Full wwPDB X-ray Structure Validation Report (i)

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PDB ID	:	4V2E
Title	:	FLRT3 LRR domain
Authors	:	Seiradake, E.; del Toro, D.; Nagel, D.; Cop, F.; Haertl, R.; Ruff, T.; Seyit-Bremer, G.; Harlos, K.; Border, E.C.; Acker-Palmer, A.; Jones, E.Y.; Klein, R.
Deposited on	:	2014-10-08
Resolution	:	2.50 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
http://wwpdb.org/validation/2016/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

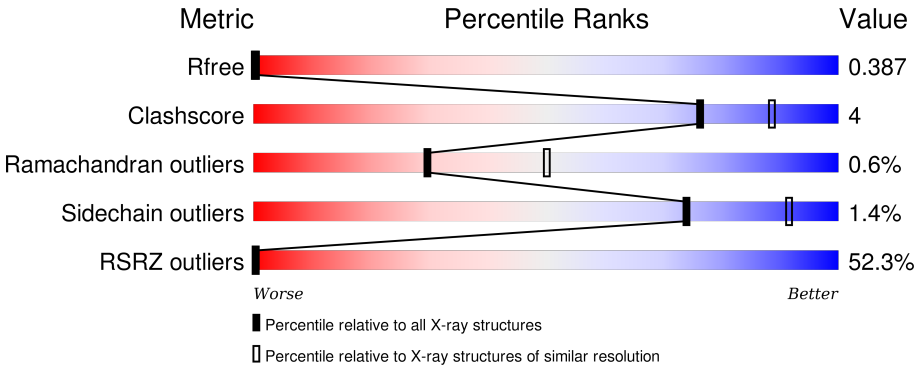
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	trunk26865

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 2.50 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}	91344	3553 (2.50-2.50)
Clashscore	102246	4242 (2.50-2.50)
Ramachandran outliers	100387	4156 (2.50-2.50)
Sidechain outliers	100360	4158 (2.50-2.50)
RSRZ outliers	91569	3562 (2.50-2.50)

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 on the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria. 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	A	331	38% 85% 12% ·
1	B	331	63% 86% 11% ·

2 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 5118 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 FIBRONECTIN LEUCINE RICH TRANSMEMBRANE PROTEIN 3.

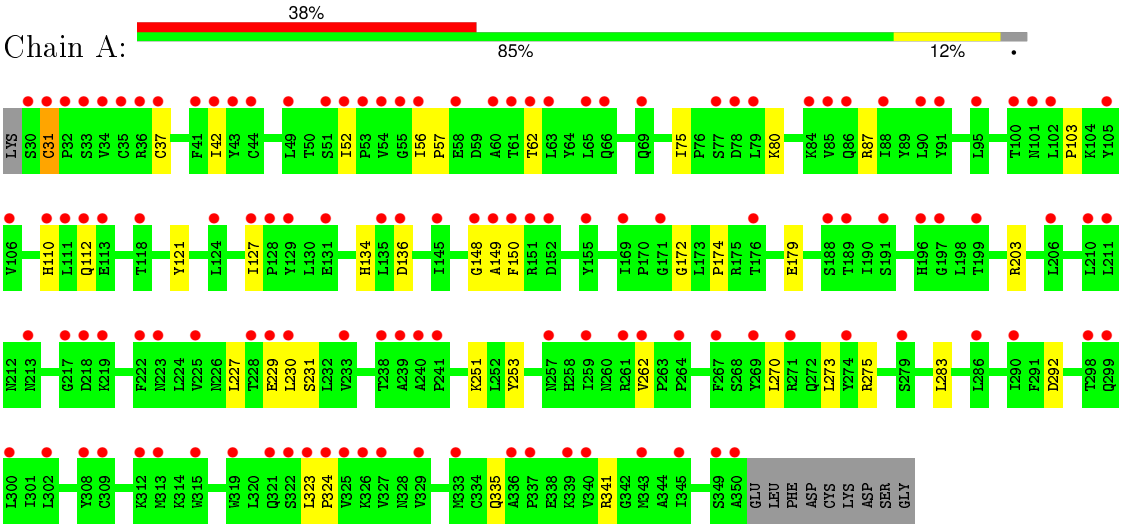
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	321	Total	C	N	O	S	0	0	0
			2559	1615	453	480	11			
1	B	321	Total	C	N	O	S	0	0	0
			2559	1615	453	480	11			

