



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 06:50 AM UTC

PDB ID : 1DEQ / pdb_00001deq
Title : THE CRYSTAL STRUCTURE OF MODIFIED BOVINE FIBRINOGEN (AT 4 ANGSTROM RESOLUTION)
Authors : Brown, J.H.; Volkmann, N.; Jun, G.; Henschen-Edman, A.H.; Cohen, C.
Deposited on : 1999-11-15
Resolution : 3.50 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

<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

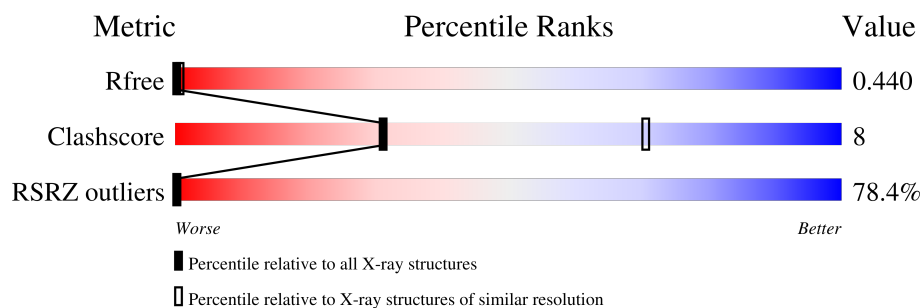
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.50 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}	180053	1085 (3.54-3.46)
Clashscore	190562	1140 (3.54-3.46)
RSRZ outliers	180081	1084 (3.54-3.46)

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	390	
1	D	390	
1	N	390	
1	Q	390	
2	B	408	
2	E	408	
2	O	408	

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Mol	Chain	Length	Quality of chain
2	R	408	76% 93% 7%
3	C	411	69% 90% 10%
3	F	411	71% 89% 10%
3	P	411	78% 90% 10%
3	S	411	75% 90% 10%
4	M	90	87% 13%
4	Z	90	87% 13%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 3900 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 FIBRINOGEN (ALPHA CHAIN).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
1	A	180	Total C 180 180	0	0	180
1	D	180	Total C 180 180	0	0	180
1	N	180	Total C 180 180	0	0	180
1	Q	180	Total C 180 180	0	0	180

- Molecule 2 is a protein called FIBRINOGEN (BETA CHAIN).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
2	B	380	Total C 380 380	0	0	380
2	E	380	Total C 380 380	0	0	380
2	O	380	Total C 380 380	0	0	380
2	R	380	Total C 380 380	0	0	380

- Molecule 3 is a protein called FIBRINOGEN (GAMMA CHAIN).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
3	C	370	Total C 370 370	0	0	370
3	F	370	Total C 370 370	0	0	370
3	P	370	Total C 370 370	0	0	370
3	S	370	Total C 370 370	0	0	370

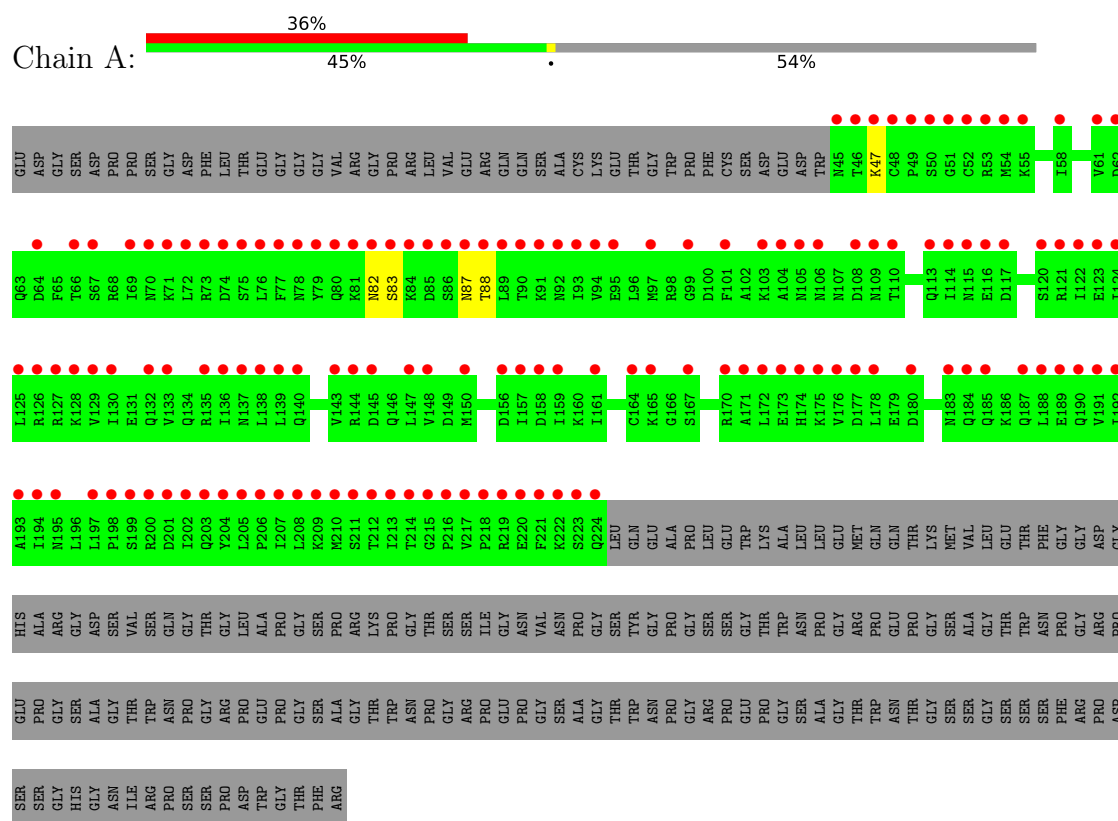
- Molecule 4 is a protein called FIBRINOGEN.

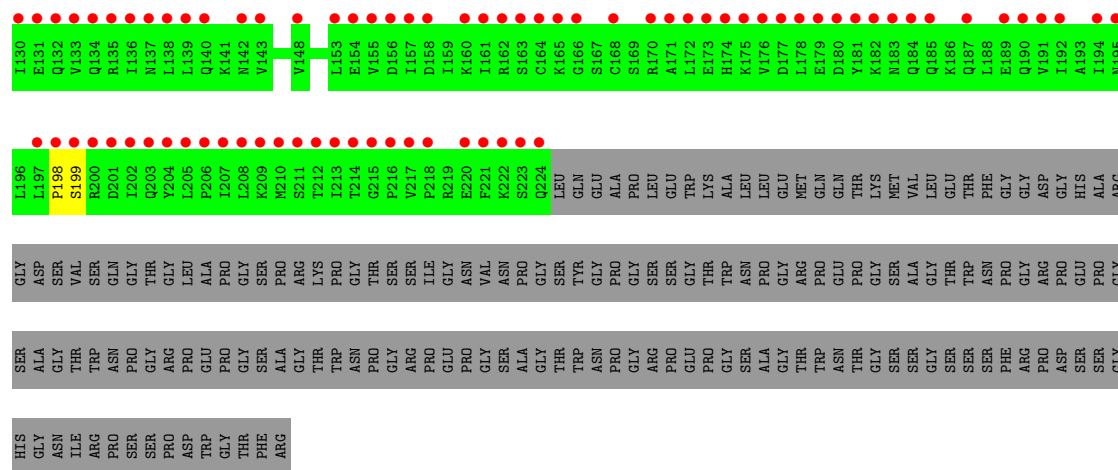
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf	Trace
4	M	90	Total	C	0	0	90
			90	90			
4	Z	90	Total	C	0	0	90
			90	90			

3 Residue-property plots [i](#)

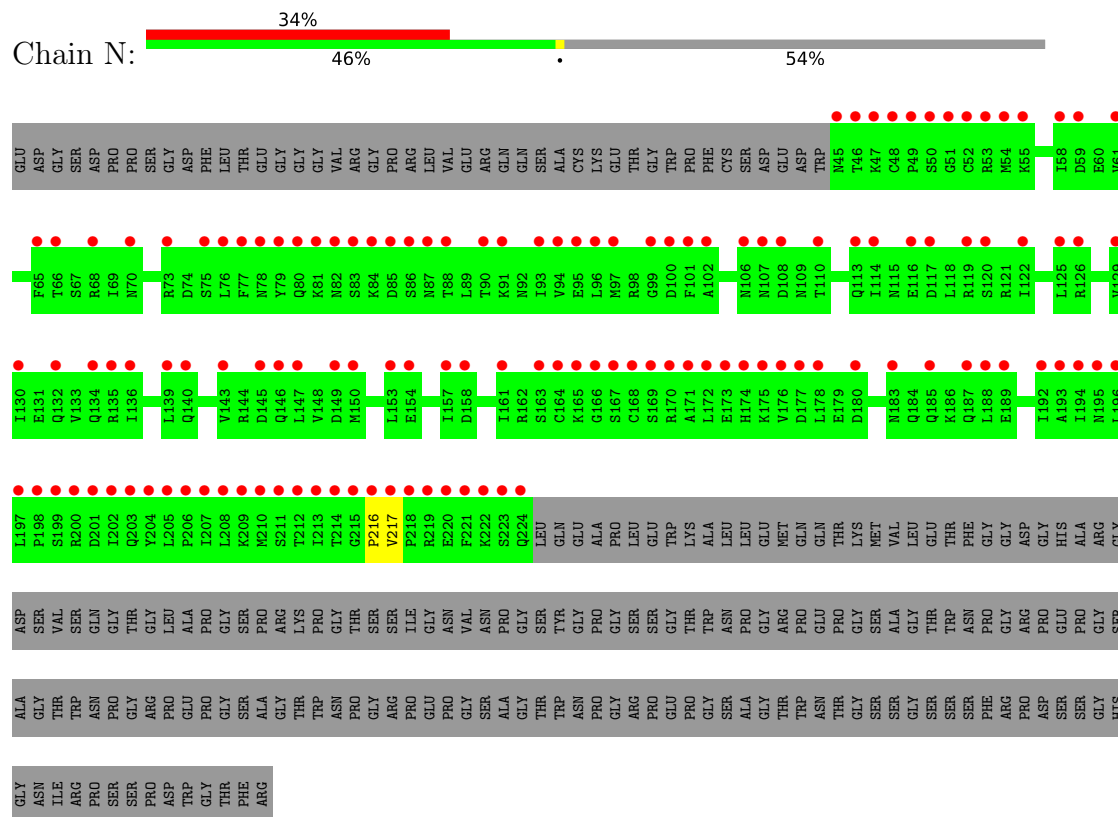
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: FIBRINOGEN (ALPHA CHAIN)

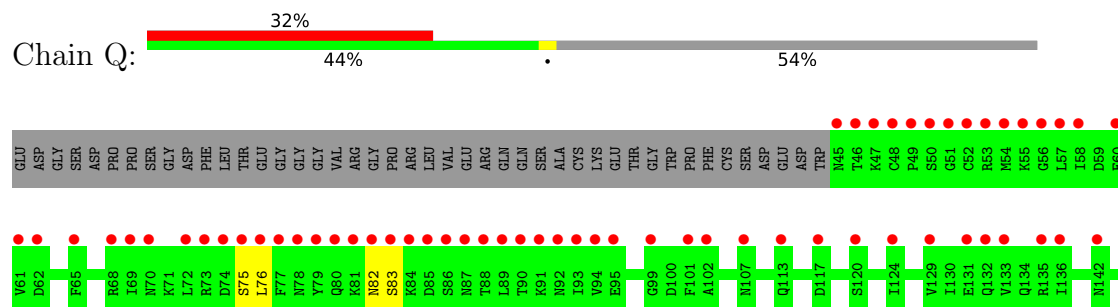


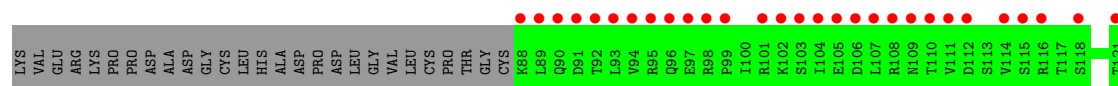


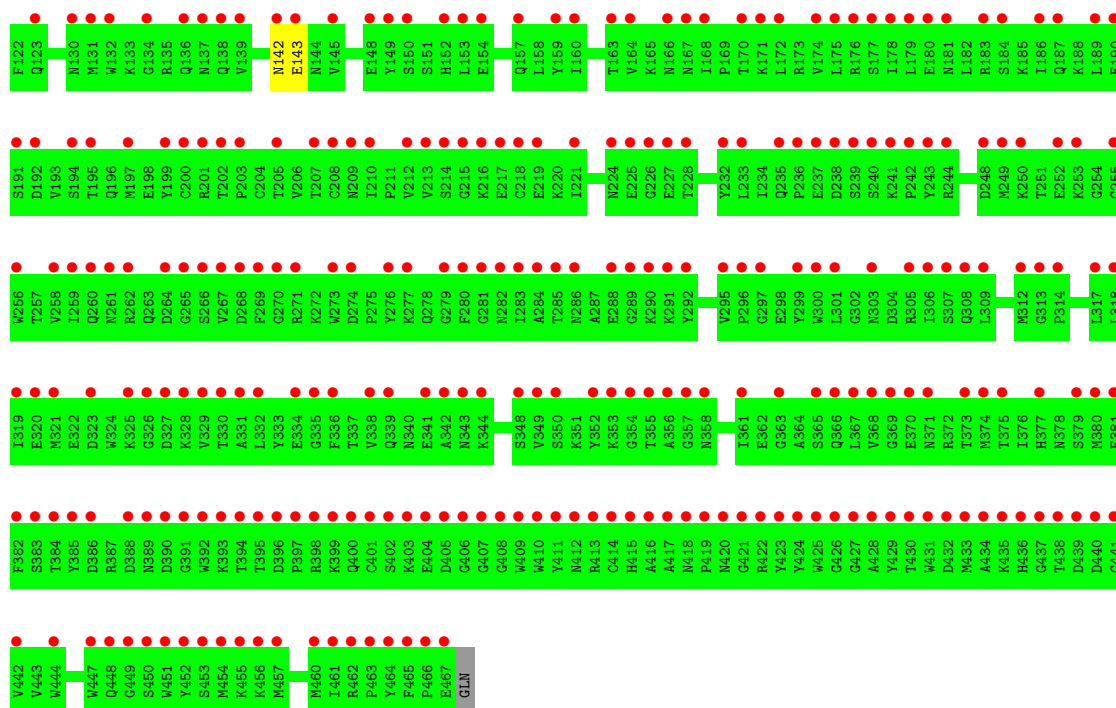
• Molecule 1: FIBRINOGEN (ALPHA CHAIN)



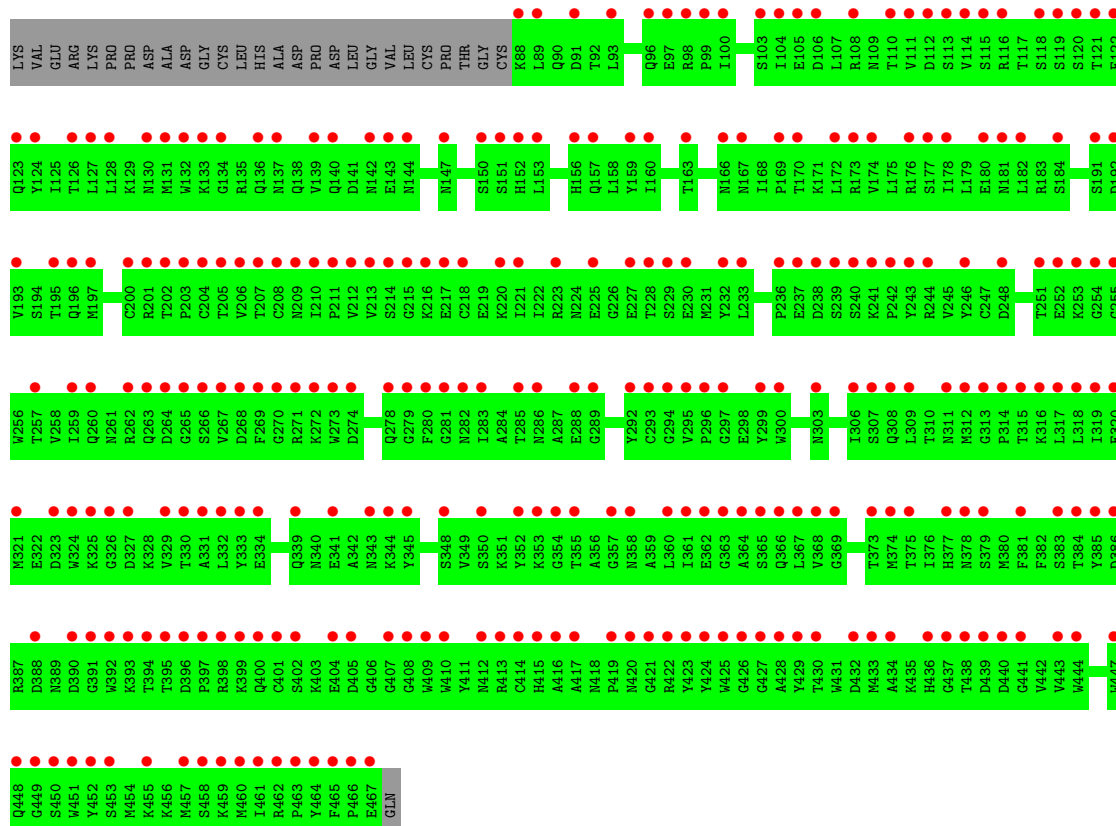
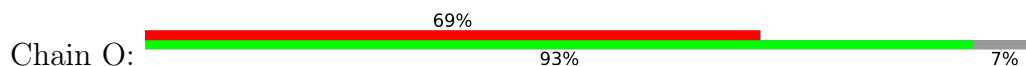
• Molecule 1: FIBRINOGEN (ALPHA CHAIN)





