



# Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 07:00 PM GMT

PDB ID : 1DEQ  
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](mailto:validation@mail.wwpdb.org)  
A user guide is available at  
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>  
with specific help available everywhere you see the ⓘ symbol.

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The following versions of software and data (see [references ⓘ](#)) 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

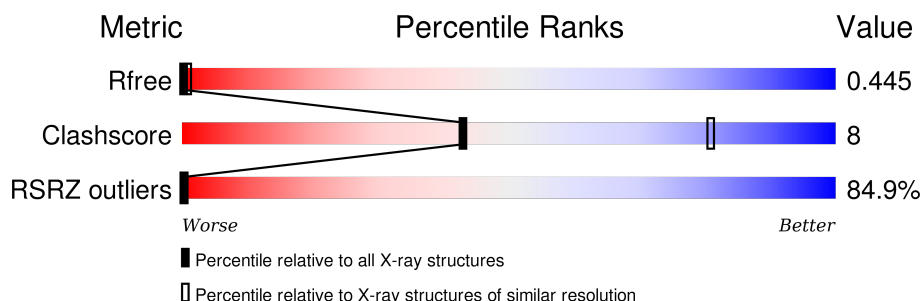
# 1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 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))
$R_{free}$	91344	1051 (3.60-3.40)
Clashscore	102246	1157 (3.60-3.40)
RSRZ outliers	91569	1058 (3.60-3.40)

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  $\geq 3$ , 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  $\leq 5\%$ . 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	<div> <div>39%</div> <div>45%</div> <div>54%</div> </div>
1	D	390	<div> <div>43%</div> <div>44%</div> <div>54%</div> </div>
1	N	390	<div> <div>38%</div> <div>46%</div> <div>54%</div> </div>
1	Q	390	<div> <div>44%</div> <div>44%</div> <div>54%</div> </div>
2	B	408	<div> <div>74%</div> <div>93%</div> <div>7%</div> </div>
2	E	408	<div> <div>80%</div> <div>93%</div> <div>7%</div> </div>
2	O	408	<div> <div>72%</div> <div>93%</div> <div>7%</div> </div>
2	R	408	<div> <div>86%</div> <div>93%</div> <div>7%</div> </div>

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Mol	Chain	Length	Quality of chain
3	C	411	<div><div></div><div>74%90%10%</div></div>
3	F	411	<div><div></div><div>70%89%10%</div></div>
3	P	411	<div><div></div><div>76%90%10%</div></div>
3	S	411	<div><div></div><div>83%90%10%</div></div>
4	M	90	<div><div></div><div>87%13%</div></div>
4	Z	90	<div><div></div><div>87%13%</div></div>

## 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

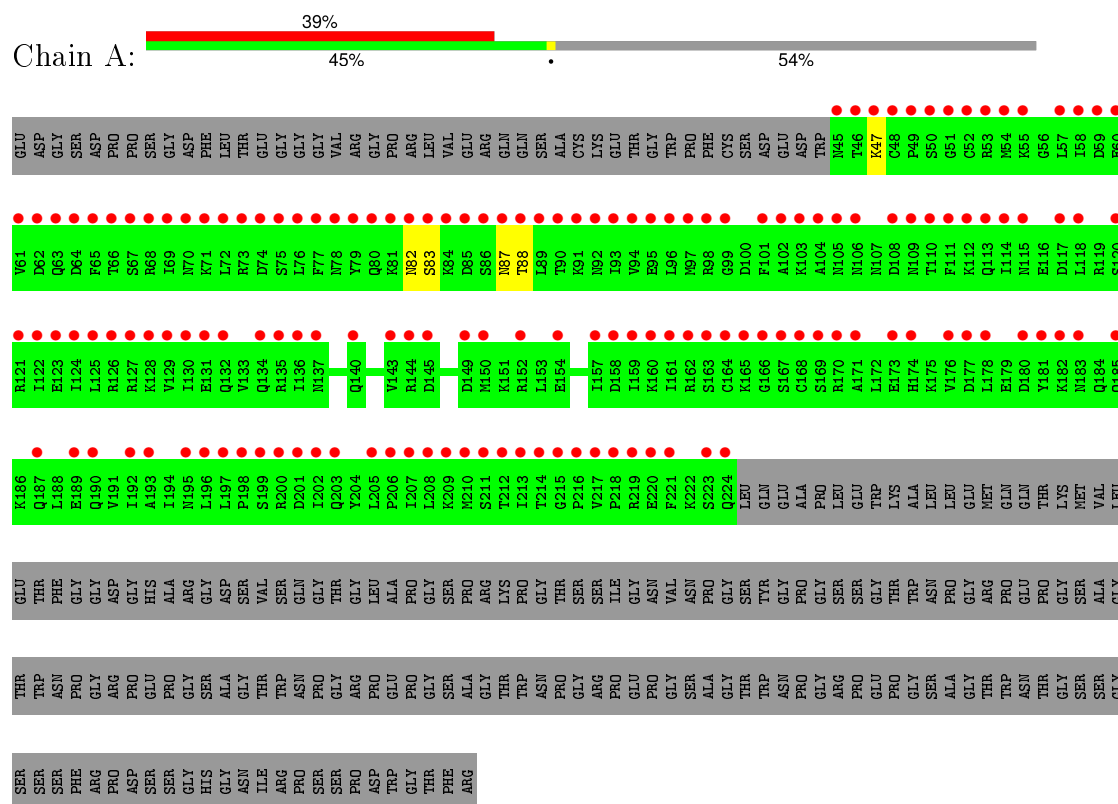
- Molecule 4 is a protein called FIBRINOGEN.