3 Residue-property plots (i)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

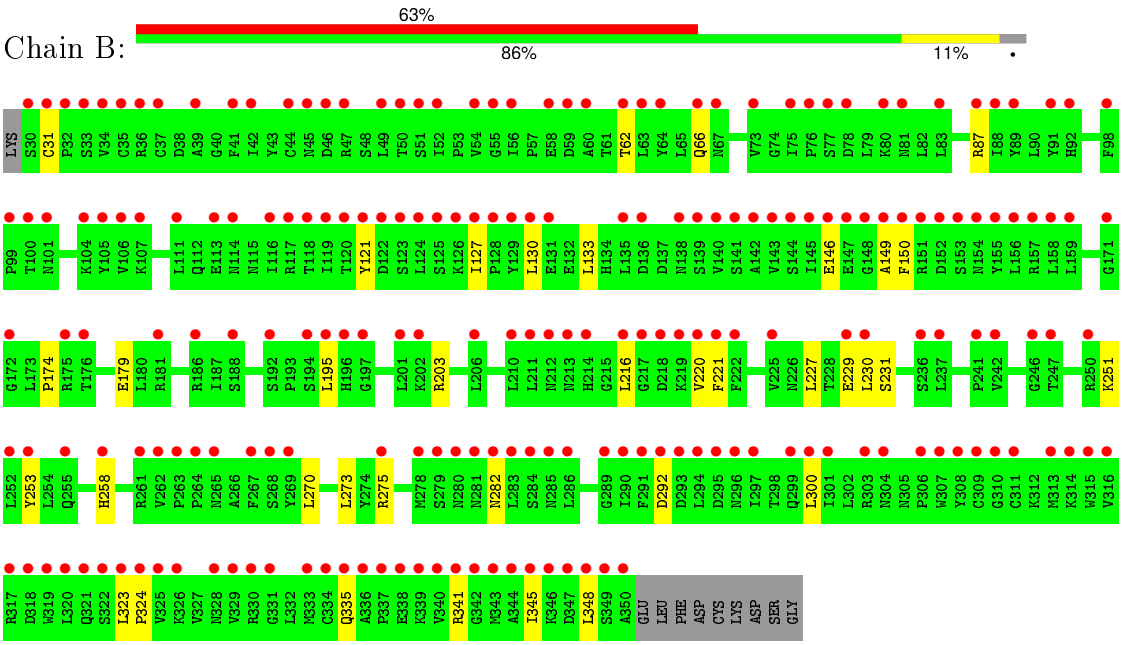
- Molecule 1: FIBRONECTIN LEUCINE RICH TRANSMEMBRANE PROTEIN 3

Chain A:



- Molecule 1: FIBRONECTIN LEUCINE RICH TRANSMEMBRANE PROTEIN 3

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	59.81Å 61.97Å 92.97Å 90.00° 106.38° 90.00°	Depositor
Resolution (Å)	57.38 – 2.50 44.60 – 2.50	Depositor EDS
% Data completeness (in resolution range)	90.2 (57.38-2.50) 80.5 (44.60-2.50)	Depositor EDS
R_{merge}	0.46	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.30 (at 2.51Å)	Xtriage
Refinement program	BUSTER 2.11.2	Depositor
R, R_{free}	0.345 , 0.351 0.399 , 0.387	Depositor DCC
R_{free} test set	1051 reflections (5.39%)	DCC
Wilson B-factor (Å^2)	22.6	Xtriage
Anisotropy	0.828	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.30 , -3.0	EDS
Estimated twinning fraction	0.026 for h,-k,-h-l	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.45$, $< L^2 > = 0.28$	Xtriage
Outliers	0 of 20595 reflections	Xtriage
F_o,F_c correlation	0.67	EDS
Total number of atoms	5118	wwPDB-VP
Average B, all atoms (Å^2)	40.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.81% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 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	0.39	0/2609	0.55	0/3548
1	B	0.38	0/2609	0.54	0/3548
All	All	0.38	0/5218	0.55	0/7096

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

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	2559	0	2573	23	0
1	B	2559	0	2573	16	0
All	All	5118	0	5146	39	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 4.