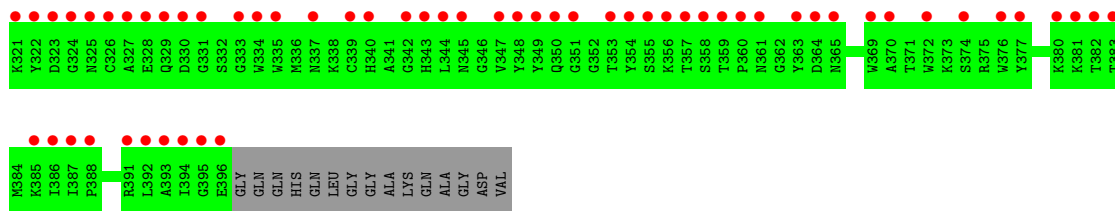


● Molecule 2: FIBRINOGEN (BETA CHAIN)

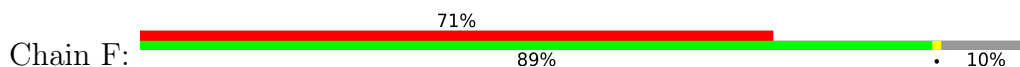


● Molecule 2: FIBRINOGEN (BETA CHAIN)

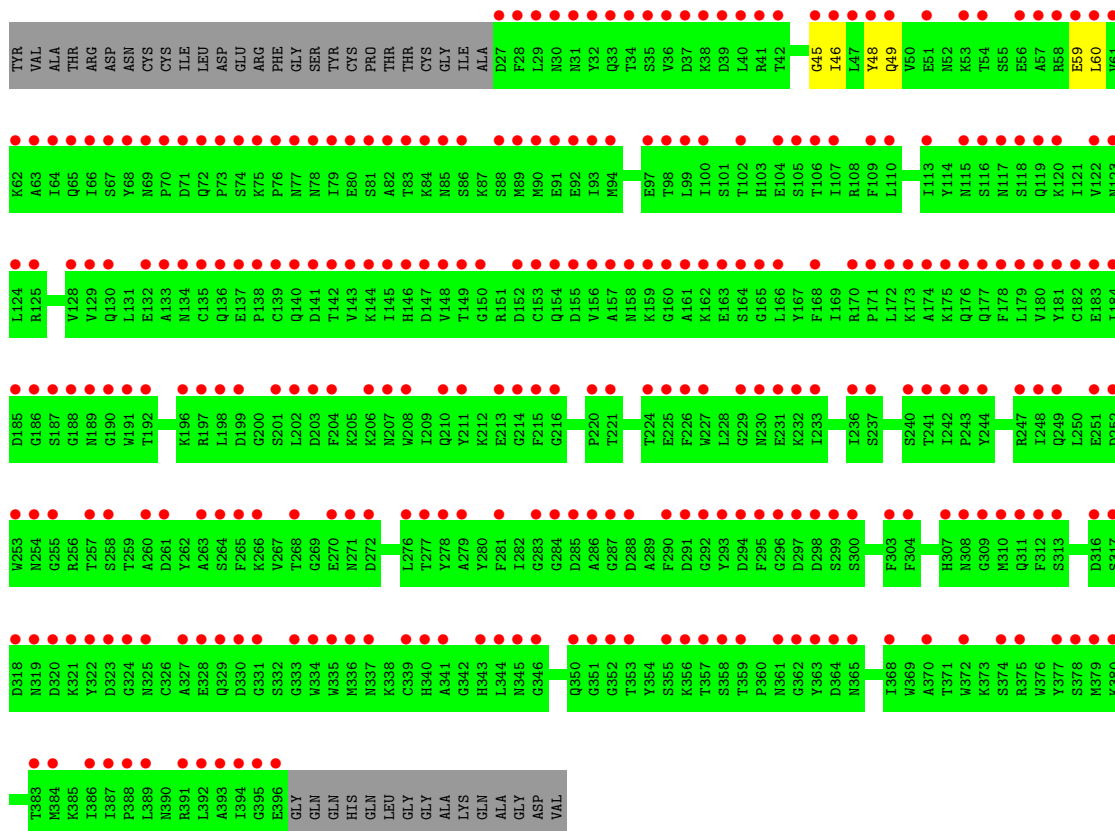




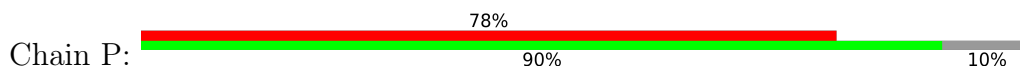
- Molecule 3: FIBRINOGEN (GAMMA CHAIN)



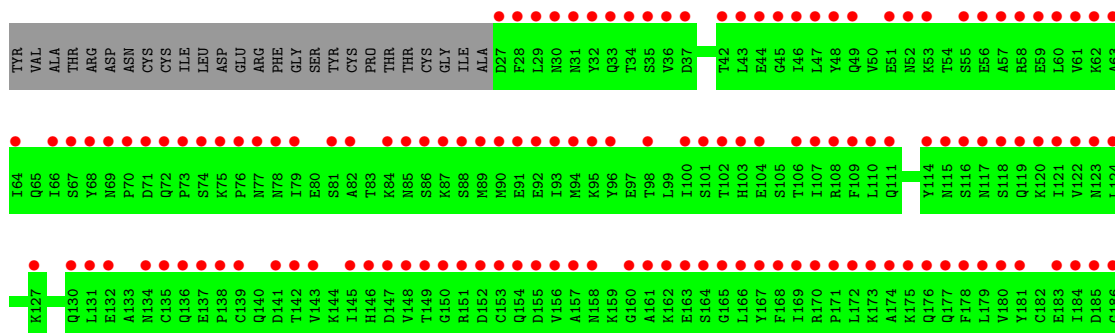
Chain F:

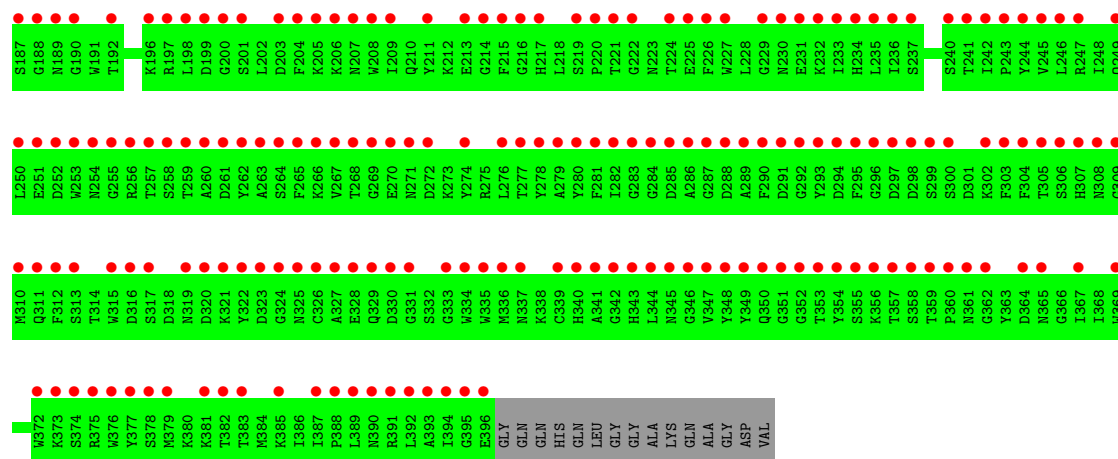


- Molecule 3: FIBRINOGEN (GAMMA CHAIN)

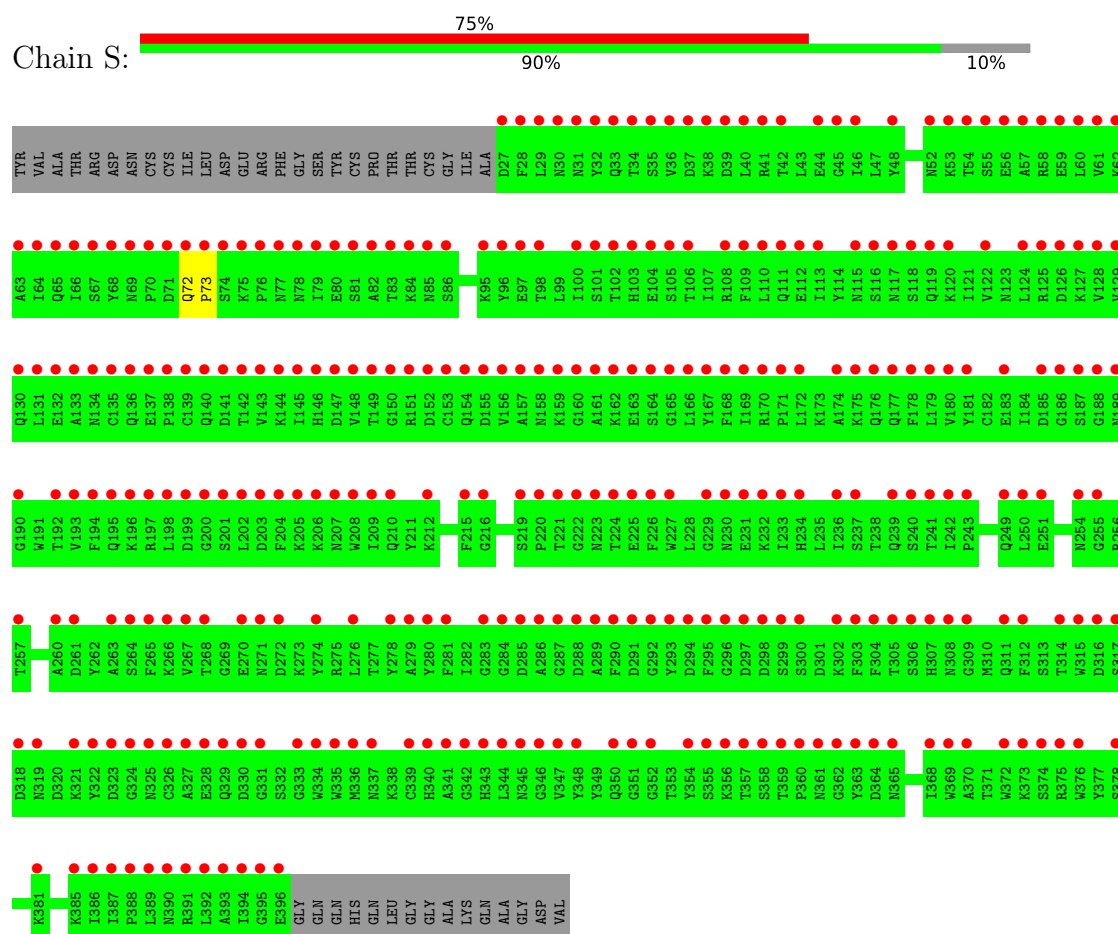


Chain P:





• Molecule 3: FIBRINOGEN (GAMMA CHAIN)

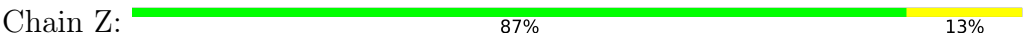


• Molecule 4: FIBRINOGEN

Chain M: 87% 13%



• Molecule 4: FIBRINOGEN



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	176.01Å 94.94Å 209.81Å 90.00° 94.41° 90.00°	Depositor
Resolution (Å)	10.00 – 3.50 10.00 – 3.50	Depositor EDS
% Data completeness (in resolution range)	86.9 (10.00-3.50) 78.8 (10.00-3.50)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.89 (at 3.33Å)	Xtriage
Refinement program	X-PLOR 3.851	Depositor
R, R_{free}	0.257 , 0.370 0.441 , 0.440	Depositor DCC
R_{free} test set	3953 reflections (4.98%)	wwPDB-VP
Wilson B-factor (Å ²)	91.6	Xtriage
Anisotropy	0.887	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.22 , 93.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.52	EDS
Total number of atoms	3900	wwPDB-VP
Average B, all atoms (Å ²)	225.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 10.82% 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).

There are no protein, RNA or DNA chains available to summarize Z scores of covalent bonds and angles.

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 [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	180	0	0	3	0
1	D	180	0	0	5	0
1	N	180	0	0	1	0
1	Q	180	0	0	4	0
2	B	380	0	0	1	0
2	E	380	0	0	1	0
2	O	380	0	0	0	0
2	R	380	0	0	1	0
3	C	370	0	0	0	0
3	F	370	0	0	3	0
3	P	370	0	0	0	0
3	S	370	0	0	1	0
4	M	90	0	0	8	0
4	Z	90	0	0	6	0
All	All	3900	0	0	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 8.

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)
2:E:142:ASN:CA	2:E:143:GLU:CA	2.09	1.29
4:M:134:UNK:CA	4:M:135:UNK:CA	2.16	1.22
4:M:43:UNK:CA	4:M:44:UNK:CA	2.18	1.21
1:Q:82:ASN:CA	1:Q:83:SER:CA	2.22	1.17
4:M:124:UNK:CA	4:M:125:UNK:CA	2.27	1.12
4:Z:124:UNK:CA	4:Z:125:UNK:CA	2.33	1.05
1:Q:216:PRO:CA	1:Q:217:VAL:CA	2.44	0.96
1:D:83:SER:CA	1:D:84:LYS:CA	2.47	0.92
3:F:48:TYR:CA	3:F:49:GLN:CA	2.50	0.89
3:S:72:GLN:CA	3:S:73:PRO:CA	2.54	0.86
4:Z:142:UNK:CA	4:Z:143:UNK:CA	2.56	0.83
4:M:142:UNK:CA	4:M:143:UNK:CA	2.56	0.83
4:M:42:UNK:CA	4:M:43:UNK:CA	2.56	0.82
3:F:59:GLU:CA	3:F:60:LEU:CA	2.60	0.80
1:D:45:ASN:CA	4:M:114:UNK:CA	2.59	0.80
4:M:133:UNK:CA	4:M:134:UNK:CA	2.64	0.76
3:F:45:GLY:CA	3:F:46:ILE:CA	2.64	0.74
1:N:216:PRO:CA	1:N:217:VAL:CA	2.68	0.71
1:D:82:ASN:CA	1:D:83:SER:CA	2.73	0.66
1:A:82:ASN:CA	1:A:83:SER:CA	2.74	0.65
2:B:120:SER:CA	2:B:121:THR:CA	2.77	0.62
4:Z:7:UNK:CA	4:Z:8:UNK:CA	2.81	0.58
1:D:198:PRO:CA	1:D:199:SER:CA	2.82	0.57
4:Z:118:UNK:CA	4:Z:119:UNK:CA	2.83	0.56
1:A:47:LYS:CA	4:M:118:UNK:CA	2.83	0.56
1:A:87:ASN:CA	1:A:88:THR:CA	2.85	0.54
4:Z:103:UNK:CA	4:Z:104:UNK:CA	2.93	0.46
2:R:108:ARG:CA	2:R:109:ASN:CA	2.95	0.45
4:Z:105:UNK:CA	4:Z:106:UNK:CA	2.96	0.44
1:D:69:ILE:CA	1:D:70:ASN:CA	2.97	0.42
1:Q:75:SER:CA	1:Q:76:LEU:CA	2.98	0.42
1:Q:217:VAL:CA	1:Q:218:PRO:CA	2.98	0.41

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

There are no protein backbone outliers to report in this entry.

5.3.2 Protein sidechains [i](#)

There are no protein residues with a non-rotameric sidechain to report in this entry.