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

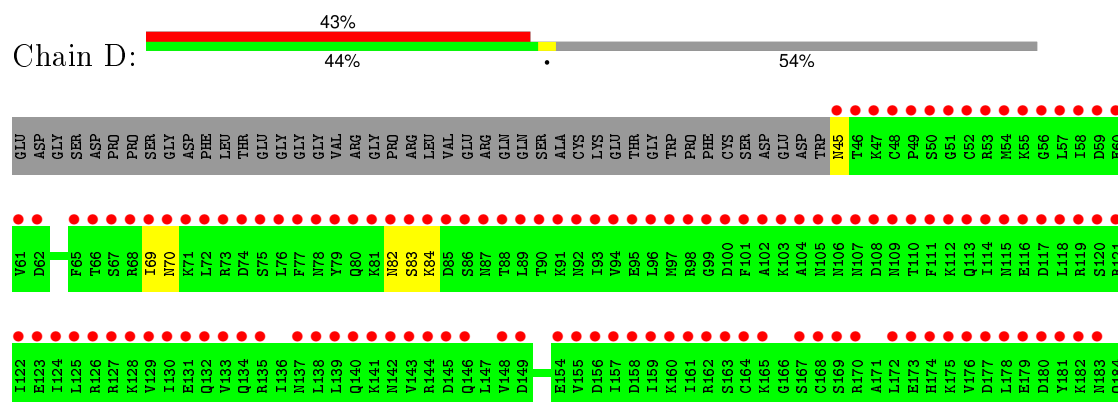
### 3 Residue-property plots

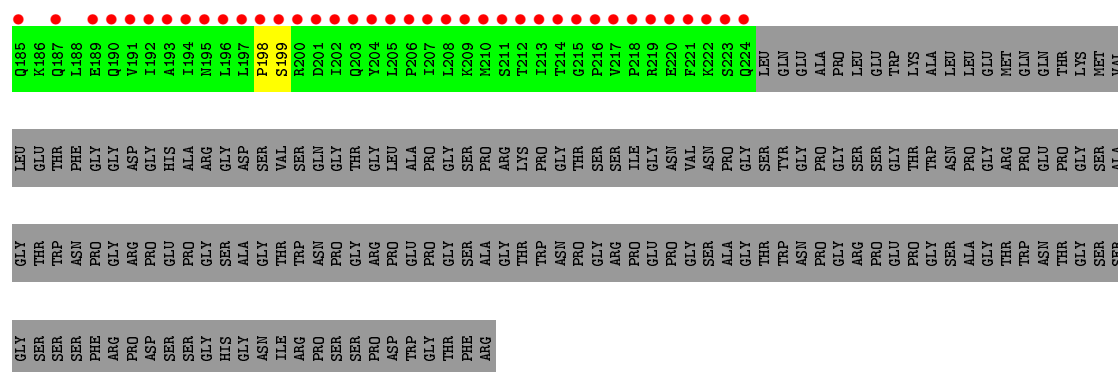
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according 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 ( $\text{RSRZ} > 2$ ). 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)