All (39) 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:56:ILE:HG23	1:A:57:PRO:HD2	1.72	0.69
1:A:42:ILE:HD13	1:A:56:ILE:HG23	1.80	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:112:GLN:HG2	1:A:136:ASP:H	1.64	0.61
1:A:62:THR:HG23	1:A:87:ARG:HG3	1.83	0.60
1:A:42:ILE:HD13	1:A:56:ILE:CG2	2.33	0.59
1:A:56:ILE:CG2	1:A:57:PRO:HD2	2.34	0.58
1:B:150:PHE:HB3	1:B:174:PRO:HD3	1.88	0.54
1:B:179:GLU:HG3	1:B:203:ARG:HB3	1.92	0.52
1:B:229:GLU:HG2	1:B:251:LYS:HB2	1.90	0.52
1:A:148:GLY:HA2	1:A:172:GLY:HA3	1.92	0.51
1:A:110:HIS:HA	1:A:134:HIS:HB2	1.93	0.50
1:A:335:GLN:HA	1:A:341:ARG:HG3	1.94	0.49
1:A:179:GLU:HG3	1:A:203:ARG:HB3	1.94	0.49
1:A:229:GLU:HG2	1:A:251:LYS:HB2	1.94	0.49
1:B:227:LEU:HD21	1:B:230:LEU:HD13	1.94	0.49
1:B:345:ILE:HA	1:B:348:LEU:HD12	1.95	0.47
1:A:37:CYS:HB3	1:A:42:ILE:HG23	1.95	0.47
1:B:335:GLN:HA	1:B:341:ARG:HG3	1.96	0.46
1:A:227:LEU:HD21	1:A:230:LEU:HD13	1.97	0.46
1:A:56:ILE:CG2	1:A:57:PRO:CD	2.95	0.45
1:A:231:SER:HA	1:A:253:TYR:HB2	1.99	0.45
1:B:62:THR:HG23	1:B:87:ARG:HG3	1.99	0.45
1:B:146:GLU:HB3	1:B:149:ALA:HB2	1.99	0.44
1:B:270:LEU:HD23	1:B:273:LEU:HD13	1.99	0.44
1:B:216:LEU:HD21	1:B:221:PHE:HE2	1.81	0.44
1:B:231:SER:HA	1:B:253:TYR:HB2	1.99	0.44
1:A:270:LEU:HD23	1:A:273:LEU:HD13	1.99	0.44
1:A:262:VAL:HG23	1:A:283:LEU:HD21	2.00	0.44
1:A:121:TYR:HD1	1:A:149:ALA:HA	1.83	0.43
1:B:121:TYR:HD1	1:B:149:ALA:HA	1.84	0.43
1:B:251:LYS:HG2	1:B:275:ARG:HB3	2.01	0.42
1:A:31:CYS:SG	1:A:37:CYS:N	2.93	0.42
1:A:52:ILE:HD12	1:A:75:ILE:HA	2.00	0.42
1:A:150:PHE:HB3	1:A:174:PRO:HD3	2.01	0.42
1:A:251:LYS:HG2	1:A:275:ARG:HB3	2.01	0.42
1:A:80:LYS:HA	1:A:103:PRO:HA	2.01	0.41
1:B:195:LEU:HB2	1:B:220:VAL:HG22	2.02	0.41
1:B:130:LEU:HD21	1:B:133:LEU:HD13	2.03	0.41
1:B:258:HIS:HA	1:B:282:ASN:HD22	1.86	0.41

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	319/331 (96%)	292 (92%)	25 (8%)	2 (1%)	30 50
1	B	319/331 (96%)	294 (92%)	23 (7%)	2 (1%)	30 50
All	All	638/662 (96%)	586 (92%)	48 (8%)	4 (1%)	30 50

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	324	PRO
1	B	324	PRO
1	A	323	LEU
1	B	323	LEU

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 sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	296/305 (97%)	293 (99%)	3 (1%)	82 95
1	B	296/305 (97%)	291 (98%)	5 (2%)	68 89
All	All	592/610 (97%)	584 (99%)	8 (1%)	74 91