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	180/390 (46%)	6.16	142 (78%) 0 0	4, 93, 999, 999	0
1	D	180/390 (46%)	5.95	139 (77%) 0 0	25, 131, 999, 999	0
1	N	180/390 (46%)	6.05	131 (72%) 0 0	2, 88, 999, 999	0
1	Q	180/390 (46%)	5.56	126 (70%) 0 0	2, 151, 999, 999	0
2	B	380/408 (93%)	5.64	291 (76%) 0 0	2, 62, 214, 999	0
2	E	380/408 (93%)	6.03	294 (77%) 0 0	2, 81, 999, 999	0
2	O	380/408 (93%)	5.21	281 (73%) 0 0	2, 63, 191, 359	0
2	R	380/408 (93%)	7.09	312 (82%) 0 0	2, 130, 358, 999	0
3	C	370/411 (90%)	5.93	283 (76%) 0 0	2, 58, 999, 999	0
3	F	370/411 (90%)	5.88	293 (79%) 0 0	2, 68, 999, 999	0
3	P	370/411 (90%)	6.92	319 (86%) 0 0	2, 96, 386, 999	0
3	S	370/411 (90%)	6.64	307 (82%) 0 0	6, 112, 999, 999	0
4	M	0/90	-	-	-	-
4	Z	0/90	-	-	-	-
All	All	3720/5016 (74%)	6.12	2918 (78%) 0 0	2, 87, 999, 999	0

All (2918) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	391	GLY	46.3
2	R	329	VAL	46.2
2	R	278	GLN	38.6
2	E	236	PRO	38.5
3	P	350	GLN	38.1
2	B	394	THR	36.9
2	R	386	ASP	36.9
2	B	202	THR	36.9
1	N	202	ILE	36.2

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Mol	Chain	Res	Type	RSRZ
2	B	112	ASP	35.5
1	N	203	GLN	34.0
1	A	192	ILE	33.5
2	R	388	ASP	33.2
2	R	317	LEU	32.6
3	F	199	ASP	31.4
3	C	266	LYS	30.7
2	E	385	TYR	30.6
3	P	174	ALA	30.4
1	A	204	TYR	30.4
2	R	330	THR	30.4
2	B	264	ASP	30.3
2	E	253	LYS	29.6
3	S	140	GLN	28.7
3	C	376	TRP	28.4
2	O	329	VAL	28.2
2	R	467	GLU	27.9
3	C	318	ASP	27.8
3	S	308	ASN	27.6
3	F	176	GLN	27.4
2	B	108	ARG	27.3
3	P	359	THR	27.1
2	E	269	PHE	27.0
3	F	288	ASP	27.0
2	B	355	THR	26.6
3	P	137	GLU	26.4
1	A	173	GLU	25.9
1	N	213	ILE	25.8
2	R	190	GLU	25.7
2	O	404	GLU	25.4
3	P	192	THR	25.2
2	E	216	LYS	25.1
3	F	90	MET	25.1
2	B	396	ASP	24.8
2	R	300	TRP	24.5
2	E	252	GLU	24.3
3	S	390	ASN	24.2
1	A	214	THR	24.2
3	P	287	GLY	24.1
3	C	152	ASP	24.1
3	P	312	PHE	24.0
2	R	367	LEU	23.9

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Mol	Chain	Res	Type	RSRZ
2	R	306	ILE	23.9
2	R	358	ASN	23.7
1	Q	212	THR	23.6
2	E	265	GLY	23.5
3	C	295	PHE	23.4
2	E	369	GLY	23.3
2	E	423	TYR	23.3
3	C	160	GLY	23.2
3	C	71	ASP	23.2
3	C	242	ILE	23.1
3	C	134	ASN	23.1
1	N	206	PRO	23.1
3	P	331	GLY	23.1
3	S	333	GLY	23.0
3	P	199	ASP	22.8
3	P	186	GLY	22.7
2	R	415	HIS	22.3
2	R	432	ASP	22.3
3	F	135	CYS	22.2
3	P	353	THR	22.0
1	Q	224	GLN	21.7
1	A	211	SER	21.6
3	F	206	LYS	21.5
2	O	160	ILE	21.4
1	N	47	LYS	21.4
2	B	306	ILE	21.3
3	F	308	ASN	21.3
3	F	379	MET	21.3
3	S	203	ASP	21.2
2	O	252	GLU	21.0
3	F	47	LEU	21.0
2	R	417	ALA	20.8
1	D	77	PHE	20.8
3	C	176	GLN	20.7
1	Q	47	LYS	20.7
2	R	394	THR	20.7
2	O	282	ASN	20.6
2	B	348	SER	20.5
1	N	193	ALA	20.5
1	N	75	SER	20.5
1	A	90	THR	20.5
2	O	396	ASP	20.5

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Mol	Chain	Res	Type	RSRZ
3	P	304	PHE	20.4
1	Q	78	ASN	20.3
2	E	358	ASN	20.2
2	E	444	TRP	20.2
3	C	201	SER	20.2
3	P	189	ASN	20.2
3	C	392	LEU	20.1
3	S	264	SER	20.0
3	F	323	ASP	20.0
1	N	219	ARG	19.9
3	S	146	HIS	19.8
3	P	361	ASN	19.7
1	D	170	ARG	19.5
2	R	139	VAL	19.4
3	F	393	ALA	19.4
3	S	199	ASP	19.4
2	E	91	ASP	19.3
2	E	386	ASP	19.3
3	S	387	ILE	19.2
3	C	325	ASN	19.2
3	S	216	GLY	19.1
3	F	74	SER	19.1
3	S	145	ILE	19.0
2	R	313	GLY	19.0
1	D	58	ILE	18.8
3	P	179	LEU	18.8
3	F	139	CYS	18.7
2	R	216	LYS	18.7
3	P	393	ALA	18.7
1	N	150	MET	18.7
2	B	253	LYS	18.7
3	P	89	MET	18.6
3	F	325	ASN	18.5
3	P	76	PRO	18.4
2	E	201	ARG	18.3
2	O	426	GLY	18.2
1	N	154	GLU	18.2
2	B	167	ASN	18.1
2	B	159	TYR	18.1
2	B	292	TYR	18.1
3	F	295	PHE	18.1
3	P	152	ASP	18.0

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Mol	Chain	Res	Type	RSRZ
2	O	204	CYS	18.0
2	B	239	SER	18.0
3	F	73	PRO	18.0
1	A	188	LEU	17.9
2	E	448	GLN	17.9
2	R	352	TYR	17.9
3	F	203	ASP	17.9
3	F	227	TRP	17.9
3	C	89	MET	17.9
1	D	76	LEU	17.9
2	R	312	MET	17.7
1	N	199	SER	17.7
2	E	112	ASP	17.6
2	R	448	GLN	17.6
2	R	404	GLU	17.6
2	B	91	ASP	17.6
3	P	78	ASN	17.5
3	P	323	ASP	17.5
3	S	101	SER	17.5
3	F	70	PRO	17.5
3	C	323	ASP	17.5
2	R	142	ASN	17.5
1	A	94	VAL	17.4
2	O	457	MET	17.4
3	S	271	ASN	17.3
3	F	185	ASP	17.3
2	B	395	THR	17.3
3	P	299	SER	17.2
3	P	297	ASP	17.2
1	A	213	ILE	17.1
2	O	242	PRO	17.1
1	D	105	ASN	17.1
2	O	374	MET	17.1
3	P	121	ILE	17.1
2	B	146	VAL	17.1
2	R	308	GLN	17.0
2	E	175	LEU	17.0
3	F	242	ILE	17.0
1	N	223	SER	17.0
1	Q	54	MET	16.8
2	E	425	TRP	16.8
2	B	255	GLY	16.8

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Mol	Chain	Res	Type	RSRZ
2	O	104	ILE	16.8
2	O	192	ASP	16.8
3	C	335	TRP	16.8
3	C	103	HIS	16.8
2	B	329	VAL	16.7
1	D	48	CYS	16.7
1	D	164	CYS	16.6
2	E	334	GLU	16.6
2	O	437	GLY	16.5
2	R	421	GLY	16.5
2	R	355	THR	16.5
2	B	392	TRP	16.5
2	R	390	ASP	16.4
3	C	39	ASP	16.4
3	S	288	ASP	16.4
2	R	253	LYS	16.3
2	O	392	TRP	16.3
3	C	395	GLY	16.2
3	P	224	THR	16.2
3	P	391	ARG	16.2
3	P	356	LYS	16.1
2	R	219	GLU	16.0
3	C	243	PRO	16.0
2	E	400	GLN	16.0
2	O	163	THR	16.0
3	F	86	SER	16.0
1	Q	164	CYS	15.9
3	S	197	ARG	15.9
3	S	178	PHE	15.9
3	F	396	GLU	15.9
3	S	152	ASP	15.9
1	A	220	GLU	15.9
3	C	165	GLY	15.9
2	B	282	ASN	15.9
1	Q	206	PRO	15.8
3	C	138	PRO	15.8
2	R	160	ILE	15.8
2	B	90	GLN	15.8
3	P	364	ASP	15.8
2	B	448	GLN	15.8
3	S	283	GLY	15.8
1	A	80	GLN	15.7

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Mol	Chain	Res	Type	RSRZ
2	O	255	GLY	15.7
3	P	231	GLU	15.7
1	A	46	THR	15.7
1	N	52	CYS	15.7
2	E	440	ASP	15.6
2	R	288	GLU	15.5
3	C	333	GLY	15.5
2	E	455	LYS	15.5
1	D	88	THR	15.4
3	S	307	HIS	15.4
2	B	218	CYS	15.4
1	D	214	THR	15.4
3	F	163	GLU	15.3
2	R	457	MET	15.3
2	O	105	GLU	15.3
2	E	291	LYS	15.3
2	E	309	LEU	15.3
3	P	278	TYR	15.3
3	P	29	LEU	15.3
2	O	288	GLU	15.3
2	O	394	THR	15.3
2	R	385	TYR	15.3
3	S	169	ILE	15.3
3	P	291	ASP	15.2
1	Q	219	ARG	15.2
2	R	93	LEU	15.2
2	R	396	ASP	15.2
3	C	361	ASN	15.2
2	O	425	TRP	15.2
2	R	389	ASN	15.2
1	Q	220	GLU	15.2
2	B	142	ASN	15.2
3	S	115	ASN	15.2
3	P	175	LYS	15.2
2	R	266	SER	15.1
3	C	322	TYR	15.1
1	N	168	CYS	15.1
1	A	200	ARG	15.1
1	D	171	ALA	15.1
3	F	33	GLN	15.0
3	C	329	GLN	15.0
2	R	290	LYS	15.0

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Mol	Chain	Res	Type	RSRZ
2	E	248	ASP	15.0
2	B	397	PRO	15.0
1	D	87	ASN	15.0
2	O	400	GLN	15.0
2	O	123	GLN	14.9
2	E	289	GLY	14.9
1	Q	86	SER	14.9
3	S	142	THR	14.9
2	E	388	ASP	14.9
1	N	208	LEU	14.8
3	F	162	LYS	14.8
3	C	179	LEU	14.8
3	S	183	GLU	14.8
2	R	444	TRP	14.8
2	O	229	SER	14.8
3	C	396	GLU	14.8
3	P	64	ILE	14.7
2	R	403	LYS	14.7
2	B	424	TYR	14.7
3	F	147	ASP	14.7
2	R	295	VAL	14.6
3	P	377	TYR	14.6
1	N	76	LEU	14.6
2	B	140	GLN	14.5
3	F	65	GLN	14.5
1	Q	216	PRO	14.5
2	O	391	GLY	14.5
3	S	48	TYR	14.4
1	N	192	ILE	14.4
3	P	395	GLY	14.4
2	R	456	LYS	14.4
1	D	133	VAL	14.4
2	O	178	ILE	14.3
3	C	206	LYS	14.3
3	C	118	SER	14.3
3	S	106	THR	14.2
2	O	150	SER	14.2
3	C	199	ASP	14.2
3	S	365	ASN	14.2
3	S	71	ASP	14.2
2	E	202	THR	14.2
2	R	107	LEU	14.2

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Mol	Chain	Res	Type	RSRZ
1	Q	215	GLY	14.1
3	S	316	ASP	14.1
3	C	267	VAL	14.1
1	Q	203	GLN	14.1
2	E	209	ASN	14.1
1	N	222	LYS	14.1
2	E	415	HIS	14.0
2	R	425	TRP	14.0
2	E	283	ILE	13.9
1	Q	142	ASN	13.9
2	E	447	TRP	13.9
1	A	58	ILE	13.9
3	F	312	PHE	13.9
2	R	420	ASN	13.9
3	S	351	GLY	13.9
1	D	139	LEU	13.9
3	P	389	LEU	13.9
2	R	462	ARG	13.8
1	A	218	PRO	13.8
3	C	97	GLU	13.8
2	R	265	GLY	13.8
3	P	236	ILE	13.7
3	P	316	ASP	13.7
3	S	151	ARG	13.7
2	B	269	PHE	13.7
2	B	192	ASP	13.7
2	R	143	GLU	13.7
3	P	257	THR	13.6
3	S	181	TYR	13.6
1	D	206	PRO	13.6
2	B	457	MET	13.6
2	O	172	LEU	13.6
3	P	355	SER	13.6
3	P	185	ASP	13.6
3	S	312	PHE	13.6
3	F	297	ASP	13.6
2	E	300	TRP	13.5
2	O	399	LYS	13.5
3	P	293	TYR	13.5
1	Q	89	LEU	13.5
2	O	405	ASP	13.5
3	S	229	GLY	13.5

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Mol	Chain	Res	Type	RSRZ
3	P	322	TYR	13.4
3	C	74	SER	13.4
3	P	329	GLN	13.4
2	O	93	LEU	13.4
2	R	211	PRO	13.4
3	S	375	ARG	13.4
3	S	330	ASP	13.3
1	D	161	ILE	13.3
2	O	365	SER	13.3
1	N	136	ILE	13.3
2	R	301	LEU	13.3
3	P	201	SER	13.3
3	C	139	CYS	13.3
1	Q	199	SER	13.2
3	C	324	GLY	13.2
3	F	138	PRO	13.2
3	S	231	GLU	13.1
1	Q	184	GLN	13.1
2	E	88	LYS	13.1
2	O	455	LYS	13.1
2	R	214	SER	13.1
2	E	405	ASP	13.1
3	P	177	GLN	13.1
3	F	134	ASN	13.1
3	C	115	ASN	13.0
1	A	74	ASP	13.0
2	R	195	THR	13.0
2	E	319	ILE	13.0
2	O	202	THR	13.0
2	R	235	GLN	13.0
2	R	270	GLY	13.0
3	F	290	PHE	12.9
3	S	31	ASN	12.9
2	O	401	CYS	12.9
1	D	45	ASN	12.9
3	F	335	TRP	12.9
1	D	174	HIS	12.9
1	N	212	THR	12.9
2	E	306	ILE	12.9
1	D	209	LYS	12.8
3	S	329	GLN	12.8
3	S	396	GLU	12.8

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Mol	Chain	Res	Type	RSRZ
3	S	136	GLN	12.8
2	R	419	PRO	12.8
3	S	205	LYS	12.8
1	Q	74	ASP	12.8
2	R	422	ARG	12.8
3	S	372	TRP	12.8
2	B	266	SER	12.7
3	S	281	PHE	12.7
3	S	294	ASP	12.7
3	F	149	THR	12.7
3	S	268	THR	12.7
1	N	97	MET	12.7
3	F	220	PRO	12.7
3	S	135	CYS	12.7
3	P	122	VAL	12.6
3	C	136	GLN	12.6
1	Q	113	GLN	12.6
2	E	280	PHE	12.6
2	E	462	ARG	12.6
1	N	171	ALA	12.6
3	C	33	GLN	12.5
2	R	451	TRP	12.5
2	R	414	CYS	12.5
3	S	220	PRO	12.5
3	S	67	SER	12.5
3	C	231	GLU	12.5
1	Q	51	GLY	12.5
3	P	58	ARG	12.5
3	C	391	ARG	12.4
2	E	396	ASP	12.4
3	S	392	LEU	12.4
3	F	363	TYR	12.4
3	S	70	PRO	12.4
3	C	334	TRP	12.4
1	Q	102	ALA	12.3
3	P	109	PHE	12.2
2	B	353	LYS	12.2
3	F	236	ILE	12.2
3	C	149	THR	12.2
2	E	115	SER	12.2
1	Q	94	VAL	12.2
2	E	353	LYS	12.2

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Mol	Chain	Res	Type	RSRZ
2	B	458	SER	12.2
3	P	267	VAL	12.2
3	P	339	CYS	12.1
3	F	56	GLU	12.1
2	R	202	THR	12.1
3	F	202	LEU	12.1
3	C	365	ASN	12.1
2	E	317	LEU	12.1
3	S	388	PRO	12.1
3	C	81	SER	12.1
2	B	300	TRP	12.0
3	C	317	SER	12.0
1	N	201	ASP	12.0
3	P	157	ALA	12.0
1	A	144	ARG	12.0
3	C	131	LEU	12.0
3	F	97	GLU	12.0
1	Q	73	ARG	12.0
1	Q	166	GLY	12.0
2	O	238	ASP	11.9
2	B	313	GLY	11.9
3	S	160	GLY	11.9
3	S	34	THR	11.9
3	C	36	VAL	11.9
3	F	394	ILE	11.9
1	D	177	ASP	11.9
2	R	279	GLY	11.9
2	E	436	HIS	11.9
2	E	365	SER	11.9
2	R	241	LYS	11.9
1	D	46	THR	11.9
3	P	107	ILE	11.9
3	P	354	TYR	11.9
3	P	215	PHE	11.9
3	C	72	GLN	11.8
3	S	317	SER	11.8
3	S	186	GLY	11.8
2	R	88	LYS	11.8
2	O	266	SER	11.8
1	A	135	ARG	11.8
1	N	170	ARG	11.8
3	P	362	GLY	11.8