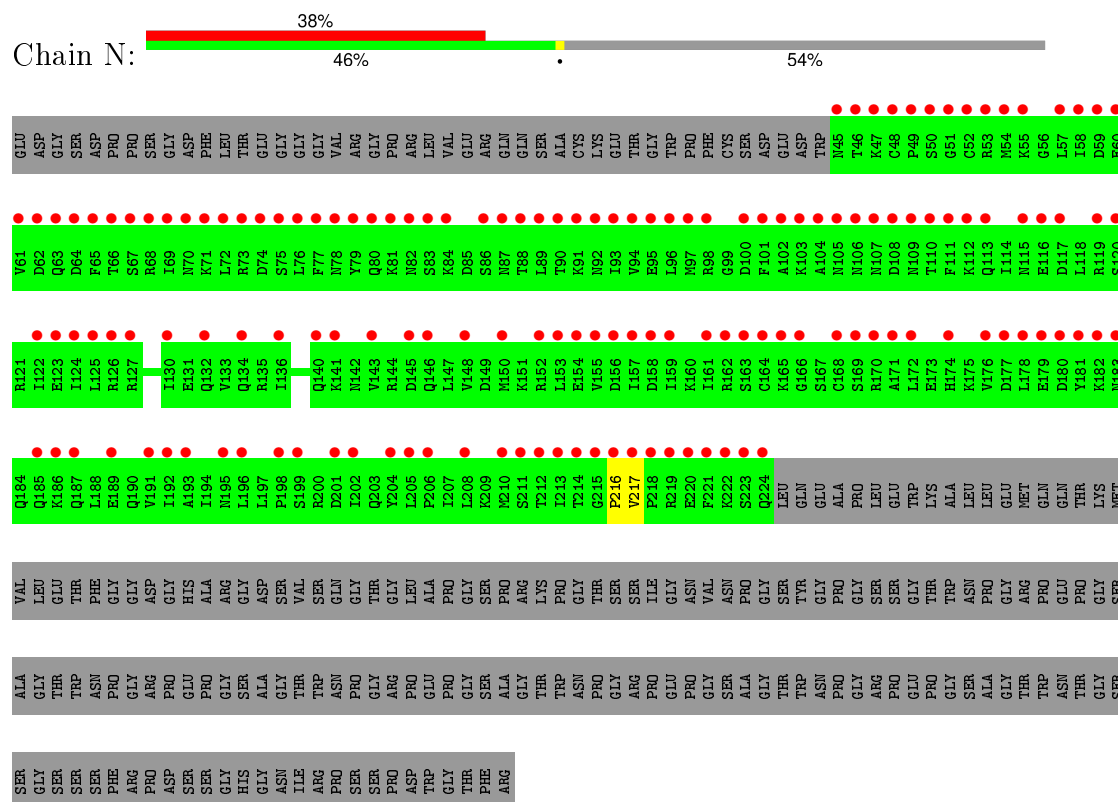


#### • Molecule 1: FIBRINOGEN (ALPHA CHAIN)

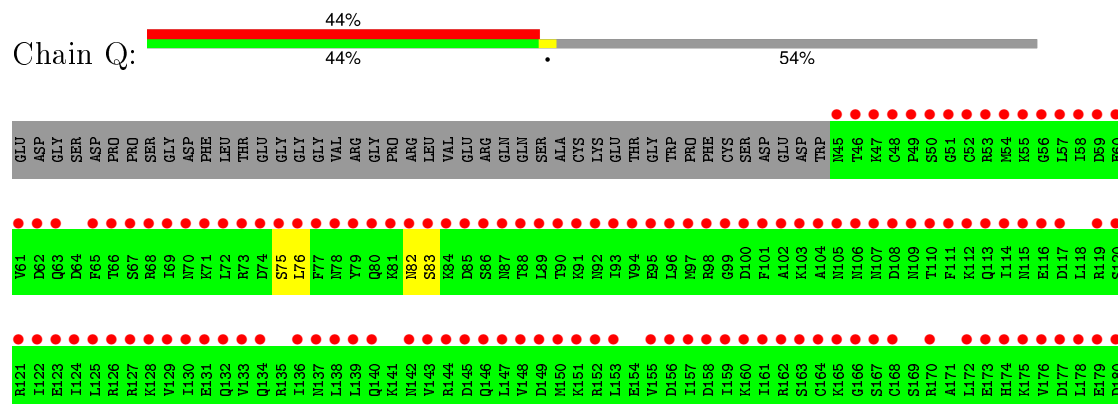


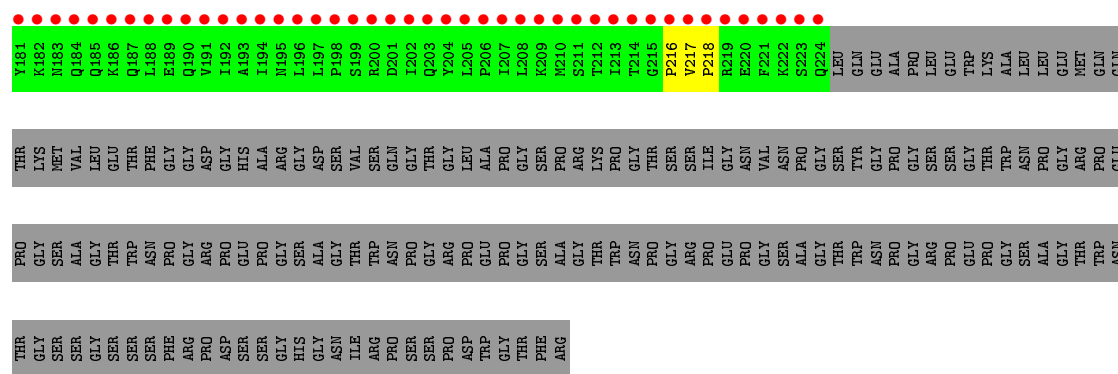


- Molecule 1: FIBRINOGEN (ALPHA CHAIN)

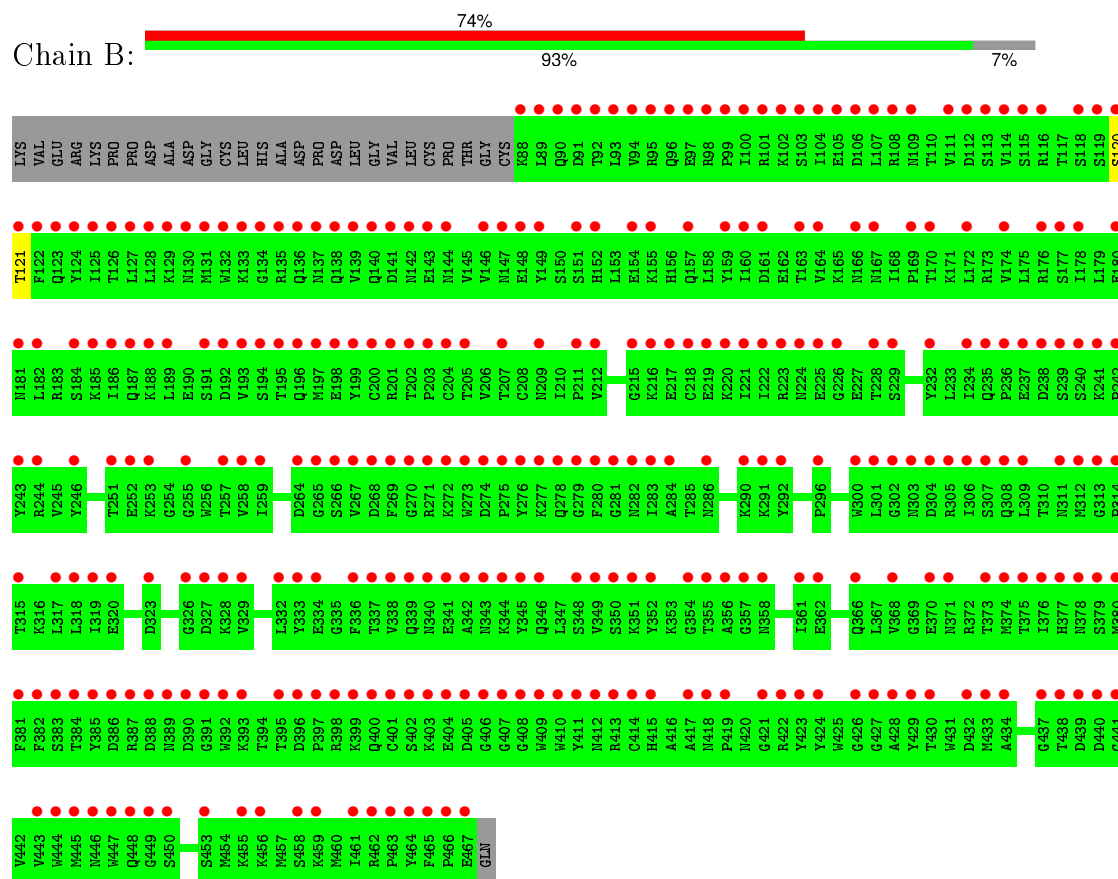


- Molecule 1: FIBRINOGEN (ALPHA CHAIN)