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

Mol	Chain	Res	Type
1	A	31	CYS
1	A	127	ILE

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Mol	Chain	Res	Type
1	A	292	ASP
1	B	31	CYS
1	B	66	GLN
1	B	127	ILE
1	B	292	ASP
1	B	300	LEU

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

Mol	Chain	Res	Type
1	A	213	ASN
1	A	243	ASN
1	A	282	ASN
1	B	66	GLN
1	B	67	ASN
1	B	282	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 carbohydrates 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

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, 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	A	321/331 (96%)	1.87	127 (39%)	0	0	10, 30, 57, 85	0
1	B	321/331 (96%)	2.83	209 (65%)	0	0	23, 44, 83, 125	0
All	All	642/662 (96%)	2.35	336 (52%)	0	0	10, 37, 72, 125	0

All (336) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	338	GLU	13.1
1	A	54	VAL	8.7
1	B	151	ARG	8.6
1	B	150	PHE	8.1
1	A	33	SER	8.0
1	B	219	LYS	7.9
1	B	296	ASN	7.6
1	B	123	SER	7.5
1	B	311	CYS	7.5
1	B	344	ALA	7.5
1	B	308	TYR	7.3
1	A	34	VAL	7.2
1	B	149	ALA	6.4
1	B	210	LEU	6.4
1	B	331	GLY	6.4
1	B	144	SER	6.3
1	B	143	VAL	6.3
1	B	340	VAL	6.2
1	B	339	LYS	6.2
1	B	220	VAL	6.1
1	B	264	PRO	6.0
1	B	154	ASN	6.0
1	A	324	PRO	6.0
1	A	43	TYR	5.8

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Mol	Chain	Res	Type	RSRZ
1	B	158	LEU	5.7
1	B	155	TYR	5.7
1	B	124	LEU	5.6
1	B	218	ASP	5.5
1	B	78	ASP	5.3
1	B	341	ARG	5.3
1	B	342	GLY	5.3
1	B	147	GLU	5.1
1	B	106	VAL	5.1
1	A	315	TRP	5.1
1	B	36	ARG	5.0
1	B	335	GLN	5.0
1	B	126	LYS	5.0
1	B	324	PRO	5.0
1	B	310	GLY	4.9
1	A	36	ARG	4.8
1	B	350	ALA	4.8
1	B	333	MET	4.8
1	A	312	LYS	4.8
1	B	39	ALA	4.8
1	B	125	SER	4.7
1	B	261	ARG	4.7
1	A	51	SER	4.6
1	A	308	TYR	4.6
1	A	41	PHE	4.6
1	B	31	CYS	4.6
1	B	35	CYS	4.5
1	B	334	CYS	4.5
1	B	139	SER	4.5
1	B	317	ARG	4.5
1	A	65	LEU	4.5
1	A	350	ALA	4.4
1	B	217	GLY	4.4
1	B	323	LEU	4.4
1	B	121	TYR	4.4
1	A	290	ILE	4.3
1	B	347	ASP	4.3
1	B	348	LEU	4.3
1	B	145	ILE	4.3
1	A	30	SER	4.3
1	B	55	GLY	4.3
1	B	64	TYR	4.3

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Mol	Chain	Res	Type	RSRZ
1	B	118	THR	4.3
1	B	122	ASP	4.2
1	A	191	SER	4.2
1	B	47	ARG	4.2
1	B	37	CYS	4.1
1	A	56	ILE	4.1
1	A	78	ASP	4.1
1	B	52	ILE	4.1
1	B	63	LEU	4.1
1	B	225	VAL	4.1
1	B	213	ASN	4.0
1	B	313	MET	4.0
1	A	325	VAL	4.0
1	A	239	ALA	4.0
1	B	214	HIS	4.0
1	B	192	SER	3.9
1	B	172	GLY	3.9
1	B	34	VAL	3.9
1	B	316	VAL	3.9
1	B	291	PHE	3.9
1	B	222	PHE	3.9
1	B	318	ASP	3.9
1	B	345	ILE	3.9
1	A	223	ASN	3.9
1	B	159	LEU	3.9
1	B	247	THR	3.8
1	B	135	LEU	3.8
1	B	100	THR	3.8
1	B	129	TYR	3.8
1	B	67	ASN	3.8
1	B	337	PRO	3.7
1	B	141	SER	3.7
1	B	320	LEU	3.7
1	B	241	PRO	3.7
1	B	152	ASP	3.7
1	A	264	PRO	3.7
1	B	131	GLU	3.7
1	A	336	ALA	3.7
1	B	343	MET	3.7
1	A	238	THR	3.6
1	A	101	ASN	3.6
1	A	42	ILE	3.6