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Mol	Chain	Res	Type	RSRZ
3	F	61	VAL	11.7
3	P	148	VAL	11.7
1	N	185	GLN	11.7
3	P	206	LYS	11.7
1	D	201	ASP	11.7
2	R	371	ASN	11.7
1	Q	207	ILE	11.7
1	N	49	PRO	11.7
1	Q	202	ILE	11.7
3	S	254	ASN	11.6
3	P	280	TYR	11.6
2	E	437	GLY	11.6
3	S	172	LEU	11.6
3	F	241	THR	11.6
3	S	147	ASP	11.6
1	Q	107	ASN	11.6
2	B	451	TRP	11.6
3	S	138	PRO	11.6
3	C	299	SER	11.6
3	S	266	LYS	11.6
2	E	368	VAL	11.6
3	P	315	TRP	11.5
3	S	149	THR	11.5
1	D	157	ILE	11.5
2	O	208	CYS	11.5
3	F	336	MET	11.5
2	O	227	GLU	11.5
3	F	35	SER	11.5
2	O	280	PHE	11.5
2	B	439	ASP	11.4
3	P	219	SER	11.4
3	S	212	LYS	11.4
2	E	150	SER	11.4
3	P	308	ASN	11.4
3	P	56	GLU	11.4
3	C	227	TRP	11.4
2	R	205	THR	11.4
1	Q	189	GLU	11.4
3	S	344	LEU	11.4
3	S	206	LYS	11.4
2	O	292	TYR	11.4
1	A	87	ASN	11.4

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Mol	Chain	Res	Type	RSRZ
2	O	106	ASP	11.3
3	F	39	ASP	11.3
2	R	229	SER	11.3
3	P	57	ALA	11.3
2	O	361	ILE	11.3
3	S	243	PRO	11.3
3	C	297	ASP	11.3
1	A	199	SER	11.3
1	D	50	SER	11.3
2	R	400	GLN	11.3
1	D	183	ASN	11.3
1	A	128	LYS	11.3
3	P	294	ASP	11.3
3	F	165	GLY	11.2
3	C	75	LYS	11.2
2	E	350	SER	11.2
3	S	165	GLY	11.2
3	S	161	ALA	11.2
1	D	83	SER	11.1
3	C	147	ASP	11.1
1	Q	52	CYS	11.1
3	P	184	ILE	11.1
2	E	430	THR	11.1
1	A	164	CYS	11.1
1	D	173	GLU	11.1
3	F	343	HIS	11.0
2	R	314	PRO	11.0
2	B	97	GLU	11.0
2	O	297	GLY	11.0
2	O	181	ASN	11.0
3	P	85	ASN	11.0
1	D	190	GLN	11.0
2	O	177	SER	11.0
3	P	115	ASN	11.0
2	E	242	PRO	11.0
2	O	203	PRO	11.0
3	F	145	ILE	11.0
2	E	308	GLN	11.0
3	S	80	GLU	11.0
2	B	425	TRP	10.9
3	F	27	ASP	10.9
2	R	325	LYS	10.9

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Mol	Chain	Res	Type	RSRZ
3	S	164	SER	10.9
2	E	139	VAL	10.9
2	B	350	SER	10.9
3	P	352	GLY	10.9
2	R	449	GLY	10.9
3	S	104	GLU	10.9
1	N	50	SER	10.9
3	S	39	ASP	10.8
3	P	168	PHE	10.8
3	P	340	HIS	10.8
2	E	422	ARG	10.8
2	O	352	TYR	10.8
1	D	208	LEU	10.8
3	F	375	ARG	10.8
2	O	366	GLN	10.8
1	D	72	LEU	10.8
1	D	53	ARG	10.8
3	S	298	ASP	10.8
2	O	89	LEU	10.8
2	B	412	ASN	10.8
3	C	32	TYR	10.7
3	F	279	ALA	10.7
2	R	461	ILE	10.7
1	Q	87	ASN	10.7
2	R	136	GLN	10.7
2	E	208	CYS	10.7
1	N	207	ILE	10.7
2	E	413	ARG	10.7
3	P	138	PRO	10.7
2	E	307	SER	10.7
2	E	273	TRP	10.7
2	B	274	ASP	10.7
1	A	203	GLN	10.7
2	O	353	LYS	10.7
3	F	59	GLU	10.6
3	P	134	ASN	10.6
2	O	432	ASP	10.6
3	S	300	SER	10.6
3	C	393	ALA	10.6
2	B	390	ASP	10.6
2	B	430	THR	10.6
3	F	142	THR	10.6

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Mol	Chain	Res	Type	RSRZ
2	O	451	TRP	10.6
1	N	220	GLU	10.5
3	C	146	HIS	10.5
2	B	290	LYS	10.5
3	P	229	GLY	10.5
2	E	94	VAL	10.5
3	C	73	PRO	10.5
3	P	178	PHE	10.5
2	E	292	TYR	10.5
2	O	393	LYS	10.5
1	D	189	GLU	10.5
3	S	386	ILE	10.5
3	C	70	PRO	10.5
3	F	72	GLN	10.5
3	P	396	GLU	10.5
2	B	421	GLY	10.5
2	R	464	TYR	10.5
3	C	114	TYR	10.5
3	F	395	GLY	10.4
2	R	264	ASP	10.4
3	C	119	GLN	10.4
1	N	82	ASN	10.4
2	E	145	VAL	10.4
1	D	172	LEU	10.4
1	D	192	ILE	10.4
2	B	399	LYS	10.4
1	Q	210	MET	10.3
2	E	218	CYS	10.3
3	P	335	TRP	10.3
3	S	176	GLN	10.3
2	B	326	GLY	10.3
1	D	82	ASN	10.2
2	R	208	CYS	10.2
3	P	70	PRO	10.2
2	E	214	SER	10.2
3	S	78	ASN	10.2
1	N	130	ILE	10.2
2	B	241	LYS	10.2
3	C	319	ASN	10.2
1	Q	200	ARG	10.2
2	R	375	THR	10.2
3	C	258	SER	10.2

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Mol	Chain	Res	Type	RSRZ
2	B	89	LEU	10.2
2	B	121	THR	10.2
1	A	190	GLN	10.2
1	Q	204	TYR	10.2
3	C	67	SER	10.2
3	P	325	ASN	10.2
2	R	106	ASP	10.1
2	R	405	ASP	10.1
3	C	125	ARG	10.1
3	S	255	GLY	10.1
3	S	389	LEU	10.1
3	C	316	ASP	10.1
2	E	342	ALA	10.1
2	E	454	MET	10.1
3	S	76	PRO	10.1
1	N	87	ASN	10.1
1	D	202	ILE	10.1
2	E	282	ASN	10.1
3	S	280	TYR	10.1
2	O	447	TRP	10.1
2	B	388	ASP	10.1
3	C	303	PHE	10.1
3	P	32	TYR	10.1
1	A	122	ILE	10.1
3	P	271	ASN	10.1
1	Q	48	CYS	10.1
2	R	94	VAL	10.1
3	F	387	ILE	10.0
2	O	320	GLU	10.0
3	F	104	GLU	10.0
1	A	212	THR	10.0
2	E	241	LYS	10.0
3	C	82	ALA	10.0
3	C	358	SER	10.0
3	P	101	SER	10.0
2	R	236	PRO	10.0
2	R	305	ARG	10.0
2	E	163	THR	10.0
2	R	109	ASN	10.0
3	S	337	ASN	10.0
2	R	215	GLY	10.0
3	F	124	LEU	10.0

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Mol	Chain	Res	Type	RSRZ
3	P	272	ASP	10.0
3	S	234	HIS	10.0
2	B	88	LYS	10.0
1	Q	168	CYS	10.0
2	R	316	LYS	10.0
1	D	79	TYR	10.0
2	R	206	VAL	10.0
2	E	221	ILE	10.0
3	S	395	GLY	9.9
1	A	222	LYS	9.9
3	P	75	LYS	9.9
2	E	352	TYR	9.9
1	Q	82	ASN	9.9
2	B	260	GLN	9.9
3	P	243	PRO	9.9
2	B	354	GLY	9.9
3	P	146	HIS	9.9
1	A	193	ALA	9.9
1	D	213	ILE	9.9
2	R	416	ALA	9.9
3	S	154	GLN	9.9
2	B	242	PRO	9.9
1	D	197	LEU	9.9
3	F	268	THR	9.9
2	R	440	ASP	9.9
3	C	59	GLU	9.9
1	Q	205	LEU	9.9
3	S	237	SER	9.9
2	B	413	ARG	9.9
2	R	207	THR	9.9
3	P	106	THR	9.9
3	S	355	SER	9.9
3	F	351	GLY	9.9
3	S	194	PHE	9.8
1	Q	201	ASP	9.8
1	A	91	LYS	9.8
1	N	85	ASP	9.8
1	N	218	PRO	9.8
3	P	326	CYS	9.8
1	A	180	ASP	9.8
3	P	381	LYS	9.8
2	B	251	THR	9.8

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Mol	Chain	Res	Type	RSRZ
3	S	30	ASN	9.8
3	S	117	ASN	9.8
1	D	211	SER	9.8
3	F	214	GLY	9.7
1	N	214	THR	9.7
3	S	33	GLN	9.7
3	C	340	HIS	9.7
3	F	57	ALA	9.7
3	S	221	THR	9.7
3	F	69	ASN	9.7
2	O	467	GLU	9.7
3	S	83	THR	9.7
3	S	239	GLN	9.7
2	O	464	TYR	9.7
3	P	333	GLY	9.7
1	A	221	PHE	9.6
2	B	357	GLY	9.6
3	F	174	ALA	9.6
3	C	350	GLN	9.6
3	P	330	ASP	9.6
1	D	142	ASN	9.6
2	R	232	TYR	9.6
3	S	227	TRP	9.6
2	O	395	THR	9.6
3	P	103	HIS	9.6
3	S	204	PHE	9.6
1	A	175	LYS	9.6
2	E	417	ALA	9.6
2	R	201	ARG	9.6
2	R	178	ILE	9.6
2	R	319	ILE	9.6
3	P	253	TRP	9.6
2	B	252	GLU	9.5
2	R	446	ASN	9.5
3	S	343	HIS	9.5
3	F	224	THR	9.5
3	S	328	GLU	9.5
1	D	49	PRO	9.5
3	P	266	LYS	9.4
3	S	148	VAL	9.4
3	F	153	CYS	9.4
3	P	55	SER	9.4

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Mol	Chain	Res	Type	RSRZ
2	O	124	TYR	9.4
3	S	339	CYS	9.4
3	C	298	ASP	9.4
1	A	72	LEU	9.4
1	A	185	GLN	9.4
3	F	321	LYS	9.4
2	E	391	GLY	9.4
1	D	224	GLN	9.4
2	R	283	ILE	9.4
3	S	119	GLN	9.4
2	B	163	THR	9.4
2	R	340	ASN	9.4
3	C	144	LYS	9.4
2	E	101	ARG	9.3
1	A	52	CYS	9.3
1	Q	50	SER	9.3
2	R	225	GLU	9.3
3	P	336	MET	9.3
3	F	177	GLN	9.3
2	E	195	THR	9.3
3	S	98	THR	9.3
3	S	323	ASP	9.3
1	A	219	ARG	9.3
2	B	211	PRO	9.3
1	Q	214	THR	9.3
2	B	222	ILE	9.3
2	E	305	ARG	9.3
2	E	303	ASN	9.3
1	N	143	VAL	9.3
2	R	248	ASP	9.2
2	R	357	GLY	9.2
2	E	235	GLN	9.2
1	D	175	LYS	9.2
3	S	303	PHE	9.2
3	C	29	LEU	9.2
2	E	406	GLY	9.2
1	A	49	PRO	9.2
2	O	463	PRO	9.2
2	B	240	SER	9.2
3	F	361	ASN	9.2
2	R	285	THR	9.2
3	P	394	ILE	9.2

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Mol	Chain	Res	Type	RSRZ
2	E	374	MET	9.1
3	P	118	SER	9.1
2	E	268	ASP	9.1
3	F	291	ASP	9.1
2	R	193	VAL	9.1
2	E	215	GLY	9.1
2	O	368	VAL	9.1
3	F	36	VAL	9.1
1	Q	120	SER	9.1
1	Q	185	GLN	9.1
2	B	157	GLN	9.1
2	E	399	LYS	9.1
1	N	204	TYR	9.1
2	O	321	MET	9.1
1	N	78	ASN	9.1
1	D	132	GLN	9.1
2	E	96	GLN	9.1
2	E	361	ILE	9.1
1	A	76	LEU	9.0
2	B	294	GLY	9.0
3	C	45	GLY	9.0
1	Q	222	LYS	9.0
2	O	415	HIS	9.0
1	D	52	CYS	9.0
3	C	109	PHE	9.0
3	S	69	ASN	9.0
2	B	215	GLY	9.0
2	O	407	GLY	9.0
2	R	327	ASP	9.0
3	P	171	PRO	9.0
2	R	273	TRP	9.0
3	S	290	PHE	9.0
3	S	171	PRO	9.0
2	E	432	ASP	9.0
2	E	414	CYS	8.9
2	O	414	CYS	8.9
2	B	341	GLU	8.9
2	R	209	ASN	8.9
3	C	69	ASN	8.9
3	F	164	SER	8.9
2	B	280	PHE	8.9
3	C	178	PHE	8.9

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Mol	Chain	Res	Type	RSRZ
3	S	72	GLN	8.9
3	P	135	CYS	8.9
3	S	129	VAL	8.9
2	E	184	SER	8.8
3	F	215	PHE	8.8
1	Q	192	ILE	8.8
2	B	406	GLY	8.8
2	O	293	CYS	8.8
3	P	73	PRO	8.8
2	R	213	VAL	8.8
3	C	281	PHE	8.8
3	P	307	HIS	8.8
1	A	48	CYS	8.8
2	O	243	TYR	8.8
3	P	27	ASP	8.8
3	S	38	LYS	8.8
3	F	80	GLU	8.8
2	B	175	LEU	8.8
3	P	392	LEU	8.8
3	F	38	LYS	8.8
2	E	450	SER	8.7
2	E	238	ASP	8.7
1	A	215	GLY	8.7
1	D	215	GLY	8.7
2	R	426	GLY	8.7
3	C	177	GLN	8.7
3	F	255	GLY	8.7
1	D	47	LYS	8.7
2	O	88	LYS	8.7
3	F	143	VAL	8.7
1	A	54	MET	8.7
2	R	374	MET	8.7
3	S	327	ALA	8.7
3	F	40	LEU	8.7
3	C	357	THR	8.7
1	N	81	LYS	8.7
2	R	341	GLU	8.7
1	N	94	VAL	8.7
3	S	103	HIS	8.6
3	S	257	THR	8.6
2	R	407	GLY	8.6
2	O	244	ARG	8.6

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Mol	Chain	Res	Type	RSRZ
2	R	223	ARG	8.6
1	D	165	LYS	8.6
2	B	243	TYR	8.6
3	F	64	ILE	8.6
3	C	192	THR	8.6
3	S	56	GLU	8.6
2	O	240	SER	8.6
2	R	242	PRO	8.6
2	R	409	TRP	8.6
2	E	207	THR	8.5
2	O	327	ASP	8.5
3	P	149	THR	8.5
3	S	170	ARG	8.5
1	N	195	ASN	8.5
3	C	56	GLU	8.5
3	S	373	LYS	8.5
2	E	203	PRO	8.5
2	R	373	THR	8.5
3	F	339	CYS	8.5
3	P	337	ASN	8.5
3	S	233	ILE	8.5
3	F	237	SER	8.5
2	E	371	ASN	8.5
1	D	156	ASP	8.5
2	E	416	ALA	8.5
2	R	342	ALA	8.5
3	C	63	ALA	8.5
3	P	170	ARG	8.5
1	N	122	ILE	8.5
3	S	209	ILE	8.5
3	C	77	ASN	8.5
2	O	214	SER	8.5
3	P	67	SER	8.5
2	O	323	ASP	8.5
2	E	392	TRP	8.5
2	O	430	THR	8.5
2	B	169	PRO	8.4
3	C	285	ASP	8.4
3	P	298	ASP	8.4
3	S	192	THR	8.4
2	E	348	SER	8.4
2	B	405	ASP	8.4

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Mol	Chain	Res	Type	RSRZ
3	F	316	ASP	8.4
2	R	204	CYS	8.4
3	C	360	PRO	8.4
3	P	198	LEU	8.4
2	E	244	ARG	8.4
2	B	283	ILE	8.3
1	A	92	ASN	8.3
1	A	83	SER	8.3
3	C	35	SER	8.3
3	S	319	ASN	8.3
2	E	105	GLU	8.3
3	P	252	ASP	8.3
1	A	51	GLY	8.3
3	P	61	VAL	8.3
1	D	184	GLN	8.3
3	C	388	PRO	8.3
2	B	258	VAL	8.3
3	S	190	GLY	8.3
3	S	79	ILE	8.3
2	R	177	SER	8.3
3	P	313	SER	8.3
3	P	310	MET	8.3
3	P	241	THR	8.2
2	O	458	SER	8.2
2	B	217	GLU	8.2
2	R	198	GLU	8.2
3	P	351	GLY	8.2
3	C	64	ILE	8.2
2	R	282	ASN	8.2
2	E	102	LYS	8.2
1	D	51	GLY	8.2
2	E	226	GLY	8.2
2	O	450	SER	8.2
3	F	266	LYS	8.2
3	P	71	ASP	8.2
3	P	288	ASP	8.2
1	Q	53	ARG	8.2
2	R	243	TYR	8.2
3	S	29	LEU	8.2
3	S	304	PHE	8.2
2	E	157	GLN	8.2
3	C	37	ASP	8.1

