLY	GLY	ARG	HIS
VAL	TYR	ILE	HIS
LYS	VAL	ILE	HIS
LYS	SER	ILE	HIS
TYR	LYS	GLY	HIS
ASN	ASP	ASP	HIS
PRO	GLN	GLY	HIS
ASN	THR	ALA	HIS
PRO	ASN	ASN	HIS
ASP	GLU	SER	HIS
	ARG	THR	HIS
	SER		HIS

4 Data and refinement statistics

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, α , β , γ	166.89Å 166.89Å 192.09Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	48.18 – 3.65 48.18 – 3.65	Depositor EDS
% Data completeness (in resolution range)	99.9 (48.18-3.65) 99.9 (48.18-3.65)	Depositor EDS
R_{merge}	0.19	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.05 (at 3.67Å)	Xtriage
Refinement program	BUSTER 2.11.2	Depositor
R, R_{free}	0.349 , 0.386 0.382 , 0.385	Depositor DCC
R_{free} test set	1751 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å ²)	178.5	Xtriage
Anisotropy	0.139	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 77.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	0.046 for -h,-k,l	Xtriage
F_o, F_c correlation	0.84	EDS
Total number of atoms	6344	wwPDB-VP
Average B, all atoms (Å ²)	124.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.53% 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	0.70	0/4088	1.10	3/5563 (0.1%)
1	B	0.70	0/2390	1.09	2/3240 (0.1%)
All	All	0.70	0/6478	1.09	5/8803 (0.1%)

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	520	GLY	N-CA-C	5.90	119.11	110.80
1	B	138	ARG	CA-C-N	5.29	128.14	120.79
1	B	138	ARG	C-N-CA	5.29	128.14	120.79
1	A	269	ARG	CA-C-N	5.08	127.34	120.38
1	A	269	ARG	C-N-CA	5.08	127.34	120.38

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	4002	0	3865	15	0
1	B	2342	0	2236	17	0
All	All	6344	0	6101	32	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 (32) 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:126:TYR:HB3	1:A:145:ILE:HD11	1.88	0.56
1:B:126:TYR:HB3	1:B:145:ILE:HD11	1.88	0.55
1:B:82:ASN:HB2	1:B:187:ASP:HB3	1.89	0.54
1:A:457:VAL:H	1:A:500:ILE:HG13	1.73	0.53
1:B:245:MET:HE2	1:B:256:PRO:HB3	1.91	0.53
1:B:91:ARG:HB2	1:B:180:GLY:H	1.74	0.52
1:A:389:GLN:HB2	1:A:393:LEU:HD13	1.92	0.52
1:A:471:ILE:HA	1:A:517:THR:HG22	1.91	0.52
1:B:105:LEU:HD12	1:B:192:ILE:HD12	1.91	0.51
1:A:443:SER:HB2	1:A:523:ASP:HB2	1.93	0.51
1:B:114:VAL:HG13	1:B:118:CYS:HB2	1.91	0.50
1:B:157:VAL:H	1:B:163:ILE:HG23	1.76	0.50
1:B:269:ARG:HH22	1:B:277:LYS:HE3	1.77	0.50
1:A:329:PRO:HG3	1:A:417:ASN:HB2	1.94	0.49
1:A:406:HIS:H	1:A:437:ASN:HB2	1.78	0.49
1:A:335:LEU:HD12	1:A:430:VAL:HG12	1.95	0.49
1:B:175:PRO:HB3	1:B:221:ALA:HB1	1.93	0.49
1:A:100:GLU:HB3	1:A:198:ARG:HB2	1.94	0.49
1:A:265:GLY:H	1:A:282:LYS:HB3	1.79	0.47
1:B:265:GLY:H	1:B:282:LYS:HB3	1.79	0.47
1:B:203:LYS:HE2	1:B:216:ASP:HB3	1.97	0.47
1:A:138:ARG:HB3	1:A:141:GLN:HB2	1.98	0.46
1:A:226:LEU:HD22	1:A:246:TYR:HB3	1.98	0.46
1:B:48:SER:HB3	1:B:49:PRO:HD3	1.98	0.44
1:A:300:VAL:HG22	1:A:308:THR:HG22	1.99	0.44
1:B:300:VAL:HG22	1:B:308:THR:HG22	1.99	0.44
1:B:30:GLU:HG3	1:B:203:LYS:H	1.83	0.44
1:B:96:ARG:HH21	1:B:222:ASP:HA	1.84	0.43
1:B:295:PRO:HD2	1:B:324:PRO:HB3	2.00	0.42
1:A:295:PRO:HD2	1:A:324:PRO:HB3	2.01	0.42
1:A:39:VAL:HG21	1:A:43:LEU:HA	2.01	0.42
1:B:255:VAL:HA	1:B:256:PRO:HD3	1.97	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	512/568 (90%)	483 (94%)	29 (6%)	0	100	100
1	B	298/568 (52%)	280 (94%)	18 (6%)	0	100	100
All	All	810/1136 (71%)	763 (94%)	47 (6%)	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	446/489 (91%)	429 (96%)	17 (4%)	29	51
1	B	259/489 (53%)	254 (98%)	5 (2%)	50	64
All	All	705/978 (72%)	683 (97%)	22 (3%)	35	55