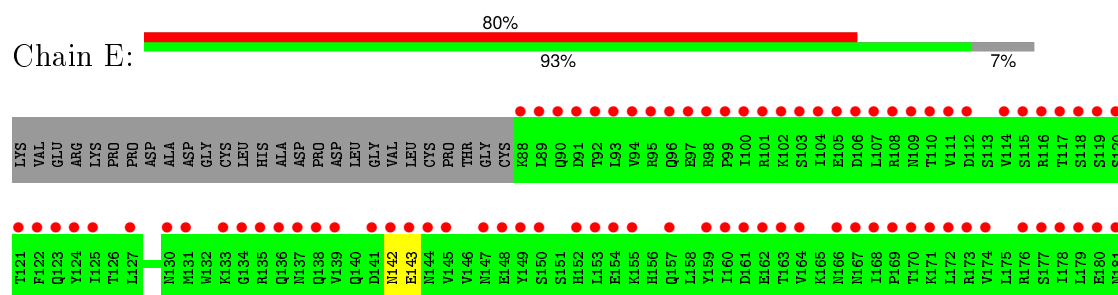




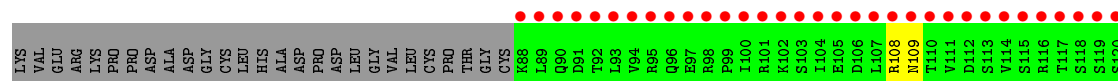
- Molecule 2: FIBRINOGEN (BETA CHAIN)

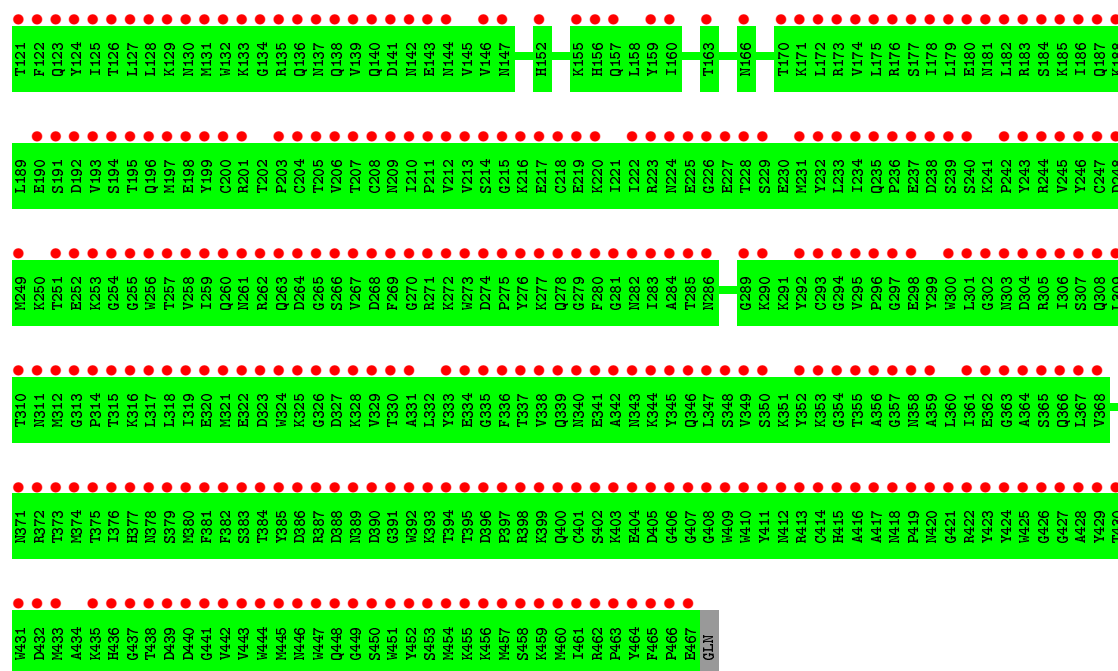


- Molecule 2: FIBRINOGEN (BETA CHAIN)