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Mol	Chain	Res	Type	RSRZ
2	R	116	ARG	8.1
1	N	149	ASP	8.1
3	F	82	ALA	8.1
3	P	155	ASP	8.1
3	P	328	GLU	8.1
2	R	354	GLY	8.1
1	A	161	ILE	8.1
2	E	237	GLU	8.1
2	O	215	GLY	8.1
3	S	150	GLY	8.1
3	F	358	SER	8.1
3	C	95	LYS	8.1
3	F	264	SER	8.1
2	O	375	THR	8.1
2	R	281	GLY	8.1
1	A	125	LEU	8.0
2	B	401	CYS	8.0
3	F	388	PRO	8.0
3	S	295	PHE	8.0
3	F	188	GLY	8.0
2	R	365	SER	8.0
1	A	121	ARG	8.0
2	B	434	ALA	8.0
1	N	51	GLY	8.0
2	R	406	GLY	8.0
3	P	365	ASN	8.0
1	D	212	THR	8.0
2	O	251	THR	8.0
3	C	27	ASP	8.0
3	P	72	GLN	8.0
3	P	220	PRO	8.0
2	O	127	LEU	8.0
3	F	180	VAL	8.0
1	Q	171	ALA	8.0
2	R	289	GLY	8.0
1	D	203	GLN	8.0
2	O	269	PHE	8.0
3	P	33	GLN	8.0
2	E	174	VAL	8.0
3	C	355	SER	8.0
3	P	317	SER	8.0
1	A	126	ARG	8.0

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Mol	Chain	Res	Type	RSRZ
1	A	178	LEU	7.9
2	R	140	GLN	7.9
2	E	344	LYS	7.9
2	B	416	ALA	7.9
3	S	74	SER	7.9
1	A	189	GLU	7.9
3	S	226	PHE	7.9
2	B	462	ARG	7.9
2	R	108	ARG	7.9
2	E	301	LEU	7.9
3	S	224	THR	7.9
3	C	161	ALA	7.9
2	R	262	ARG	7.9
2	E	109	ASN	7.9
2	O	265	GLY	7.9
3	S	302	LYS	7.9
1	A	145	ASP	7.9
3	F	270	GLU	7.9
1	Q	90	THR	7.9
2	R	284	ALA	7.9
3	S	35	SER	7.8
3	C	351	GLY	7.8
2	E	341	GLU	7.8
1	A	177	ASP	7.8
2	O	274	ASP	7.8
3	S	63	ALA	7.8
3	F	281	PHE	7.8
1	A	137	ASN	7.8
2	R	200	CYS	7.8
3	S	272	ASP	7.8
1	N	194	ILE	7.8
2	R	259	ILE	7.8
1	N	129	VAL	7.8
2	E	390	ASP	7.8
2	E	411	TYR	7.8
3	P	376	TRP	7.8
3	C	278	TYR	7.8
2	R	224	ASN	7.7
2	R	337	THR	7.7
1	D	125	LEU	7.7
2	O	295	VAL	7.7
3	P	96	TYR	7.7

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Mol	Chain	Res	Type	RSRZ
2	E	297	GLY	7.7
3	S	57	ALA	7.7
1	N	205	LEU	7.7
2	B	366	GLN	7.7
2	O	308	GLN	7.7
1	N	189	GLU	7.7
3	F	78	ASN	7.7
3	P	300	SER	7.7
3	S	325	ASN	7.7
2	O	423	TYR	7.7
3	S	348	TYR	7.7
2	R	413	ARG	7.7
2	E	384	THR	7.7
1	Q	175	LYS	7.7
3	P	59	GLU	7.7
2	E	98	ARG	7.7
2	R	326	GLY	7.7
3	C	394	ILE	7.7
3	P	348	TYR	7.7
2	B	342	ALA	7.7
3	C	42	THR	7.6
3	S	128	VAL	7.6
1	D	179	GLU	7.6
2	O	420	ASN	7.6
2	E	354	GLY	7.6
2	E	465	PHE	7.6
3	C	237	SER	7.6
3	P	240	SER	7.6
2	E	92	THR	7.6
2	R	174	VAL	7.6
2	R	465	PHE	7.6
2	B	270	GLY	7.6
2	B	126	THR	7.6
1	Q	178	LEU	7.6
2	E	412	ASN	7.6
3	P	30	ASN	7.6
1	A	197	LEU	7.6
3	S	276	LEU	7.6
1	D	200	ARG	7.6
2	R	251	THR	7.6
2	B	244	ARG	7.6
3	P	142	THR	7.6

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Mol	Chain	Res	Type	RSRZ
2	E	312	MET	7.6
2	R	99	PRO	7.6
2	R	227	GLU	7.6
3	P	165	GLY	7.6
3	F	37	ASP	7.5
2	O	111	VAL	7.5
1	A	206	PRO	7.5
2	E	199	TYR	7.5
1	A	129	VAL	7.5
2	O	460	MET	7.5
1	N	125	LEU	7.5
3	C	200	GLY	7.5
2	R	115	SER	7.5
1	Q	218	PRO	7.5
3	F	328	GLU	7.5
3	F	75	LYS	7.4
1	N	157	ILE	7.4
2	O	156	HIS	7.4
2	R	294	GLY	7.4
1	A	47	LYS	7.4
3	C	120	LYS	7.4
3	C	127	LYS	7.4
2	B	323	ASP	7.4
3	F	298	ASP	7.4
2	B	454	MET	7.4
3	F	45	GLY	7.4
2	E	153	LEU	7.4
3	S	335	TRP	7.4
1	A	79	TYR	7.4
3	P	268	THR	7.4
1	D	210	MET	7.4
3	C	153	CYS	7.4
2	E	288	GLU	7.4
3	F	391	ARG	7.4
3	C	320	ASP	7.4
2	E	463	PRO	7.4
2	O	459	LYS	7.4
3	S	356	LYS	7.4
3	P	156	VAL	7.4
1	N	134	GLN	7.4
2	R	293	CYS	7.4
2	O	318	LEU	7.4

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Mol	Chain	Res	Type	RSRZ
2	R	353	LYS	7.3
1	Q	56	GLY	7.3
2	E	90	GLN	7.3
2	B	116	ARG	7.3
2	E	336	PHE	7.3
2	R	387	ARG	7.3
2	B	411	TYR	7.3
2	R	252	GLU	7.3
2	R	260	GLN	7.3
1	A	157	ILE	7.3
2	B	408	GLY	7.3
1	N	80	GLN	7.3
1	N	177	ASP	7.3
3	S	381	LYS	7.3
3	C	30	ASN	7.3
2	E	99	PRO	7.3
2	E	281	GLY	7.3
1	D	90	THR	7.3
3	S	96	TYR	7.3
2	B	172	LEU	7.3
2	O	413	ARG	7.3
1	A	224	GLN	7.3
1	N	224	GLN	7.3
2	E	227	GLU	7.3
3	P	209	ILE	7.3
3	C	222	GLY	7.3
3	F	30	ASN	7.2
3	P	319	ASN	7.2
1	Q	198	PRO	7.2
3	F	60	LEU	7.2
1	A	176	VAL	7.2
3	C	311	GLN	7.2
3	C	356	LYS	7.2
3	C	339	CYS	7.2
3	P	303	PHE	7.2
3	P	147	ASP	7.2
3	S	200	GLY	7.2
3	C	142	THR	7.2
3	S	61	VAL	7.2
1	Q	62	ASP	7.2
1	Q	124	ILE	7.2
1	D	182	LYS	7.2

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Mol	Chain	Res	Type	RSRZ
2	R	280	PHE	7.2
1	N	61	VAL	7.2
3	C	158	ASN	7.2
3	S	45	GLY	7.2
3	S	37	ASP	7.2
2	E	110	THR	7.1
2	E	189	LEU	7.1
2	O	211	PRO	7.1
3	P	84	LYS	7.1
1	D	85	ASP	7.1
3	S	285	ASP	7.1
1	Q	208	LEU	7.1
2	B	124	TYR	7.1
3	P	341	ALA	7.1
3	S	342	GLY	7.1
3	S	65	GLN	7.1
2	R	186	ILE	7.1
2	R	423	TYR	7.1
2	B	265	GLY	7.1
2	B	131	MET	7.1
1	A	62	ASP	7.1
3	S	64	ILE	7.1
2	B	267	VAL	7.1
3	C	171	PRO	7.1
3	F	230	ASN	7.1
3	F	307	HIS	7.1
2	R	399	LYS	7.1
3	F	173	LYS	7.1
1	N	173	GLU	7.1
3	P	286	ALA	7.1
2	R	203	PRO	7.1
1	Q	45	ASN	7.1
2	B	176	ARG	7.1
1	D	74	ASP	7.1
3	F	330	ASP	7.1
3	C	62	LYS	7.0
3	C	205	LYS	7.0
3	C	233	ILE	7.0
2	O	362	GLU	7.0
1	N	139	LEU	7.0
1	Q	172	LEU	7.0
3	F	29	LEU	7.0

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Mol	Chain	Res	Type	RSRZ
1	A	140	GLN	7.0
2	B	109	ASN	7.0
2	R	392	TRP	7.0
2	O	390	ASP	7.0
2	O	313	GLY	7.0
1	N	113	GLN	7.0
2	O	319	ILE	7.0
3	C	326	CYS	7.0
2	O	436	HIS	7.0
3	P	234	HIS	7.0
3	C	172	LEU	7.0
3	S	376	TRP	7.0
1	D	185	GLN	7.0
3	P	35	SER	7.0
2	E	321	MET	7.0
1	D	129	VAL	7.0
3	P	172	LEU	7.0
2	B	414	CYS	7.0
1	Q	187	GLN	7.0
1	N	79	TYR	7.0
2	B	352	TYR	7.0
3	P	181	TYR	7.0
3	S	97	GLU	6.9
1	A	223	SER	6.9
2	E	95	ARG	6.9
2	O	96	GLN	6.9
3	P	369	TRP	6.9
2	B	464	TYR	6.9
3	F	32	TYR	6.9
1	A	69	ILE	6.9
1	Q	70	ASN	6.9
2	O	306	ILE	6.9
1	D	54	MET	6.9
3	C	173	LYS	6.9
2	O	99	PRO	6.9
2	O	100	ILE	6.9
2	O	108	ARG	6.9
2	R	155	LYS	6.9
1	A	202	ILE	6.9
2	R	91	ASP	6.9
3	S	297	ASP	6.9
1	A	84	LYS	6.9

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Mol	Chain	Res	Type	RSRZ
3	P	44	GLU	6.9
1	D	216	PRO	6.9
2	R	454	MET	6.8
3	C	221	THR	6.8
3	F	357	THR	6.8
3	S	185	ASP	6.8
2	B	428	ALA	6.8
2	E	103	SER	6.8
3	P	334	TRP	6.8
3	C	47	LEU	6.8
2	B	291	LYS	6.8
3	F	196	LYS	6.8
2	O	388	ASP	6.8
1	A	132	GLN	6.8
2	B	262	ARG	6.8
3	S	58	ARG	6.8
1	Q	217	VAL	6.8
1	A	55	LYS	6.8
2	O	350	SER	6.8
2	O	309	LEU	6.8
2	R	276	TYR	6.8
3	S	222	GLY	6.8
1	D	135	ARG	6.8
2	O	241	LYS	6.8
3	P	265	PHE	6.8
3	S	357	THR	6.8
2	E	240	SER	6.8
2	R	184	SER	6.8
2	E	106	ASP	6.8
2	E	114	VAL	6.8
1	Q	83	SER	6.8
2	E	407	GLY	6.8
3	S	336	MET	6.7
2	E	295	VAL	6.7
3	F	62	LYS	6.7
1	N	45	ASN	6.7
2	O	453	SER	6.7
3	F	148	VAL	6.7
3	F	141	ASP	6.7
1	Q	186	LYS	6.7
3	P	260	ALA	6.7
2	R	410	TRP	6.7

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Mol	Chain	Res	Type	RSRZ
2	B	433	MET	6.7
2	B	327	ASP	6.7
3	S	162	LYS	6.7
2	B	453	SER	6.7
3	P	258	SER	6.7
2	E	457	MET	6.7
2	O	142	ASN	6.7
3	C	123	ASN	6.7
3	S	394	ILE	6.7
3	S	168	PHE	6.7
2	R	292	TYR	6.7
3	F	309	GLY	6.7
3	C	31	ASN	6.7
3	P	31	ASN	6.7
3	C	76	PRO	6.7
3	C	272	ASP	6.6
1	D	96	LEU	6.6
2	E	93	LEU	6.6
3	F	146	HIS	6.6
2	E	205	THR	6.6
3	F	109	PHE	6.6
1	N	147	LEU	6.6
3	F	329	GLN	6.6
3	P	154	GLN	6.6
2	B	164	VAL	6.6
3	S	180	VAL	6.6
3	S	347	VAL	6.6
2	R	380	MET	6.6
3	F	389	LEU	6.6
1	Q	211	SER	6.6
2	O	228	THR	6.6
2	B	426	GLY	6.6
1	Q	150	MET	6.6
3	C	141	ASP	6.6
1	A	45	ASN	6.6
2	O	428	ALA	6.6
2	R	212	VAL	6.6
3	S	321	LYS	6.6
3	S	340	HIS	6.6
3	C	80	GLU	6.6
1	Q	221	PHE	6.6
3	F	249	GLN	6.5

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Mol	Chain	Res	Type	RSRZ
2	B	435	LYS	6.5
2	B	154	GLU	6.5
3	C	377	TYR	6.5
3	S	68	TYR	6.5
2	E	327	ASP	6.5
3	F	84	LYS	6.5
1	A	183	ASN	6.5
2	E	367	LEU	6.5
2	E	398	ARG	6.5
2	B	465	PHE	6.5
3	C	57	ALA	6.5
3	F	254	ASN	6.5
3	S	132	GLU	6.5
3	P	114	TYR	6.5
2	B	285	THR	6.5
3	S	270	GLU	6.5
2	O	381	PHE	6.5
3	C	344	LEU	6.4
1	A	88	THR	6.4
2	B	105	GLU	6.4
3	F	34	THR	6.4
2	B	238	ASP	6.4
3	S	46	ILE	6.4
3	F	92	GLU	6.4
3	P	28	PHE	6.4
1	D	112	LYS	6.4
1	A	50	SER	6.4
1	N	211	SER	6.4
2	B	171	LYS	6.4
2	B	216	LYS	6.4
3	P	139	CYS	6.4
3	F	71	ASP	6.4
3	P	169	ILE	6.4
1	D	207	ILE	6.4
2	B	273	TRP	6.4
3	C	79	ILE	6.4
3	C	354	TYR	6.4
2	E	285	THR	6.3
3	C	182	CYS	6.3
2	O	223	ARG	6.3
3	C	58	ARG	6.3
2	R	459	LYS	6.3

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Mol	Chain	Res	Type	RSRZ
1	A	105	ASN	6.3
1	A	115	ASN	6.3
2	E	249	MET	6.3
3	F	158	ASN	6.3
2	R	268	ASP	6.3
2	E	107	LEU	6.3
3	C	342	GLY	6.3
2	B	93	LEU	6.3
2	B	208	CYS	6.3
2	R	102	LYS	6.3
2	R	110	THR	6.3
3	C	65	GLN	6.3
2	E	420	ASN	6.2
3	F	150	GLY	6.2
3	P	237	SER	6.2
3	S	260	ALA	6.2
3	F	191	TRP	6.2
1	A	75	SER	6.2
2	B	371	ASN	6.2
2	O	409	TRP	6.2
2	R	256	TRP	6.2
3	C	315	TRP	6.2
3	C	296	GLY	6.2
2	B	259	ILE	6.2
2	E	121	THR	6.2
2	B	281	GLY	6.2
2	O	103	SER	6.2
3	P	255	GLY	6.2
2	R	105	GLU	6.2
3	S	82	ALA	6.2
3	F	178	PHE	6.2
2	B	449	GLY	6.2
1	N	183	ASN	6.2
3	S	293	TYR	6.2
2	O	205	THR	6.2
3	C	84	LYS	6.2
3	F	233	ILE	6.2
3	S	309	GLY	6.2
3	S	361	ASN	6.2
2	E	424	TYR	6.1
1	N	48	CYS	6.1
1	N	46	THR	6.1