All (22) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	64	ASN
1	A	105	LEU
1	A	107	ASP
1	A	300	VAL
1	A	335	LEU
1	A	339	VAL
1	A	369	CYS
1	A	386	TYR

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Mol	Chain	Res	Type
1	A	389	GLN
1	A	446	LEU
1	A	450	LYS
1	A	463	GLU
1	A	476	VAL
1	A	483	GLN
1	A	500	ILE
1	A	516	ARG
1	A	534	THR
1	B	67	ILE
1	B	89	ILE
1	B	218	ILE
1	B	300	VAL
1	B	325	CYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	64	ASN
1	A	80	GLN
1	A	131	ASN
1	A	236	ASN
1	A	389	GLN
1	A	408	ASN
1	A	497	ASN
1	B	64	ASN
1	B	131	ASN
1	B	167	ASN
1	B	236	ASN
1	B	266	HIS
1	B	296	HIS

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 [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	514/568 (90%)	1.14	95 (18%) 3 4	77, 116, 186, 300	0
1	B	300/568 (52%)	1.41	81 (27%) 1 2	65, 115, 228, 300	0
All	All	814/1136 (71%)	1.24	176 (21%) 2 3	65, 116, 212, 300	0

All (176) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	140	ASN	9.5
1	A	287	ASP	8.3
1	B	254	LEU	7.8
1	B	298	TYR	7.6
1	A	373	ASP	7.6
1	A	333	LEU	7.2
1	B	287	ASP	7.1
1	B	248	GLY	6.4
1	B	219	THR	6.3
1	B	255	VAL	6.3
1	B	218	ILE	6.1
1	A	425	ASN	5.8
1	B	226	LEU	5.6
1	B	301	TRP	5.4
1	B	261	LEU	5.4
1	A	272	GLU	5.3
1	A	32	THR	5.0
1	B	243	PRO	5.0
1	A	326	THR	4.9
1	B	246	TYR	4.8
1	A	156	GLN	4.7
1	A	165	LYS	4.7
1	B	311	ARG	4.6
1	B	249	ALA	4.6

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Mol	Chain	Res	Type	RSRZ
1	B	257	ILE	4.6
1	A	478	TYR	4.5
1	A	150	ALA	4.4
1	B	162	ARG	4.4
1	B	139	GLU	4.4
1	A	428	GLN	4.4
1	A	521	TYR	4.4
1	B	229	VAL	4.4
1	B	235	ASN	4.3
1	B	256	PRO	4.3
1	A	332	PRO	4.3
1	B	136	PHE	4.3
1	B	160	GLY	4.3
1	A	414	TRP	4.1
1	B	252	GLU	4.1
1	A	162	ARG	4.1
1	B	161	ASP	4.0
1	A	423	ASN	4.0
1	A	232	SER	3.9
1	B	310	ASP	3.8
1	A	506	LEU	3.8
1	B	227	VAL	3.8
1	B	184	ALA	3.7
1	A	331	ALA	3.7
1	A	454	ARG	3.6
1	A	154	PHE	3.6
1	B	220	GLY	3.6
1	A	110	SER	3.6
1	A	27	PRO	3.5
1	B	263	ASN	3.5
1	B	258	GLY	3.5
1	A	254	LEU	3.5
1	A	534	THR	3.5
1	B	188	VAL	3.4
1	A	195	VAL	3.3
1	A	31	VAL	3.3
1	A	170	ILE	3.3
1	A	415	ALA	3.2
1	A	159	ILE	3.2
1	A	163	ILE	3.2
1	A	537	SER	3.2
1	B	237	SER	3.2