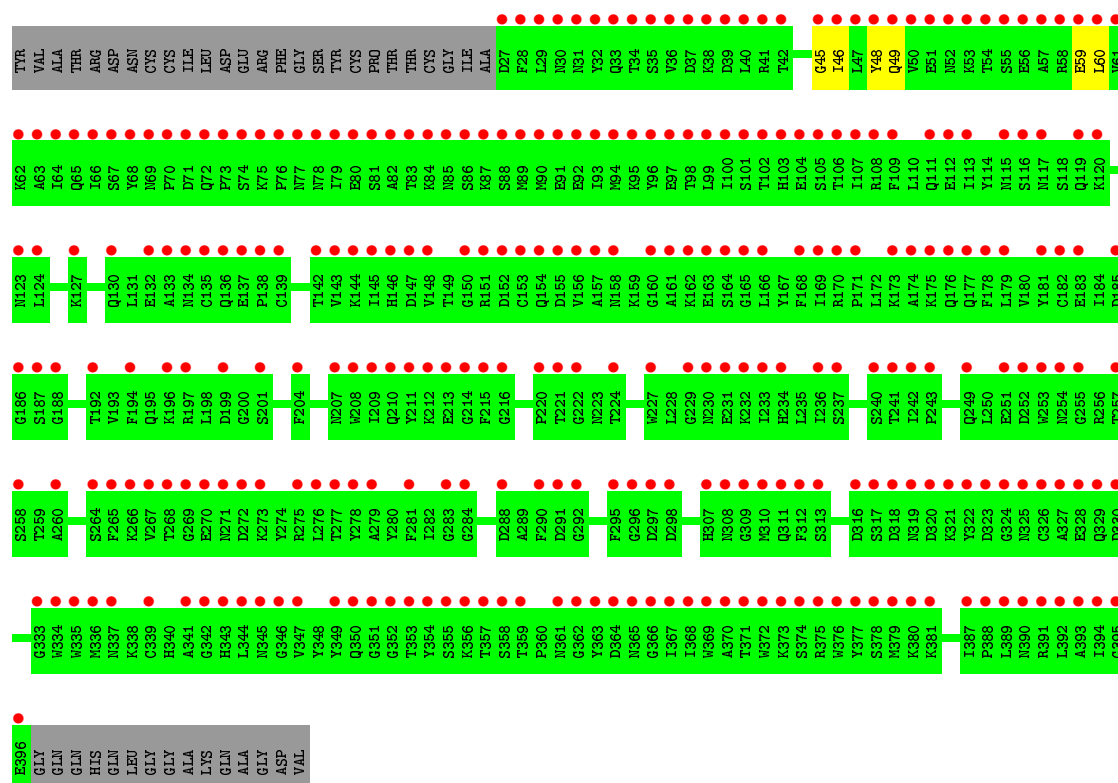


• Molecule 3: FIBRINOGEN (GAMMA CHAIN)

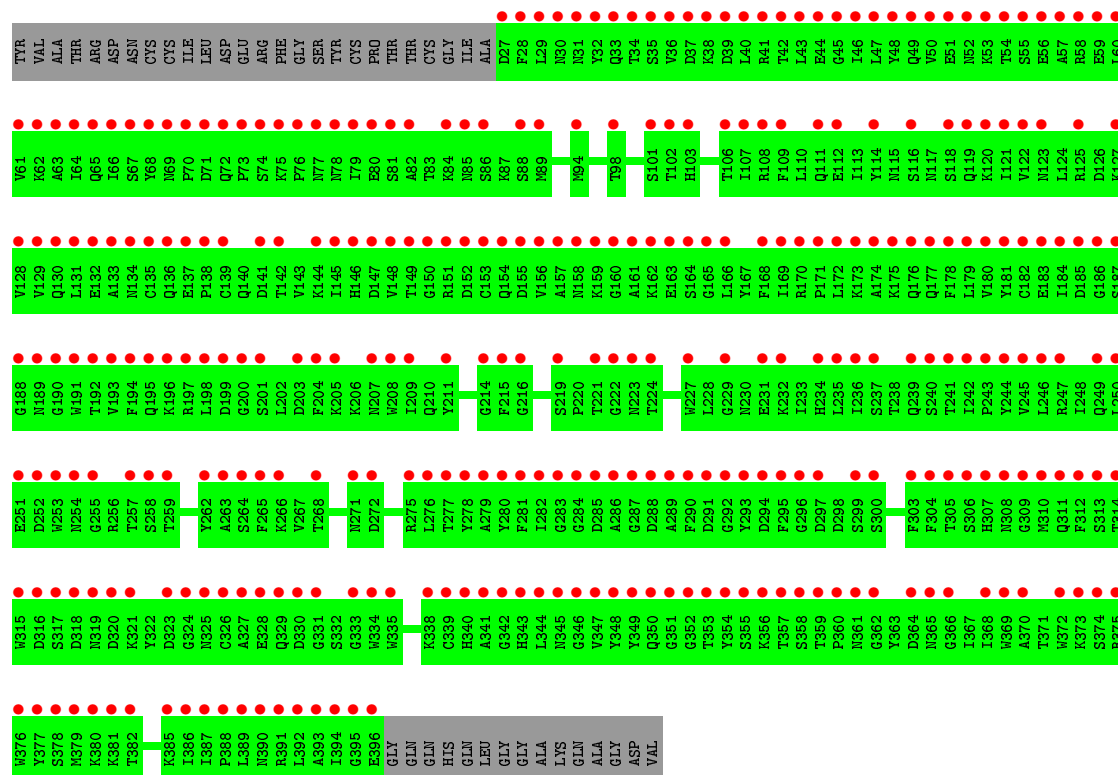
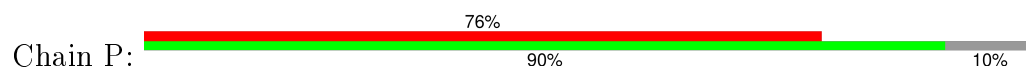


• Molecule 3: FIBRINOGEN (GAMMA CHAIN)





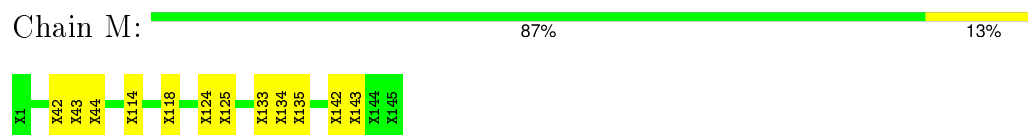
• Molecule 3: FIBRINOGEN (GAMMA CHAIN)



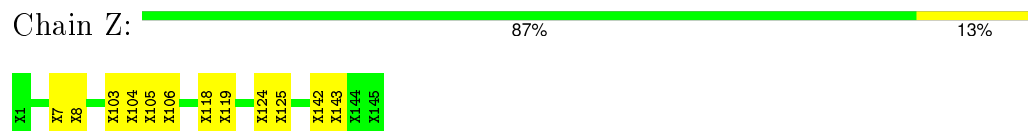
- Molecule 3: FIBRINOGEN (GAMMA CHAIN)