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Mol	Chain	Res	Type	RSRZ
1	Q	159	ILE	6.1
2	B	325	LYS	6.1
2	E	279	GLY	6.1
2	R	258	VAL	6.1
3	C	28	PHE	6.1
2	O	283	ILE	6.1
3	F	132	GLU	6.1
1	Q	147	LEU	6.1
2	O	386	ASP	6.1
1	D	86	SER	6.1
1	Q	223	SER	6.1
3	S	36	VAL	6.1
1	A	82	ASN	6.1
1	D	70	ASN	6.1
3	S	44	GLU	6.1
3	P	360	PRO	6.1
2	E	427	GLY	6.1
2	B	368	VAL	6.1
1	Q	55	LYS	6.1
2	O	377	HIS	6.1
2	R	332	LEU	6.1
2	O	402	SER	6.1
3	S	318	ASP	6.1
2	O	417	ALA	6.1
1	A	159	ILE	6.1
2	B	113	SER	6.1
1	D	84	LYS	6.0
1	Q	191	VAL	6.0
2	R	428	ALA	6.0
2	R	455	LYS	6.0
3	P	222	GLY	6.0
3	P	379	MET	6.0
3	C	128	VAL	6.0
3	C	46	ILE	6.0
2	B	379	SER	6.0
3	C	374	SER	6.0
3	P	349	TYR	6.0
1	N	110	THR	6.0
3	F	221	THR	6.0
2	R	361	ILE	6.0
1	A	85	ASP	6.0
1	A	209	LYS	6.0

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Mol	Chain	Res	Type	RSRZ
2	R	303	ASN	6.0
1	Q	85	ASP	6.0
2	R	172	LEU	6.0
3	C	381	LYS	6.0
1	N	140	GLN	6.0
2	O	136	GLN	6.0
1	A	194	ILE	6.0
3	C	186	GLY	6.0
3	S	326	CYS	6.0
3	C	302	LYS	6.0
2	O	397	PRO	6.0
3	S	230	ASN	6.0
3	P	221	THR	6.0
1	D	94	VAL	6.0
1	N	215	GLY	6.0
2	B	437	GLY	6.0
2	E	239	SER	5.9
3	P	264	SER	5.9
1	N	221	PHE	5.9
3	C	348	TYR	5.9
2	R	364	ALA	5.9
1	D	153	LEU	5.9
2	E	325	LYS	5.9
2	B	151	SER	5.9
1	Q	65	PHE	5.9
1	N	59	ASP	5.9
1	N	117	ASP	5.9
2	B	404	GLU	5.9
3	P	292	GLY	5.9
3	S	95	LYS	5.9
1	D	221	PHE	5.9
3	S	159	LYS	5.9
1	A	201	ASP	5.9
2	E	134	GLY	5.9
1	A	136	ILE	5.9
1	Q	165	LYS	5.9
3	S	278	TYR	5.9
3	C	135	CYS	5.9
2	E	111	VAL	5.8
2	R	244	ARG	5.8
2	O	440	ASP	5.8
2	R	196	GLN	5.8

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Mol	Chain	Res	Type	RSRZ
1	A	130	ILE	5.8
2	B	224	ASN	5.8
2	R	185	LYS	5.8
3	C	288	ASP	5.8
2	O	119	SER	5.8
2	R	222	ILE	5.8
3	C	312	PHE	5.8
2	E	171	LYS	5.8
3	F	320	ASP	5.8
1	Q	174	HIS	5.8
3	C	307	HIS	5.8
2	O	260	GLN	5.8
2	E	212	VAL	5.8
2	O	212	VAL	5.8
3	F	284	GLY	5.8
3	F	324	GLY	5.8
2	E	177	SER	5.8
3	C	364	ASP	5.8
3	P	375	ARG	5.8
2	R	291	LYS	5.8
2	R	344	LYS	5.8
2	R	429	TYR	5.8
2	R	240	SER	5.8
2	R	368	VAL	5.8
2	R	466	PRO	5.8
1	D	55	LYS	5.8
3	F	310	MET	5.7
1	N	217	VAL	5.7
2	E	314	PRO	5.7
3	P	290	PHE	5.7
3	C	257	THR	5.7
2	E	97	GLU	5.7
3	P	270	GLU	5.7
2	E	104	ILE	5.7
1	Q	81	LYS	5.7
3	C	220	PRO	5.7
3	S	240	SER	5.7
3	S	299	SER	5.7
2	O	303	ASN	5.7
3	F	179	LEU	5.7
3	S	202	LEU	5.7
2	O	218	CYS	5.7

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Mol	Chain	Res	Type	RSRZ
1	Q	46	THR	5.7
3	F	257	THR	5.7
1	N	210	MET	5.7
3	F	231	GLU	5.7
2	B	361	ILE	5.7
2	B	303	ASN	5.7
3	C	204	PHE	5.7
2	R	430	THR	5.7
2	E	160	ILE	5.7
3	S	60	LEU	5.7
3	F	197	ARG	5.7
2	O	358	ASN	5.7
2	B	138	GLN	5.7
3	F	243	PRO	5.7
1	A	171	ALA	5.7
1	D	205	LEU	5.7
2	R	112	ASP	5.7
3	C	66	ILE	5.6
3	F	333	GLY	5.6
2	E	172	LEU	5.6
1	D	136	ILE	5.6
3	F	66	ILE	5.6
2	R	194	SER	5.6
2	E	255	GLY	5.6
2	O	200	CYS	5.6
2	R	435	LYS	5.6
3	S	75	LYS	5.6
1	D	176	VAL	5.6
3	F	207	ASN	5.6
3	P	282	ILE	5.6
3	S	370	ALA	5.6
2	R	164	VAL	5.6
2	B	386	ASP	5.6
3	S	100	ILE	5.6
2	O	184	SER	5.6
2	O	357	GLY	5.6
3	P	62	LYS	5.6
3	S	175	LYS	5.6
3	F	94	MET	5.6
1	A	143	VAL	5.6
2	O	193	VAL	5.6
2	R	111	VAL	5.6

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Mol	Chain	Res	Type	RSRZ
3	C	68	TYR	5.6
1	A	106	ASN	5.5
1	D	73	ARG	5.5
1	N	180	ASP	5.6
1	D	195	ASN	5.5
3	F	260	ALA	5.6
3	C	219	SER	5.5
3	F	355	SER	5.5
3	P	136	GLN	5.5
3	P	256	ARG	5.5
3	S	108	ARG	5.5
3	P	320	ASP	5.5
2	O	263	GLN	5.5
2	R	345	TYR	5.5
1	A	158	ASP	5.5
2	R	197	MET	5.5
1	A	133	VAL	5.5
2	B	96	GLN	5.5
2	O	448	GLN	5.5
3	F	28	PHE	5.5
1	D	204	TYR	5.5
1	D	75	SER	5.5
2	E	453	SER	5.5
3	C	241	THR	5.5
3	P	102	THR	5.5
3	C	126	ASP	5.5
3	F	110	LEU	5.5
3	P	162	LYS	5.5
1	Q	79	TYR	5.5
1	Q	75	SER	5.5
1	D	109	ASN	5.5
3	P	382	THR	5.5
3	S	314	THR	5.5
3	F	168	PHE	5.5
2	O	182	LEU	5.5
3	C	372	TRP	5.5
1	D	194	ILE	5.5
3	S	345	ASN	5.5
3	P	346	GLY	5.4
3	P	141	ASP	5.4
2	E	381	PHE	5.4
2	E	402	SER	5.4

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Mol	Chain	Res	Type	RSRZ
3	P	94	MET	5.4
3	S	141	ASP	5.4
3	P	167	TYR	5.4
2	R	286	ASN	5.4
3	S	158	ASN	5.4
1	D	187	GLN	5.4
3	P	311	GLN	5.4
1	Q	157	ILE	5.4
2	R	379	SER	5.4
1	A	195	ASN	5.4
1	Q	129	VAL	5.4
2	O	137	ASN	5.4
2	R	254	GLY	5.4
2	B	321	MET	5.4
2	R	192	ASP	5.4
2	B	288	GLU	5.4
1	N	91	LYS	5.4
2	E	355	THR	5.4
3	S	241	THR	5.4
2	R	463	PRO	5.4
3	F	204	PHE	5.4
2	O	421	GLY	5.4
3	P	188	GLY	5.4
2	B	400	GLN	5.4
1	N	83	SER	5.3
3	P	66	ILE	5.3
2	B	115	SER	5.3
1	A	205	LEU	5.3
3	S	134	ASN	5.3
1	Q	132	GLN	5.3
3	S	32	TYR	5.3
2	B	438	THR	5.3
2	R	261	ASN	5.3
3	S	109	PHE	5.3
3	P	183	GLU	5.3
2	B	250	LYS	5.3
3	P	205	LYS	5.3
2	E	270	GLY	5.3
3	S	153	CYS	5.3
2	R	398	ARG	5.3
3	C	385	LYS	5.3
1	A	139	LEU	5.3

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Mol	Chain	Res	Type	RSRZ
3	C	359	THR	5.3
3	S	267	VAL	5.3
3	P	160	GLY	5.3
2	B	444	TRP	5.3
3	C	194	PHE	5.3
3	C	100	ILE	5.3
2	B	236	PRO	5.2
2	O	97	GLU	5.2
2	R	320	GLU	5.2
3	F	129	VAL	5.2
1	N	163	SER	5.2
2	B	95	ARG	5.2
2	E	323	ASP	5.2
3	S	265	PHE	5.2
1	D	143	VAL	5.2
3	S	59	GLU	5.2
2	O	330	THR	5.2
2	O	333	TYR	5.2
1	N	86	SER	5.2
3	C	101	SER	5.2
3	S	187	SER	5.2
3	S	296	GLY	5.2
2	B	393	LYS	5.2
2	O	433	MET	5.2
1	Q	76	LEU	5.2
2	B	332	LEU	5.2
2	E	89	LEU	5.2
2	E	409	TRP	5.2
2	E	418	ASN	5.2
3	C	337	ASN	5.2
3	S	261	ASP	5.2
2	E	395	THR	5.2
3	P	204	PHE	5.2
1	Q	197	LEU	5.2
2	E	460	MET	5.2
3	F	144	LYS	5.2
2	O	196	GLN	5.2
1	N	100	ASP	5.2
2	R	230	GLU	5.2
2	E	366	GLN	5.2
2	O	130	ASN	5.2
3	C	308	ASN	5.2

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Mol	Chain	Res	Type	RSRZ
3	P	117	ASN	5.2
2	O	112	ASP	5.2
3	F	303	PHE	5.2
3	P	373	LYS	5.2
1	A	110	THR	5.2
3	S	358	SER	5.2
3	C	279	ALA	5.1
2	E	258	VAL	5.1
3	C	321	LYS	5.1
1	N	119	ARG	5.1
3	F	359	THR	5.1
2	E	452	TYR	5.1
3	F	322	TYR	5.1
2	B	459	LYS	5.1
3	F	232	LYS	5.1
2	E	116	ARG	5.1
2	E	262	ARG	5.1
2	O	279	GLY	5.1
2	E	339	GLN	5.1
2	E	428	ALA	5.1
3	C	111	GLN	5.1
3	F	31	ASN	5.1
3	F	365	ASN	5.1
2	B	205	THR	5.1
2	O	270	GLY	5.1
3	P	263	ALA	5.1
3	S	322	TYR	5.1
2	O	296	PRO	5.1
2	O	315	THR	5.1
2	R	395	THR	5.1
2	O	281	GLY	5.1
3	S	284	GLY	5.1
1	Q	173	GLU	5.1
3	F	133	ALA	5.1
3	S	279	ALA	5.1
1	N	176	VAL	5.1
2	B	387	ARG	5.1
2	O	120	SER	5.1
3	F	81	SER	5.1
3	F	190	GLY	5.1
3	P	87	LYS	5.1
3	P	342	GLY	5.1

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Mol	Chain	Res	Type	RSRZ
3	S	144	LYS	5.1
3	P	327	ALA	5.1
3	S	350	GLN	5.1
2	B	432	ASP	5.1
1	D	191	VAL	5.1
2	E	389	ASN	5.0
1	D	71	LYS	5.0
3	C	54	THR	5.0
3	F	159	LYS	5.0
3	P	68	TYR	5.0
1	N	200	ARG	5.0
3	C	129	VAL	5.0
1	D	137	ASN	5.0
2	R	418	ASN	5.0
3	P	166	LEU	5.0
3	F	294	ASP	5.0
1	D	131	GLU	5.0
2	R	334	GLU	5.0
3	C	91	GLU	5.0
2	B	317	LEU	5.0
2	B	100	ILE	5.0
2	B	195	THR	5.0
3	F	42	THR	5.0
3	P	150	GLY	5.0
2	R	237	GLU	5.0
3	S	334	TRP	5.0
2	E	377	HIS	5.0
2	O	314	PRO	5.0
2	E	137	ASN	5.0
2	R	304	ASP	5.0
3	C	185	ASP	5.0
3	P	358	SER	5.0
1	A	198	PRO	4.9
2	R	401	CYS	4.9
3	F	229	GLY	4.9
2	E	148	GLU	4.9
3	P	36	VAL	4.9
3	S	354	TYR	4.9
2	R	402	SER	4.9
2	R	318	LEU	4.9
2	R	397	PRO	4.9
2	B	279	GLY	4.9

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Mol	Chain	Res	Type	RSRZ
3	C	207	ASN	4.9
1	A	210	MET	4.9
3	P	372	TRP	4.9
3	S	86	SER	4.9
2	B	203	PRO	4.9
2	E	228	THR	4.9
1	A	104	ALA	4.9
2	O	207	THR	4.9
2	B	297	GLY	4.9
3	C	130	GLN	4.9
3	P	284	GLY	4.9
3	P	254	ASN	4.9
2	O	216	LYS	4.9
2	O	217	GLU	4.9
3	P	262	TYR	4.9
3	F	362	GLY	4.9
1	Q	136	ILE	4.9
2	B	114	VAL	4.9
2	B	374	MET	4.9
1	N	65	PHE	4.9
2	R	362	GLU	4.8
2	O	355	THR	4.8
2	R	315	THR	4.8
1	D	99	GLY	4.8
3	F	63	ALA	4.8
1	Q	177	ASP	4.8
2	E	217	GLU	4.8
3	P	244	TYR	4.8
3	F	277	THR	4.8
3	S	346	GLY	4.8
3	F	152	ASP	4.8
2	R	411	TYR	4.8
3	P	90	MET	4.8
3	P	309	GLY	4.8
1	A	77	PHE	4.8
2	O	271	ARG	4.8
2	R	453	SER	4.8
3	F	248	ILE	4.8
3	F	386	ILE	4.8
2	E	192	ASP	4.8
2	R	323	ASP	4.8
3	F	346	GLY	4.8

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Mol	Chain	Res	Type	RSRZ
1	N	126	ARG	4.8
2	R	100	ILE	4.8
3	P	390	ASN	4.8
2	O	299	TYR	4.7
1	N	102	ALA	4.7
1	N	132	GLN	4.7
3	S	360	PRO	4.7
3	S	201	SER	4.7
2	B	418	ASN	4.7
3	S	207	ASN	4.7
3	S	157	ALA	4.7
3	S	359	THR	4.7
2	E	397	PRO	4.7
2	R	296	PRO	4.7
3	F	79	ILE	4.7
3	S	363	TYR	4.7
2	R	228	THR	4.7
3	C	268	THR	4.7
1	A	216	PRO	4.7
2	B	304	ASP	4.7
1	D	178	LEU	4.7
3	F	368	ILE	4.7
3	P	233	ILE	4.7
3	P	281	PHE	4.7
3	P	127	LYS	4.7
3	S	305	THR	4.7
2	B	466	PRO	4.7
3	F	299	SER	4.7
1	Q	154	GLU	4.7
2	B	356	ALA	4.7
1	Q	49	PRO	4.7
3	S	378	SER	4.7
1	N	158	ASP	4.7
3	C	345	ASN	4.7
3	P	120	LYS	4.7
1	A	174	HIS	4.7
2	O	452	TYR	4.7
3	P	143	VAL	4.7
3	C	190	GLY	4.7
3	S	116	SER	4.6
3	S	27	ASP	4.6
3	F	253	TRP	4.6

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Mol	Chain	Res	Type	RSRZ
2	O	360	LEU	4.6
2	B	286	ASN	4.6
2	R	434	ALA	4.6
1	Q	88	THR	4.6
2	R	169	PRO	4.6
2	O	268	ASP	4.6
3	C	250	LEU	4.6
2	B	104	ILE	4.6
2	E	225	GLU	4.6
2	O	341	GLU	4.6
2	E	375	THR	4.6
3	F	130	GLN	4.6
3	F	88	SER	4.6
3	F	201	SER	4.6
3	P	74	SER	4.6
3	C	40	LEU	4.6
2	B	101	ARG	4.6
1	D	124	ILE	4.6
1	Q	213	ILE	4.6
2	B	161	ASP	4.6
3	F	272	ASP	4.6
3	P	289	ALA	4.6
2	E	166	ASN	4.6
3	P	274	TYR	4.6
2	B	150	SER	4.6
3	C	41	ARG	4.6
3	F	58	ARG	4.6
1	A	207	ILE	4.6
3	S	133	ALA	4.6
3	F	319	ASN	4.6
1	D	101	PHE	4.6
1	D	199	SER	4.6
1	Q	209	LYS	4.6
2	O	434	ALA	4.6
3	F	157	ALA	4.6
1	D	220	GLU	4.6
2	B	237	GLU	4.6
2	E	320	GLU	4.6
2	R	97	GLU	4.6
3	C	300	SER	4.6
3	C	328	GLU	4.6
3	P	52	ASN	4.6