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Mol	Chain	Res	Type	RSRZ
1	B	216	LEU	3.6
1	B	279	SER	3.6
1	B	309	CYS	3.6
1	B	329	VAL	3.6
1	B	346	LYS	3.6
1	A	300	LEU	3.5
1	B	73	VAL	3.5
1	B	46	ASP	3.5
1	A	35	CYS	3.5
1	B	265	ASN	3.5
1	B	41	PHE	3.5
1	B	328	ASN	3.5
1	A	105	TYR	3.4
1	B	45	ASN	3.4
1	A	124	LEU	3.4
1	B	319	TRP	3.4
1	A	241	PRO	3.4
1	B	127	ILE	3.4
1	B	33	SER	3.3
1	B	303	ARG	3.3
1	B	292	ASP	3.3
1	B	321	GLN	3.3
1	B	157	ARG	3.3
1	B	307	TRP	3.3
1	B	88	ILE	3.3
1	B	285	ASN	3.3
1	B	62	THR	3.3
1	B	128	PRO	3.3
1	B	142	ALA	3.3
1	B	286	LEU	3.3
1	A	77	SER	3.3
1	B	153	SER	3.3
1	B	32	PRO	3.2
1	B	263	PRO	3.2
1	B	60	ALA	3.2
1	B	77	SER	3.2
1	A	58	GLU	3.2
1	A	100	THR	3.2
1	B	242	VAL	3.2
1	B	89	TYR	3.2
1	B	269	TYR	3.2
1	A	152	ASP	3.2

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Mol	Chain	Res	Type	RSRZ
1	B	117	ARG	3.2
1	B	148	GLY	3.2
1	A	95	LEU	3.2
1	B	111	LEU	3.1
1	A	228	THR	3.1
1	B	75	ILE	3.1
1	A	327	VAL	3.1
1	B	146	GLU	3.1
1	A	31	CYS	3.1
1	A	333	MET	3.0
1	A	60	ALA	3.0
1	B	349	SER	3.0
1	B	49	LEU	3.0
1	A	44	CYS	3.0
1	A	319	TRP	3.0
1	A	131	GLU	3.0
1	B	295	ASP	3.0
1	B	130	LEU	3.0
1	B	54	VAL	3.0
1	B	275	ARG	3.0
1	B	120	THR	3.0
1	B	281	ASN	3.0
1	B	50	THR	3.0
1	A	261	ARG	3.0
1	A	145	ILE	3.0
1	A	90	LEU	2.9
1	A	63	LEU	2.9
1	B	304	ASN	2.9
1	B	315	TRP	2.9
1	A	79	LEU	2.9
1	A	222	PHE	2.9
1	A	52	ILE	2.9
1	A	169	ILE	2.9
1	A	150	PHE	2.9
1	A	298	THR	2.9
1	B	253	TYR	2.8
1	A	257	ASN	2.8
1	B	289	GLY	2.8
1	A	199	THR	2.8
1	A	84	LYS	2.8
1	A	112	GLN	2.8
1	A	267	PHE	2.8

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Mol	Chain	Res	Type	RSRZ
1	A	128	PRO	2.8
1	B	66	GLN	2.8
1	B	56	ILE	2.8
1	A	230	LEU	2.8
1	B	114	ASN	2.8
1	A	88	ILE	2.7
1	B	301	ILE	2.7
1	A	229	GLU	2.7
1	B	300	LEU	2.7
1	B	322	SER	2.7
1	A	279	SER	2.7
1	B	107	LYS	2.7
1	B	230	LEU	2.7
1	A	111	LEU	2.7
1	B	201	LEU	2.7
1	B	171	GLY	2.7
1	B	246	GLY	2.7
1	B	176	THR	2.7
1	A	91	TYR	2.7
1	B	80	LYS	2.7
1	A	313	MET	2.6
1	B	202	LYS	2.6
1	A	274	TYR	2.6
1	A	69	GLN	2.6
1	A	196	HIS	2.6
1	B	92	HIS	2.6
1	B	250	ARG	2.6
1	A	129	TYR	2.6
1	A	309	CYS	2.6
1	B	255	GLN	2.6
1	A	218	ASP	2.6
1	B	290	ILE	2.6
1	A	61	THR	2.6
1	A	321	GLN	2.6
1	A	340	VAL	2.6
1	A	217	GLY	2.6
1	B	119	ILE	2.6
1	B	175	ARG	2.5
1	A	213	ASN	2.5
1	B	138	ASN	2.5
1	A	302	LEU	2.5
1	B	237	LEU	2.5