- Molecule 4: FIBRINOGEN



- Molecule 4: FIBRINOGEN



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	176.01Å 94.94Å 209.81Å 90.00° 94.41° 90.00°	Depositor
Resolution (Å)	10.00 – 3.50 209.18 – 3.34	Depositor EDS
% Data completeness (in resolution range)	86.9 (10.00-3.50) 78.8 (209.18-3.34)	Depositor EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.89 (at 3.33Å)	Xtriage
Refinement program	X-PLOR 3.851	Depositor
R, $R_{free}$	0.257 , 0.370 0.438 , 0.445	Depositor DCC
$R_{free}$ test set	3661 reflections (5.02%)	DCC
Wilson B-factor (Å <sup>2</sup> )	91.6	Xtriage
Anisotropy	0.887	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.30 , 153.0	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.29$	Xtriage
Outliers	3 of 79450 reflections (0.004%)	Xtriage
$F_o, F_c$ correlation	0.72	EDS
Total number of atoms	3900	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	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.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 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 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 [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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	180/390 (46%)	8.27	153 (85%)  	4, 93, 999, 999	0
1	D	180/390 (46%)	10.44	167 (92%)  	25, 131, 999, 999	0
1	N	180/390 (46%)	8.61	148 (82%)  	2, 88, 999, 999	0
1	Q	180/390 (46%)	10.21	173 (96%)  	2, 151, 999, 999	0
2	B	380/408 (93%)	9.88	302 (79%)  	2, 62, 214, 999	0
2	E	380/408 (93%)	11.69	326 (85%)  	2, 81, 999, 999	0
2	O	380/408 (93%)	9.80	292 (76%)  	2, 63, 191, 359	0
2	R	380/408 (93%)	15.79	349 (91%)  	2, 130, 358, 999	0
3	C	370/411 (90%)	9.27	303 (81%)  	2, 58, 999, 999	0
3	F	370/411 (90%)	9.38	288 (77%)  	2, 68, 999, 999	0
3	P	370/411 (90%)	13.45	313 (84%)  	2, 96, 386, 999	0
3	S	370/411 (90%)	13.06	343 (92%)  	6, 112, 999, 999	0
4	M	0/90	-	-	-	-
4	Z	0/90	-	-	-	-
All	All	3720/5016 (74%)	11.13	3157 (84%)  	2, 87, 999, 999	0

All (3157) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	E	390	ASP	73.2
2	R	453	SER	62.3
2	R	198	GLU	58.1
2	R	450	SER	57.5
3	C	176	GLN	57.2
1	A	58	ILE	56.4
3	P	199	ASP	54.9
2	R	257	THR	52.8
1	Q	183	ASN	52.8

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
3	P	328	GLU	51.9
1	N	72	LEU	51.3
2	R	386	ASP	51.0
2	R	266	SER	50.4
3	S	134	ASN	49.5
1	D	107	ASN	49.0
3	P	388	PRO	47.7
2	R	394	THR	46.6
3	C	241	THR	46.6
2	R	433	MET	46.4
3	C	357	THR	46.1
3	P	67	SER	45.5
2	B	107	LEU	45.4
2	B	313	GLY	45.4
3	P	357	THR	44.9
3	P	192	THR	44.3
2	E	237	GLU	44.3
2	E	144	ASN	44.3
2	R	120	SER	43.9
2	B	439	ASP	43.7
2	R	115	SER	43.2
1	N	47	LYS	43.1
3	S	308	ASN	42.3
2	E	118	SER	42.2
2	B	120	SER	41.8
2	B	131	MET	41.7
2	B	108	ARG	41.4
2	R	274	ASP	41.3
3	P	36	VAL	41.1
1	Q	142	ASN	40.8
3	P	42	THR	40.7
3	S	158	ASN	40.5
3	P	285	ASP	40.3
2	R	200	CYS	40.2
1	N	53	ARG	40.0
2	B	274	ASP	39.9
1	D	110	THR	39.9
3	S	387	ILE	39.8
3	S	152	ASP	39.1
3	F	90	MET	39.1
3	S	133	ALA	38.6
3	S	103	HIS	38.6

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Mol	Chain	Res	Type	RSRZ
2	E	303	ASN	38.4
2	O	227	GLU	38.1
2	O	238	ASP	38.1
3	F	185	ASP	38.1
2	R	314	PRO	38.0
2	R	443	VAL	38.0
3	F	138	PRO	37.9
1	Q	107	ASN	37.7
2	E	327	ASP	37.5
3	P	354	TYR	37.5
3	F	136	GLN	37.2
3	C	54	THR	37.2
2	O	388	ASP	37.1
2	R	178	ILE	37.1
3	P	157	ALA	36.7
3	S	176	GLN	36.6
1	A	180	ASP	36.5
2	R	103	SER	36.4
2	R	389	ASN	36.4
1	D	89	LEU	36.3
2	O	138	GLN	36.2
3	S	160	GLY	35.9
2	B	91	ASP	35.8
2	R	375	THR	35.4
2	R	256	TRP	35.2
1	D	142	ASN	35.2
3	P	34	THR	35.0
3	P	364	ASP	34.9
2	R	303	ASN	34.6
3	P	390	ASN	34.6
3	F	339	CYS	34.6
2	E	422	ARG	34.6
2	B	130	ASN	34.5
2	R	383	SER	34.5
3	S	231	GLU	34.3
1	Q	184	GLN	34.3
2	B	157	GLN	34.3
2	R	142	ASN	34.2
2	R	252	GLU	34.0
3	P	137	GLU	34.0
3	F	137	GLU	33.9
3	P	376	TRP	33.9

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Mol	Chain	Res	Type	RSRZ
2	R	255	GLY	33.7
2	B	112	ASP	33.7
2	R	196	GLN	33.7
2	B	401	CYS	33.6
3	P	187	SER	33.6
3	P	39	ASP	33.5
2	O	314	PRO	33.5
1	N	45	ASN	33.5
2	E	169	PRO	33.5
2	B	92	THR	33.4
3	P	236	ILE	33.4
2	O	198	GLU	33.3
3	C	81	SER	33.3
1	A	195	ASN	33.2
3	P	55	SER	33.2
2	E	393	LYS	33.1
2	R	393	LYS	32.9
3	P	356	LYS	32.9
2	R	292	TYR	32.9
2	R	454	MET	32.8
2	R	340	ASN	32.8
3	P	237	SER	32.8
3	P	77	ASN	32.7
2	B	391	GLY	32.6
3	C	258	SER	32.5
2	O	95	ARG	32.4
2	O	103	SER	32.4
3	P	359	THR	32.3
3	C	48	TYR	32.2
3	S	234	HIS	32.2
3	P	56	GLU	32.1
3	F	364	ASP	32.1
2	R	248	ASP	32.0
2	O	96	GLN	32.0
3	P	299	SER	31.8
3	F	85	ASN	31.7
3	P	188	GLY	31.7
2	E	401	CYS	31.6
3	P	74	SER	31.5
3	P	153	CYS	31.5
2	B	100	ILE	31.4
3	S	104	GLU	31.4