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Mol	Chain	Res	Type	RSRZ
3	P	230	ASN	4.6
3	S	118	SER	4.6
3	F	89	MET	4.6
3	F	370	ALA	4.5
2	B	129	LYS	4.5
2	E	382	PHE	4.5
1	D	106	ASN	4.5
2	E	170	THR	4.5
2	O	239	SER	4.5
3	F	68	TYR	4.5
2	O	332	LEU	4.5
2	O	98	ARG	4.5
2	B	460	MET	4.5
3	F	392	LEU	4.5
2	R	170	THR	4.5
2	E	286	ASN	4.5
2	O	232	TYR	4.5
3	F	340	HIS	4.5
3	S	139	CYS	4.5
2	O	118	SER	4.5
2	B	452	TYR	4.5
2	E	149	TYR	4.5
2	R	343	ASN	4.5
3	F	76	PRO	4.5
2	E	194	SER	4.5
2	E	330	THR	4.5
3	F	98	THR	4.5
2	E	296	PRO	4.5
3	F	113	ILE	4.5
2	R	445	MET	4.4
1	N	166	GLY	4.4
3	S	196	LYS	4.4
2	E	467	GLU	4.4
2	R	447	TRP	4.4
3	C	215	PHE	4.4
3	C	116	SER	4.4
3	P	116	SER	4.4
3	S	127	LYS	4.4
2	R	175	LEU	4.4
2	R	369	GLY	4.4
2	B	409	TRP	4.4
3	P	46	ILE	4.4

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Mol	Chain	Res	Type	RSRZ
3	P	387	ILE	4.4
2	B	201	ARG	4.4
2	R	309	LEU	4.4
2	R	255	GLY	4.4
3	F	137	GLU	4.4
2	B	209	ASN	4.4
3	C	189	ASN	4.4
3	F	293	TYR	4.4
2	R	234	ILE	4.4
1	N	172	LEU	4.4
2	B	106	ASP	4.4
3	P	296	GLY	4.4
2	E	464	TYR	4.4
1	D	128	LYS	4.4
3	C	61	VAL	4.4
3	F	161	ALA	4.4
1	N	164	CYS	4.4
3	F	285	ASP	4.4
2	O	438	THR	4.4
2	R	384	THR	4.4
3	C	188	GLY	4.4
3	C	347	VAL	4.4
2	B	107	LEU	4.4
2	E	451	TRP	4.4
2	O	132	TRP	4.4
2	B	178	ILE	4.4
3	F	41	ARG	4.3
2	R	458	SER	4.3
1	D	103	LYS	4.3
3	S	73	PRO	4.3
2	O	462	ARG	4.3
3	S	391	ARG	4.3
2	R	267	VAL	4.3
3	P	69	ASN	4.3
3	S	286	ALA	4.3
2	B	365	SER	4.3
2	O	324	TRP	4.3
3	P	324	GLY	4.3
2	B	141	ASP	4.3
2	O	209	ASN	4.3
2	E	461	ILE	4.3
2	O	272	LYS	4.3

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Mol	Chain	Res	Type	RSRZ
3	C	331	GLY	4.3
2	B	173	ARG	4.3
1	D	62	ASP	4.3
1	D	117	ASP	4.3
3	S	155	ASP	4.3
2	B	299	TYR	4.3
1	A	78	ASN	4.3
2	E	261	ASN	4.3
2	B	403	LYS	4.3
1	Q	69	ILE	4.3
3	F	334	TRP	4.3
3	F	155	ASP	4.3
1	Q	84	LYS	4.3
2	B	220	LYS	4.3
3	C	196	LYS	4.3
2	O	339	GLN	4.3
3	F	91	GLU	4.3
3	P	207	ASN	4.2
1	A	73	ARG	4.2
1	Q	99	GLY	4.2
2	E	373	THR	4.2
2	R	226	GLY	4.2
1	N	196	LEU	4.2
3	P	110	LEU	4.2
2	B	156	HIS	4.2
1	Q	80	GLN	4.2
2	E	224	ASN	4.2
3	F	186	GLY	4.2
3	S	42	THR	4.2
3	C	60	LEU	4.2
3	P	276	LEU	4.2
1	Q	170	ARG	4.2
2	E	138	GLN	4.2
1	D	160	LYS	4.2
1	N	55	LYS	4.2
1	A	86	SER	4.2
1	D	104	ALA	4.2
2	B	402	SER	4.2
2	E	180	GLU	4.2
3	F	278	TYR	4.2
3	F	115	ASN	4.2
3	P	77	ASN	4.2

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Mol	Chain	Res	Type	RSRZ
3	S	364	ASP	4.2
1	D	57	LEU	4.2
2	E	349	VAL	4.2
3	S	167	TYR	4.2
2	E	152	HIS	4.2
2	E	181	ASN	4.2
2	O	147	ASN	4.2
1	Q	180	ASP	4.2
1	Q	93	ILE	4.2
2	B	135	ARG	4.2
1	A	95	GLU	4.2
2	O	424	TYR	4.2
1	N	153	LEU	4.2
3	S	189	ASN	4.2
2	O	264	ASP	4.1
2	R	437	GLY	4.1
2	O	419	PRO	4.1
2	B	133	LYS	4.1
2	B	301	LEU	4.1
2	R	199	TYR	4.1
2	B	168	ILE	4.1
3	P	45	GLY	4.1
1	N	84	LYS	4.1
3	C	151	ARG	4.1
2	B	132	TRP	4.1
2	E	410	TRP	4.1
1	Q	161	ILE	4.1
2	E	159	TYR	4.1
2	R	322	GLU	4.1
3	C	112	GLU	4.1
1	N	90	THR	4.1
3	P	42	THR	4.1
1	D	81	LYS	4.1
2	R	191	SER	4.1
3	S	306	SER	4.1
2	R	246	TYR	4.1
2	E	379	SER	4.1
2	E	356	ALA	4.1
1	A	114	ILE	4.1
3	F	93	ILE	4.1
3	C	38	LYS	4.1
2	E	426	GLY	4.1

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Mol	Chain	Res	Type	RSRZ
2	R	152	HIS	4.1
3	F	67	SER	4.1
3	F	118	SER	4.1
3	P	246	LEU	4.1
1	N	58	ILE	4.1
1	N	161	ILE	4.1
2	B	227	GLU	4.1
3	F	122	VAL	4.1
3	P	81	SER	4.1
1	Q	77	PHE	4.0
2	O	91	ASP	4.0
2	R	436	HIS	4.0
3	C	122	VAL	4.0
2	B	289	GLY	4.0
2	E	394	THR	4.0
3	S	55	SER	4.0
3	P	345	ASN	4.0
3	P	176	GLN	4.0
1	N	54	MET	4.0
2	R	412	ASN	4.0
2	B	235	GLN	4.0
1	Q	176	VAL	4.0
2	O	116	ARG	4.0
3	C	293	TYR	4.0
3	F	364	ASP	4.0
3	P	145	ILE	4.0
3	S	369	TRP	4.0
3	S	174	ALA	4.0
1	A	184	GLN	4.0
3	F	350	GLN	4.0
1	A	53	ARG	4.0
2	E	433	MET	4.0
3	C	148	VAL	3.9
3	P	232	LYS	3.9
3	F	171	PRO	3.9
3	F	107	ILE	3.9
3	P	119	GLN	3.9
3	F	166	LEU	3.9
1	Q	179	GLU	3.9
3	F	287	GLY	3.9
3	C	286	ALA	3.9
2	O	201	ARG	3.9

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Mol	Chain	Res	Type	RSRZ
3	F	49	GLN	3.9
1	A	67	SER	3.9
2	B	194	SER	3.9
2	B	314	PRO	3.9
3	C	330	ASP	3.9
1	N	187	GLN	3.9
1	D	89	LEU	3.9
2	B	249	MET	3.9
1	D	168	CYS	3.9
3	S	137	GLU	3.9
3	S	125	ARG	3.9
2	B	144	ASN	3.9
2	R	274	ASP	3.9
3	F	311	GLN	3.9
3	C	88	SER	3.9
3	F	258	SER	3.9
2	O	289	GLY	3.9
3	C	382	THR	3.9
2	B	148	GLU	3.9
2	E	250	LYS	3.9
2	E	233	LEU	3.9
2	O	444	TRP	3.9
2	R	89	LEU	3.9
3	S	179	LEU	3.9
1	A	148	VAL	3.9
2	B	271	ARG	3.8
3	F	247	ARG	3.8
2	R	377	HIS	3.8
2	B	139	VAL	3.8
3	F	210	GLN	3.8
2	R	130	ASN	3.8
3	S	77	ASN	3.8
3	F	187	SER	3.8
2	E	259	ILE	3.8
2	O	254	GLY	3.8
2	E	213	VAL	3.8
3	C	245	VAL	3.8
2	R	129	LYS	3.8
3	C	294	ASP	3.8
3	P	250	LEU	3.8
3	C	157	ALA	3.8
3	C	255	GLY	3.8

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Mol	Chain	Res	Type	RSRZ
3	F	327	ALA	3.8
1	A	116	GLU	3.8
2	E	219	GLU	3.8
3	S	163	GLU	3.8
2	E	191	SER	3.8
3	F	344	LEU	3.8
3	F	170	ARG	3.8
1	N	99	GLY	3.8
3	P	161	ALA	3.8
2	B	232	TYR	3.8
3	S	111	GLN	3.8
1	D	163	SER	3.8
3	S	131	LEU	3.8
3	P	227	TRP	3.8
2	R	257	THR	3.8
3	F	263	ALA	3.8
1	D	180	ASP	3.8
2	E	329	VAL	3.8
3	F	154	GLN	3.7
1	N	70	ASN	3.7
3	P	63	ALA	3.7
3	F	213	GLU	3.7
3	P	295	PHE	3.7
3	F	189	ASN	3.7
3	P	279	ALA	3.7
2	B	456	LYS	3.7
3	S	385	LYS	3.7
1	A	208	LEU	3.7
2	E	276	TYR	3.7
2	E	136	GLN	3.7
2	O	169	PRO	3.7
3	P	49	GLN	3.7
2	B	170	THR	3.7
3	C	369	TRP	3.7
3	P	86	SER	3.7
3	S	177	GLN	3.7
2	B	181	ASN	3.7
3	C	327	ALA	3.7
3	F	123	ASN	3.7
1	A	93	ILE	3.7
2	B	223	ARG	3.7
2	O	364	ALA	3.7

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Mol	Chain	Res	Type	RSRZ
2	O	461	ILE	3.7
3	F	83	THR	3.7
3	S	352	GLY	3.7
2	O	131	MET	3.7
1	N	146	GLN	3.7
3	P	92	GLU	3.7
2	O	210	ILE	3.6
2	R	247	CYS	3.6
3	C	236	ILE	3.6
3	P	214	GLY	3.6
3	P	216	GLY	3.6
2	B	351	LYS	3.6
2	O	344	LYS	3.6
2	E	267	VAL	3.6
3	P	124	LEU	3.6
2	B	345	TYR	3.6
1	A	156	ASP	3.6
3	S	102	THR	3.6
3	S	324	GLY	3.6
2	E	277	LYS	3.6
2	O	206	VAL	3.6
2	O	213	VAL	3.6
2	E	401	CYS	3.6
3	P	111	GLN	3.6
3	P	388	PRO	3.6
2	O	246	TYR	3.6
2	B	415	HIS	3.6
2	E	335	GLY	3.6
2	B	381	PHE	3.6
2	B	198	GLU	3.6
3	C	232	LYS	3.6
1	N	53	ARG	3.6
2	R	233	LEU	3.6
3	C	202	LEU	3.6
3	C	269	GLY	3.6
3	F	353	THR	3.6
1	Q	155	VAL	3.6
2	O	267	VAL	3.6
3	S	156	VAL	3.6
3	P	164	SER	3.6
2	B	125	ILE	3.6
1	A	150	MET	3.6

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Mol	Chain	Res	Type	RSRZ
2	O	343	ASN	3.5
2	R	167	ASN	3.5
1	D	97	MET	3.5
1	N	209	LYS	3.5
3	P	302	LYS	3.5
2	O	180	GLU	3.5
2	B	189	LEU	3.5
2	E	331	ALA	3.5
2	O	465	PHE	3.5
3	C	174	ALA	3.5
3	F	156	VAL	3.5
1	D	223	SER	3.5
2	B	184	SER	3.5
3	S	113	ILE	3.5
3	S	374	SER	3.5
2	B	261	ASN	3.5
3	S	223	ASN	3.5
2	O	225	GLU	3.5
3	C	265	PHE	3.5
2	E	421	GLY	3.5
2	B	389	ASN	3.5
2	R	393	LYS	3.5
3	F	77	ASN	3.5
3	F	261	ASP	3.5
3	F	244	TYR	3.5
1	D	114	ILE	3.5
3	C	283	GLY	3.5
3	F	184	ILE	3.5
2	O	285	THR	3.5
3	P	190	GLY	3.5
3	F	380	LYS	3.5
3	F	226	PHE	3.5
3	S	143	VAL	3.5
2	B	182	LEU	3.5
3	F	337	ASN	3.5
3	F	345	ASN	3.5
1	A	127	ARG	3.5
2	O	237	GLU	3.5
1	Q	151	LYS	3.5
3	C	34	THR	3.5
3	C	94	MET	3.5
1	D	65	PHE	3.5

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Mol	Chain	Res	Type	RSRZ
2	O	286	ASN	3.5
1	A	108	ASP	3.4
3	F	100	ILE	3.4
2	E	393	LYS	3.4
2	O	385	TYR	3.4
2	B	298	GLU	3.4
2	B	373	THR	3.4
3	F	54	THR	3.4
2	O	166	ASN	3.4
1	A	81	LYS	3.4
2	B	212	VAL	3.4
2	B	370	GLU	3.4
3	F	276	LEU	3.4
2	R	239	SER	3.4
1	D	198	PRO	3.4
2	R	221	ILE	3.4
3	C	169	ILE	3.4
3	S	85	ASN	3.4
1	N	197	LEU	3.4
3	C	43	LEU	3.4
3	C	280	TYR	3.4
1	A	167	SER	3.4
2	O	191	SER	3.4
3	P	269	GLY	3.4
3	C	197	ARG	3.4
1	A	138	LEU	3.4
1	N	198	PRO	3.4
2	R	231	MET	3.4
1	A	191	VAL	3.4
2	O	379	SER	3.4
3	S	105	SER	3.4
2	R	163	THR	3.4
3	C	291	ASP	3.4
3	C	121	ILE	3.4
3	F	120	LYS	3.4
3	F	356	LYS	3.4
2	E	123	GLN	3.4
1	A	147	LEU	3.4
2	O	317	LEU	3.4
1	Q	193	ALA	3.4
2	O	113	SER	3.4
3	F	240	SER	3.4

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Mol	Chain	Res	Type	RSRZ
3	C	98	THR	3.4
3	C	208	TRP	3.4
2	E	419	PRO	3.4
3	S	219	SER	3.4
3	P	211	TYR	3.4
2	R	179	LEU	3.3
2	R	189	LEU	3.3
3	F	208	TRP	3.3
2	R	460	MET	3.3
1	A	70	ASN	3.3
2	B	229	SER	3.3
3	P	283	GLY	3.3
3	S	236	ILE	3.3
3	S	242	ILE	3.3
1	Q	91	LYS	3.3
1	D	78	ASN	3.3
2	O	262	ARG	3.3
2	R	101	ARG	3.3
3	F	99	LEU	3.3
3	S	198	LEU	3.3
1	D	181	TYR	3.3
2	E	232	TYR	3.3
2	R	96	GLN	3.3
3	F	119	GLN	3.3
2	O	416	ALA	3.3
2	R	287	ALA	3.3
2	B	398	ARG	3.3
2	E	142	ASN	3.3
3	P	153	CYS	3.3
2	R	333	TYR	3.3
2	R	363	GLY	3.3
3	F	211	TYR	3.3
3	P	51	GLU	3.3
3	S	232	LYS	3.3
1	D	108	ASP	3.3
1	D	130	ILE	3.3
1	N	93	ILE	3.3
2	E	176	ARG	3.3
2	R	271	ARG	3.3
2	R	302	GLY	3.3
3	F	283	GLY	3.3
1	N	88	THR	3.3

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Mol	Chain	Res	Type	RSRZ
3	C	343	HIS	3.3
1	A	217	VAL	3.3
1	N	216	PRO	3.3
3	P	242	ILE	3.3
2	E	274	ASP	3.3
3	F	331	GLY	3.3
3	C	238	THR	3.3
3	P	259	THR	3.3
3	F	251	GLU	3.3
3	P	321	LYS	3.3
2	O	153	LEU	3.2
2	R	356	ALA	3.2
2	E	266	SER	3.2
2	O	443	VAL	3.2
2	B	130	ASN	3.2
2	R	427	GLY	3.2
3	F	53	LYS	3.2
2	E	299	TYR	3.2
3	C	349	TYR	3.2
2	O	140	GLN	3.2
3	F	140	GLN	3.2
1	A	101	PHE	3.2
1	N	174	HIS	3.2
2	O	152	HIS	3.2
1	N	120	SER	3.2
2	O	383	SER	3.2
2	E	264	ASP	3.2
2	E	326	GLY	3.2
3	P	123	ASN	3.2
2	O	170	THR	3.2
2	R	92	THR	3.2
1	A	89	LEU	3.2
2	E	429	TYR	3.2
1	D	140	GLN	3.2
3	F	46	ILE	3.2
3	C	306	SER	3.2
3	P	374	SER	3.2
3	F	175	LYS	3.2
1	Q	117	ASP	3.2
3	P	305	THR	3.2
3	P	79	ILE	3.2
2	R	250	LYS	3.2