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Mol	Chain	Res	Type	RSRZ
1	A	328	PRO	3.2
1	B	158	ASP	3.2
1	A	261	LEU	3.2
1	A	161	ASP	3.1
1	B	299	SER	3.1
1	B	217	THR	3.1
1	B	284	LEU	3.1
1	B	259	ASN	3.1
1	A	438	GLN	3.0
1	B	92	GLU	3.0
1	B	135	ARG	3.0
1	B	228	GLU	3.0
1	B	245	MET	3.0
1	A	388	PRO	3.0
1	B	312	GLY	3.0
1	B	231	GLY	3.0
1	B	155	THR	2.9
1	A	257	ILE	2.9
1	A	43	LEU	2.9
1	A	59	ILE	2.9
1	A	325	CYS	2.9
1	A	491	VAL	2.8
1	A	168	THR	2.8
1	B	88	TRP	2.8
1	B	303	GLY	2.8
1	B	216	ASP	2.7
1	B	247	CYS	2.7
1	A	455	TYR	2.7
1	B	278	ILE	2.7
1	A	427	ASP	2.7
1	A	535	VAL	2.7
1	B	262	CYS	2.7
1	B	244	LYS	2.7
1	A	311	ARG	2.7
1	A	341	GLU	2.7
1	A	166	LEU	2.7
1	A	241	ASP	2.6
1	A	540	ILE	2.6
1	B	166	LEU	2.6
1	B	251	GLY	2.6
1	A	416	VAL	2.6
1	A	58	SER	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	421	LYS	2.5
1	A	157	VAL	2.5
1	B	206	LEU	2.5
1	A	536	PRO	2.5
1	B	326	THR	2.5
1	A	301	TRP	2.5
1	A	149	ALA	2.5
1	B	185	PHE	2.5
1	B	213	GLN	2.5
1	B	314	PHE	2.5
1	A	46	ILE	2.5
1	A	164	MET	2.5
1	A	40	GLN	2.5
1	A	356	GLY	2.5
1	A	539	ILE	2.5
1	B	242	VAL	2.5
1	B	66	PRO	2.5
1	A	300	VAL	2.5
1	B	138	ARG	2.5
1	B	221	ALA	2.4
1	A	132	ASP	2.4
1	B	302	GLU	2.4
1	A	499	ASP	2.4
1	B	238	GLU	2.4
1	B	39	VAL	2.4
1	B	156	GLN	2.4
1	A	471	ILE	2.4
1	A	529	GLU	2.4
1	B	59	ILE	2.3
1	B	194	LEU	2.3
1	A	358	GLN	2.3
1	A	57	VAL	2.3
1	A	92	GLU	2.3
1	A	67	ILE	2.3
1	B	300	VAL	2.3
1	B	141	GLN	2.3
1	A	112	PRO	2.3
1	A	505	PRO	2.3
1	A	422	TYR	2.2
1	B	212	ALA	2.2
1	A	125	TYR	2.2
1	B	95	GLN	2.2

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Mol	Chain	Res	Type	RSRZ
1	B	209	ARG	2.2
1	A	271	GLY	2.2
1	A	370	GLY	2.2
1	A	392	GLY	2.2
1	A	511	PHE	2.2
1	A	430	VAL	2.2
1	A	268	GLU	2.2
1	A	446	LEU	2.2
1	A	96	ARG	2.1
1	A	312	GLY	2.1
1	B	114	VAL	2.1
1	B	234	VAL	2.1
1	A	371	ALA	2.1
1	B	208	VAL	2.1
1	B	250	ASP	2.1
1	A	501	LYS	2.1
1	A	45	TRP	2.0
1	A	86	THR	2.0
1	A	317	ASP	2.0
1	A	531	THR	2.0
1	A	413	ILE	2.0
1	A	98	TYR	2.0
1	B	100	GLU	2.0
1	B	131	ASN	2.0
1	B	296	HIS	2.0
1	A	28	ALA	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.