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Mol	Chain	Res	Type	RSRZ
1	D	132	GLN	31.3
3	S	123	ASN	31.3
2	E	223	ARG	31.2
2	B	159	TYR	31.2
3	P	78	ASN	31.2
2	E	251	THR	31.2
3	F	102	THR	31.2
2	B	397	PRO	31.2
2	R	343	ASN	31.1
2	O	390	ASP	31.1
3	F	393	ALA	31.1
3	S	153	CYS	31.1
1	D	174	HIS	31.0
3	P	296	GLY	30.9
2	R	407	GLY	30.9
2	E	441	GLY	30.8
1	N	46	THR	30.8
3	S	135	CYS	30.7
3	P	80	GLU	30.6
2	E	330	THR	30.6
3	S	113	ILE	30.5
3	P	160	GLY	30.5
2	E	415	HIS	30.5
3	P	320	ASP	30.5
3	S	109	PHE	30.4
2	R	117	THR	30.4
3	P	353	THR	30.3
3	F	88	SER	30.3
1	D	181	TYR	30.3
1	D	99	GLY	30.2
2	R	312	MET	30.1
3	P	158	ASN	30.1
3	F	153	CYS	30.1
3	S	372	TRP	30.1
2	E	463	PRO	30.0
2	E	450	SER	29.9
1	D	104	ALA	29.8
3	P	241	THR	29.8
3	P	330	ASP	29.8
2	E	219	GLU	29.8
1	N	97	MET	29.7
2	E	323	ASP	29.7

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Mol	Chain	Res	Type	RSRZ
3	S	390	ASN	29.7
2	R	374	MET	29.7
2	R	384	THR	29.7
1	D	105	ASN	29.5
3	P	163	GLU	29.5
3	S	275	ARG	29.5
3	S	322	TYR	29.4
2	O	402	SER	29.4
1	N	54	MET	29.4
3	S	319	ASN	29.3
2	E	436	HIS	29.3
3	C	185	ASP	29.2
3	C	319	ASN	29.2
3	S	329	GLN	29.1
2	R	447	TRP	29.1
3	P	35	SER	29.1
3	P	152	ASP	29.1
2	R	308	GLN	29.0
2	R	440	ASP	29.0
1	A	177	ASP	28.9
2	B	238	ASP	28.9
3	F	150	GLY	28.8
2	R	190	GLU	28.8
3	S	209	ILE	28.8
3	P	257	THR	28.7
2	R	352	TYR	28.7
3	P	142	THR	28.7
3	S	323	ASP	28.7
3	S	136	GLN	28.7
2	R	418	ASN	28.6
1	N	64	ASP	28.6
2	R	359	ALA	28.6
3	F	151	ARG	28.6
3	P	242	ILE	28.6
3	S	98	THR	28.5
3	F	201	SER	28.4
1	N	75	SER	28.4
2	O	202	THR	28.4
2	R	296	PRO	28.3
3	S	99	LEU	28.3
3	S	276	LEU	28.3
3	P	149	THR	28.2

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Mol	Chain	Res	Type	RSRZ
3	S	272	ASP	28.2
2	R	143	GLU	28.2
3	P	138	PRO	28.2
2	R	130	ASN	28.2
2	R	182	LEU	28.1
1	D	106	ASN	28.0
2	B	140	GLN	27.9
2	R	421	GLY	27.9
2	R	93	LEU	27.9
2	O	119	SER	27.8
3	S	96	TYR	27.8
3	P	75	LYS	27.8
2	R	127	LEU	27.8
3	P	63	ALA	27.7
2	O	374	MET	27.7
2	B	96	GLN	27.7
2	O	140	GLN	27.6
2	E	460	MET	27.6
3	P	222	GLY	27.6
1	Q	187	GLN	27.5
2	R	304	ASP	27.5
3	P	319	ASN	27.5
2	E	265	GLY	27.4
3	P	361	ASN	27.4
2	R	219	GLU	27.4
2	E	410	TRP	27.4
2	O	391	GLY	27.3
2	O	88	LYS	27.3
3	P	326	CYS	27.3
3	C	243	PRO	27.3
3	S	297	ASP	27.3
2	E	163	THR	27.3
3	C	80	GLU	27.2
2	O	268	ASP	27.2
3	P	312	PHE	27.2
3	F	53	LYS	27.2
3	P	389	LEU	27.1
3	F	389	LEU	27.1
1	D	117	ASP	27.0
3	C	312	PHE	27.0
3	F	86	SER	26.9
3	P	345	ASN	26.9

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Mol	Chain	Res	Type	RSRZ
2	E	216	LYS	26.8
2	R	341	GLU	26.8
2	E	402	SER	26.8
2	R	414	CYS	26.8
3	F	135	CYS	26.7
2	E	161	ASP	26.7
2	E	238	ASP	26.7
2	E	448	GLN	26.7
3	P	316	ASP	26.6
3	S	350	GLN	26.6
2	E	180	GLU	26.6
3	S	326	CYS	26.6
2	E	283	ILE	26.6
3	F	100	ILE	26.6
2	B	453	SER	26.6
2	B	121	THR	26.5
3	S	328	GLU	26.5
3	S	330	ASP	26.5
2	R	439	ASP	26.5
2	R	139	VAL	26.5
2	E	385	TYR	26.4
2	E	329	VAL	26.4
1	D	86	SER	26.4
3	P	313	SER	26.4
2	R	445	MET	26.3
2	R	461	ILE	26.3
2	B	326	GLY	26.2
1	Q	138	LEU	26.2
3	P	251	GLU	26.2
3	P	318	ASP	26.2
3	C	333	GLY	26.2
3	F	89	MET	26.1
2	B	202	THR	26.1
3	F	94	MET	26.0
3	F	297	ASP	26.0
2	R	376	ILE	26.0
2	E	391	GLY	26.0
3	P	164	SER	25.9
2	E	465	PHE	25.9
3	C	160	GLY	25.9
2	O	273	TRP	25.9
3	F	187	SER	25.9