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Mol	Chain	Res	Type	RSRZ
2	O	134	GLY	3.2
3	S	287	GLY	3.2
2	B	420	ASN	3.2
3	C	277	THR	3.2
2	O	429	TYR	3.2
3	C	213	GLU	3.2
1	Q	160	LYS	3.2
2	E	328	LYS	3.2
3	F	117	ASN	3.2
1	N	116	GLU	3.2
3	P	385	LYS	3.2
3	F	378	SER	3.2
2	E	178	ILE	3.1
1	A	99	GLY	3.1
2	O	273	TRP	3.1
2	O	197	MET	3.1
2	B	319	ILE	3.1
3	C	310	MET	3.1
3	F	372	TRP	3.1
3	P	130	GLN	3.1
3	P	208	TRP	3.1
1	D	115	ASN	3.1
3	C	260	ALA	3.1
3	F	116	SER	3.1
3	P	60	LEU	3.1
3	P	187	SER	3.1
2	R	210	ILE	3.1
2	O	257	THR	3.1
2	O	157	GLN	3.1
1	Q	92	ASN	3.1
2	R	431	TRP	3.1
2	B	191	SER	3.1
2	B	284	ALA	3.1
2	E	338	VAL	3.1
2	R	450	SER	3.1
2	R	104	ILE	3.1
1	D	218	PRO	3.1
1	N	73	ARG	3.1
3	S	41	ARG	3.1
3	C	383	THR	3.1
3	P	383	THR	3.1
2	R	307	SER	3.1

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Mol	Chain	Res	Type	RSRZ
3	C	271	ASN	3.1
3	F	51	GLU	3.1
2	B	98	ARG	3.1
3	S	291	ASP	3.1
2	O	312	MET	3.1
2	R	157	GLN	3.1
3	P	158	ASN	3.1
2	R	381	PHE	3.1
3	C	137	GLU	3.1
3	P	108	ARG	3.1
1	A	117	ASP	3.1
3	F	252	ASP	3.1
2	R	90	GLN	3.0
2	O	221	ILE	3.0
3	S	66	ILE	3.0
2	B	158	LEU	3.0
3	P	47	LEU	3.0
3	F	296	GLY	3.0
1	N	66	THR	3.0
2	O	384	THR	3.0
3	P	357	THR	3.0
2	O	114	VAL	3.0
3	C	187	SER	3.0
1	D	138	LEU	3.0
2	B	467	GLU	3.0
2	E	179	LEU	3.0
2	B	315	THR	3.0
2	R	272	LYS	3.0
3	S	263	ALA	3.0
2	B	367	LEU	3.0
2	E	108	ARG	3.0
2	R	433	MET	3.0
3	S	166	LEU	3.0
3	C	386	ILE	3.0
3	S	362	GLY	3.0
3	F	102	THR	3.0
3	P	34	THR	3.0
1	D	148	VAL	3.0
2	O	236	PRO	3.0
2	E	186	ILE	3.0
2	E	210	ILE	3.0
3	S	53	LYS	3.0

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Mol	Chain	Res	Type	RSRZ
2	R	335	GLY	3.0
3	F	136	GLN	3.0
3	S	28	PHE	3.0
1	D	155	VAL	3.0
2	O	173	ARG	3.0
3	C	254	ASN	3.0
3	F	377	TYR	3.0
3	S	52	ASN	3.0
1	Q	95	GLU	3.0
2	B	200	CYS	3.0
3	C	251	GLU	3.0
2	O	300	TRP	3.0
3	F	198	LEU	3.0
2	E	164	VAL	3.0
2	O	174	VAL	3.0
1	Q	60	GLU	2.9
3	C	93	ILE	2.9
3	P	225	GLU	2.9
2	R	132	TRP	2.9
3	P	43	LEU	2.9
2	O	294	GLY	2.9
1	D	217	VAL	2.9
2	E	118	SER	2.9
3	F	128	VAL	2.9
3	S	195	GLN	2.9
3	S	120	LYS	2.9
2	B	147	ASN	2.9
2	R	166	ASN	2.9
2	R	441	GLY	2.9
2	B	145	VAL	2.9
2	E	260	GLN	2.9
1	D	102	ALA	2.9
2	E	434	ALA	2.9
3	C	289	ALA	2.9
1	A	103	LYS	2.9
2	B	447	TRP	2.9
2	O	408	GLY	2.9
3	P	247	ARG	2.9
2	B	228	THR	2.9
2	O	220	LYS	2.9
2	R	218	CYS	2.9
1	N	145	ASP	2.9

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Mol	Chain	Res	Type	RSRZ
2	B	312	MET	2.9
2	R	370	GLU	2.9
2	B	245	VAL	2.9
2	B	455	LYS	2.9
3	C	99	LEU	2.9
3	P	131	LEU	2.9
3	F	384	MET	2.9
1	D	158	ASP	2.9
1	N	95	GLU	2.9
2	O	439	ASP	2.9
3	C	216	GLY	2.9
1	D	93	ILE	2.9
3	S	393	ALA	2.9
1	A	170	ARG	2.9
2	O	159	TYR	2.9
2	B	268	ASP	2.8
2	R	154	GLU	2.9
2	E	441	GLY	2.8
3	P	249	GLN	2.8
3	C	106	THR	2.8
3	F	192	THR	2.8
2	R	328	LYS	2.8
2	E	190	GLU	2.8
3	F	183	GLU	2.8
1	N	178	LEU	2.8
2	B	123	GLN	2.8
2	B	134	GLY	2.8
2	B	427	GLY	2.8
2	E	439	ASP	2.8
3	C	107	ILE	2.8
2	E	466	PRO	2.8
2	O	143	GLU	2.8
3	C	229	GLY	2.8
2	O	398	ARG	2.8
2	B	210	ILE	2.8
3	C	181	TYR	2.8
2	B	166	ASN	2.8
2	E	404	GLU	2.8
2	O	449	GLY	2.8
2	B	92	THR	2.8
3	P	261	ASP	2.8
3	P	173	LYS	2.8

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Mol	Chain	Res	Type	RSRZ
2	B	463	PRO	2.8
2	O	139	VAL	2.8
2	E	357	GLY	2.8
2	R	181	ASN	2.8
2	E	284	ALA	2.8
2	O	331	ALA	2.8
2	O	248	ASP	2.8
3	P	100	ILE	2.8
1	A	113	GLN	2.8
2	R	134	GLY	2.8
3	C	163	GLU	2.8
3	C	309	GLY	2.8
3	F	160	GLY	2.8
1	A	109	ASN	2.8
2	B	277	LYS	2.8
2	E	438	THR	2.8
2	O	316	LYS	2.8
2	E	271	ARG	2.7
2	R	443	VAL	2.7
1	D	92	ASN	2.7
1	N	68	ARG	2.7
1	A	61	VAL	2.7
1	Q	133	VAL	2.7
3	C	48	TYR	2.7
2	E	130	ASN	2.7
2	O	373	THR	2.7
2	O	422	ARG	2.7
3	F	172	LEU	2.7
3	P	277	THR	2.7
2	B	214	SER	2.7
3	C	87	LYS	2.7
3	F	105	SER	2.7
1	N	101	PHE	2.7
3	S	250	LEU	2.7
3	S	292	GLY	2.7
1	D	154	GLU	2.7
3	P	367	ILE	2.7
1	D	162	ARG	2.7
1	N	135	ARG	2.7
1	Q	58	ILE	2.7
3	S	368	ILE	2.7
3	C	230	ASN	2.7

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Mol	Chain	Res	Type	RSRZ
1	A	165	LYS	2.7
1	N	165	LYS	2.7
2	B	344	LYS	2.7
2	O	307	SER	2.7
3	F	265	PHE	2.7
3	P	180	VAL	2.7
2	R	238	ASP	2.7
2	E	363	GLY	2.7
1	D	110	THR	2.7
2	B	122	PHE	2.7
1	Q	169	SER	2.7
3	F	313	SER	2.7
3	S	122	VAL	2.6
2	R	176	ARG	2.6
3	P	196	LYS	2.6
3	S	54	THR	2.6
2	E	383	SER	2.6
2	O	115	SER	2.6
1	A	66	THR	2.6
1	Q	158	ASP	2.6
3	S	126	ASP	2.6
2	E	370	GLU	2.6
3	C	90	MET	2.6
2	O	122	PHE	2.6
2	O	233	LEU	2.6
2	O	311	ASN	2.6
2	O	151	SER	2.6
3	C	156	VAL	2.6
2	E	168	ILE	2.6
2	O	325	LYS	2.6
3	S	341	ALA	2.6
2	B	257	THR	2.6
2	O	121	THR	2.6
3	F	383	THR	2.6
1	A	123	GLU	2.6
2	B	336	PHE	2.6
3	P	203	ASP	2.6
3	P	88	SER	2.6
2	E	442	VAL	2.6
1	Q	68	ARG	2.6
1	Q	135	ARG	2.6
2	O	369	GLY	2.6

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Mol	Chain	Res	Type	RSRZ
2	R	424	TYR	2.6
3	C	102	THR	2.6
2	O	363	GLY	2.6
2	E	431	TRP	2.6
3	C	363	TYR	2.6
3	P	163	GLU	2.6
1	N	175	LYS	2.6
2	R	98	ARG	2.6
3	P	347	VAL	2.6
3	C	133	ALA	2.6
1	N	77	PHE	2.6
2	B	152	HIS	2.5
3	P	343	HIS	2.5
2	E	143	GLU	2.5
2	O	348	SER	2.5
1	A	64	ASP	2.5
1	N	106	ASN	2.5
3	P	344	LEU	2.5
1	A	97	MET	2.5
2	O	466	PRO	2.5
2	R	339	GLN	2.5
2	B	461	ILE	2.5
3	P	217	HIS	2.5
1	N	167	SER	2.5
2	O	176	ARG	2.5
3	F	300	SER	2.5
3	S	193	VAL	2.5
3	P	98	THR	2.5
2	R	372	ARG	2.5
2	E	256	TRP	2.5
2	R	298	GLU	2.5
3	S	40	LEU	2.5
1	N	107	ASN	2.5
3	F	182	CYS	2.5
1	N	108	ASP	2.5
1	D	134	GLN	2.5
3	F	341	ALA	2.5
3	C	150	GLY	2.5
3	C	50	VAL	2.5
3	C	212	LYS	2.5
3	C	263	ALA	2.5
3	S	249	GLN	2.5

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Mol	Chain	Res	Type	RSRZ
3	C	83	THR	2.5
3	C	214	GLY	2.5
2	O	195	THR	2.5
2	R	336	PHE	2.4
2	B	328	LYS	2.4
3	P	213	GLU	2.4
2	E	380	MET	2.4
3	F	318	ASP	2.4
2	E	200	CYS	2.4
2	R	245	VAL	2.4
1	Q	181	TYR	2.4
3	F	304	PHE	2.4
2	B	377	HIS	2.4
1	Q	72	LEU	2.4
1	D	80	GLN	2.4
2	E	167	ASN	2.4
3	P	197	ARG	2.4
2	E	408	GLY	2.4
3	F	352	GLY	2.4
3	S	188	GLY	2.4
2	B	442	VAL	2.4
3	P	53	LYS	2.4
1	A	172	LEU	2.4
1	Q	57	LEU	2.4
2	E	318	LEU	2.4
3	P	104	GLU	2.4
3	P	132	GLU	2.4
3	P	151	ARG	2.4
3	C	209	ILE	2.4
3	P	251	GLU	2.4
3	C	275	ARG	2.4
2	B	278	GLN	2.4
2	E	132	TRP	2.4
2	E	197	MET	2.4
3	C	210	GLN	2.4
3	S	210	GLN	2.4
2	O	412	ASN	2.4
3	S	81	SER	2.4
3	P	245	VAL	2.4
2	B	160	ILE	2.4
2	B	204	CYS	2.4
1	D	107	ASN	2.4

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Mol	Chain	Res	Type	RSRZ
2	B	324	TRP	2.4
2	R	220	LYS	2.4
3	C	380	LYS	2.4
2	R	173	ARG	2.4
2	B	180	GLU	2.4
2	O	230	GLU	2.4
1	A	187	GLN	2.3
3	C	162	LYS	2.4
1	A	120	SER	2.3
3	C	284	GLY	2.3
3	S	331	GLY	2.3
2	E	183	ARG	2.3
3	P	82	ALA	2.3
1	D	122	ILE	2.3
1	Q	163	SER	2.3
2	B	318	LEU	2.3
2	O	345	TYR	2.3
3	C	244	TYR	2.3
3	S	311	GLN	2.3
1	N	114	ILE	2.3
3	C	387	ILE	2.3
2	B	119	SER	2.3
2	O	167	ASN	2.3
2	B	337	THR	2.3
2	O	410	TRP	2.3
1	A	71	LYS	2.3
2	E	290	LYS	2.3
2	E	435	LYS	2.3
1	N	96	LEU	2.3
1	A	124	ILE	2.3
2	E	187	GLN	2.3
2	B	441	GLY	2.3
2	O	326	GLY	2.3
3	F	216	GLY	2.3
2	O	378	ASN	2.3
3	C	314	THR	2.3
2	E	131	MET	2.3
2	O	253	LYS	2.3
1	Q	101	PHE	2.3
3	P	378	SER	2.3
3	C	353	THR	2.3
2	B	417	ALA	2.3

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Mol	Chain	Res	Type	RSRZ
2	O	334	GLU	2.3
3	F	317	SER	2.3
3	S	225	GLU	2.3
2	B	155	LYS	2.3
2	B	407	GLY	2.3
3	F	292	GLY	2.3
2	O	126	THR	2.2
2	R	182	LEU	2.2
3	S	110	LEU	2.2
3	S	315	TRP	2.2
3	P	226	PHE	2.2
3	S	215	PHE	2.2
3	F	286	ALA	2.2
2	R	149	TYR	2.2
2	B	118	SER	2.2
2	B	330	THR	2.2
2	B	376	ILE	2.2
1	Q	61	VAL	2.2
2	B	320	GLU	2.2
2	E	154	GLU	2.2
3	F	125	ARG	2.2
2	B	293	CYS	2.2
3	F	106	THR	2.2
1	D	222	LYS	2.2
3	S	289	ALA	2.2
2	R	103	SER	2.2
3	S	251	GLU	2.2
2	B	296	PRO	2.2
3	F	271	ASN	2.2
2	O	133	LYS	2.2
2	O	278	GLN	2.2
2	E	313	GLY	2.2
2	O	259	ILE	2.2
2	R	311	ASN	2.2
3	C	370	ALA	2.2
1	Q	188	LEU	2.2
3	F	181	TYR	2.2
2	R	122	PHE	2.2
3	S	84	LYS	2.2
2	E	332	LEU	2.2
3	P	235	LEU	2.2
2	E	449	GLY	2.1

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Mol	Chain	Res	Type	RSRZ
1	N	188	LEU	2.1
2	O	367	LEU	2.1
2	R	95	ARG	2.1
3	F	374	SER	2.1
2	B	193	VAL	2.1
3	C	282	ILE	2.1
3	C	253	TRP	2.1
3	F	48	TYR	2.1
3	P	95	LYS	2.1
2	B	226	GLY	2.1
2	B	275	PRO	2.1
2	O	110	THR	2.1
2	B	422	ARG	2.1
2	E	343	ASN	2.1
2	O	144	ASN	2.1
1	N	169	SER	2.1
2	R	338	VAL	2.1
2	B	248	ASP	2.1
3	P	37	ASP	2.1
3	S	208	TRP	2.1
3	P	306	SER	2.1
2	B	185	LYS	2.1
3	C	49	GLN	2.1
2	B	111	VAL	2.1
1	Q	131	GLU	2.1
2	B	110	THR	2.1
3	P	93	ILE	2.1
2	E	456	LYS	2.1
3	S	62	LYS	2.1
2	O	354	GLY	2.1
3	P	48	TYR	2.1
3	F	225	GLU	2.1
3	S	112	GLU	2.1
2	B	177	SER	2.1
2	O	128	LEU	2.1
1	D	166	GLY	2.0
2	E	243	TYR	2.0
2	O	441	GLY	2.0
3	P	200	GLY	2.0
3	S	274	TYR	2.0
2	R	359	ALA	2.0
2	B	382	PHE	2.0

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Mol	Chain	Res	Type	RSRZ
1	Q	153	LEU	2.0
3	S	130	GLN	2.0
2	E	403	LYS	2.0
3	P	91	GLU	2.0
3	S	124	LEU	2.0
3	F	85	ASN	2.0
2	O	427	GLY	2.0
2	R	391	GLY	2.0
3	C	292	GLY	2.0
3	C	211	TYR	2.0
3	P	285	ASP	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.