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Mol	Chain	Res	Type	RSRZ
1	B	104	LYS	2.5
1	A	118	THR	2.5
1	B	91	TYR	2.5
1	B	51	SER	2.5
1	B	330	ARG	2.5
1	B	283	LEU	2.5
1	A	197	GLY	2.5
1	B	221	PHE	2.5
1	B	268	SER	2.5
1	A	66	GLN	2.5
1	A	322	SER	2.5
1	B	229	GLU	2.4
1	B	280	ASN	2.4
1	A	271	ARG	2.4
1	B	156	LEU	2.4
1	A	225	VAL	2.4
1	B	58	GLU	2.4
1	B	236	SER	2.4
1	B	136	ASP	2.4
1	B	278	MET	2.4
1	A	219	LYS	2.4
1	B	212	ASN	2.4
1	B	282	ASN	2.4
1	B	181	ARG	2.4
1	A	53	PRO	2.4
1	A	262	VAL	2.4
1	A	299	GLN	2.4
1	B	258	HIS	2.4
1	B	186	ARG	2.3
1	A	323	LEU	2.3
1	B	262	VAL	2.3
1	A	188	SER	2.3
1	A	113	GLU	2.3
1	A	32	PRO	2.3
1	B	306	PRO	2.3
1	B	284	SER	2.3
1	A	176	THR	2.3
1	B	140	VAL	2.3
1	A	149	ALA	2.3
1	B	59	ASP	2.3
1	B	99	PRO	2.3
1	A	349	SER	2.3

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Mol	Chain	Res	Type	RSRZ
1	B	105	TYR	2.3
1	B	188	SER	2.3
1	B	211	LEU	2.3
1	A	259	ILE	2.3
1	A	37	CYS	2.3
1	A	326	LYS	2.3
1	B	30	SER	2.2
1	B	98	PHE	2.2
1	A	49	LEU	2.2
1	B	42	ILE	2.2
1	B	196	HIS	2.2
1	A	171	GLY	2.2
1	A	210	LEU	2.2
1	B	294	LEU	2.2
1	B	101	ASN	2.2
1	A	339	LYS	2.2
1	A	337	PRO	2.2
1	A	345	ILE	2.2
1	A	206	LEU	2.2
1	B	195	LEU	2.2
1	A	62	THR	2.2
1	A	189	THR	2.2
1	A	151	ARG	2.2
1	B	314	LYS	2.2
1	A	211	LEU	2.2
1	B	83	LEU	2.2
1	A	136	ASP	2.2
1	A	155	TYR	2.1
1	B	194	SER	2.1
1	B	197	GLY	2.1
1	B	116	ILE	2.1
1	B	326	LYS	2.1
1	A	85	VAL	2.1
1	B	252	LEU	2.1
1	A	329	VAL	2.1
1	B	325	VAL	2.1
1	A	343	MET	2.1
1	B	113	GLU	2.1
1	A	286	LEU	2.1
1	B	206	LEU	2.1
1	A	110	HIS	2.1
1	A	233	VAL	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	240	ALA	2.1
1	B	293	ASP	2.1
1	A	269	TYR	2.1
1	A	55	GLY	2.1
1	B	267	PHE	2.1
1	B	81	ASN	2.1
1	B	44	CYS	2.1
1	B	336	ALA	2.0
1	A	127	ILE	2.0
1	B	297	ILE	2.0
1	B	76	PRO	2.0
1	A	86	GLN	2.0
1	A	106	VAL	2.0
1	A	148	GLY	2.0
1	B	299	GLN	2.0
1	B	87	ARG	2.0
1	A	102	LEU	2.0
1	A	135	LEU	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 carbohydrates 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.