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
3	P	64	ILE	25.8
2	R	311	ASN	25.8
2	O	101	ARG	25.8
3	P	331	GLY	25.7
3	S	48	TYR	25.7
3	P	307	HIS	25.6
2	R	96	GLN	25.6
1	N	59	ASP	25.6
2	B	390	ASP	25.5
2	R	320	GLU	25.5
3	S	86	SER	25.5
3	S	172	LEU	25.5
3	F	199	ASP	25.5
3	S	279	ALA	25.4
2	E	218	CYS	25.4
3	P	161	ALA	25.4
2	O	120	SER	25.4
3	F	231	GLU	25.3
2	R	218	CYS	25.3
2	O	137	ASN	25.2
2	R	377	HIS	25.2
2	O	89	LEU	25.2
3	S	214	GLY	25.2
2	B	241	LYS	25.1
3	S	199	ASP	25.1
2	R	354	GLY	25.1
2	R	294	GLY	25.1
3	S	318	ASP	25.1
1	Q	164	CYS	25.1
2	O	366	GLN	25.0
3	S	163	GLU	25.0
1	D	103	LYS	25.0
3	F	232	LYS	25.0
3	S	106	THR	24.9
2	E	421	GLY	24.9
3	P	245	VAL	24.9
3	S	378	SER	24.9
2	B	402	SER	24.9
2	B	400	GLN	24.9
2	E	411	TYR	24.9
3	S	212	LYS	24.9
3	P	182	CYS	24.8

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
3	P	379	MET	24.8
3	C	82	ALA	24.7
2	E	308	GLN	24.7
2	B	273	TRP	24.7
3	S	243	PRO	24.7
2	R	345	TYR	24.7
2	R	401	CYS	24.7
3	C	392	LEU	24.7
2	O	134	GLY	24.7
3	P	190	GLY	24.7
2	O	92	THR	24.7
2	O	123	GLN	24.6
3	P	134	ASN	24.6
2	O	200	CYS	24.6
2	B	122	PHE	24.6
3	P	286	ALA	24.6
2	B	424	TYR	24.6
3	P	211	TYR	24.6
1	Q	85	ASP	24.5
2	B	143	GLU	24.5
2	E	255	GLY	24.5
2	E	116	ARG	24.5
2	R	265	GLY	24.4
3	S	221	THR	24.3
2	E	388	ASP	24.3
2	E	439	ASP	24.3
2	R	278	GLN	24.3
2	E	397	PRO	24.3
2	O	283	ILE	24.3
2	R	373	THR	24.3
2	R	197	MET	24.3
2	O	93	LEU	24.3
1	A	61	VAL	24.2
2	E	318	LEU	24.1
2	R	327	ASP	24.1
2	R	208	CYS	24.1
3	P	358	SER	24.1
3	S	52	ASN	24.0
3	S	320	ASP	24.0
3	P	69	ASN	24.0
2	O	90	GLN	24.0
2	O	397	PRO	23.9

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Mol	Chain	Res	Type	RSRZ
3	C	177	GLN	23.9
3	C	339	CYS	23.9
2	R	330	THR	23.9
2	B	411	TYR	23.9
2	O	239	SER	23.8
3	P	362	GLY	23.8
2	E	264	ASP	23.8
3	C	242	ILE	23.7
3	F	388	PRO	23.7
3	P	132	GLU	23.7
3	S	237	SER	23.7
2	R	105	GLU	23.7
3	F	98	THR	23.6
3	S	395	GLY	23.6
3	P	372	TRP	23.6
3	F	308	ASN	23.6
3	C	356	LYS	23.6
3	S	345	ASN	23.6
1	Q	181	TYR	23.6
1	A	65	PHE	23.6
3	F	152	ASP	23.6
3	C	318	ASP	23.5
3	S	341	ALA	23.5
2	R	172	LEU	23.5
2	R	106	ASP	23.4
3	P	38	LYS	23.4
3	S	165	GLY	23.4
1	N	106	ASN	23.4
2	R	404	GLU	23.4
1	A	46	THR	23.4
1	D	180	ASP	23.4
2	B	161	ASP	23.3
3	S	257	THR	23.3
3	P	283	GLY	23.3
3	S	337	ASN	23.3
3	C	162	LYS	23.3
1	Q	155	VAL	23.2
1	D	109	ASN	23.2
2	E	352	TYR	23.2
1	N	48	CYS	23.1
3	C	343	HIS	23.1
2	B	449	GLY	23.1

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
2	R	179	LEU	23.1
2	O	130	ASN	23.1
3	S	127	LYS	23.1
3	P	317	SER	23.1
3	F	208	TRP	23.1
3	S	361	ASN	23.1
2	B	142	ASN	23.0
3	C	334	TRP	23.0
2	R	398	ARG	22.9
2	E	419	PRO	22.9
1	D	172	LEU	22.9
2	B	352	TYR	22.8
3	C	391	ARG	22.8
2	O	104	ILE	22.8
3	P	146	HIS	22.8
3	S	365	ASN	22.7
1	A	104	ALA	22.7
2	B	239	SER	22.7
2	R	258	VAL	22.6
3	P	243	PRO	22.6
2	B	371	ASN	22.6
2	B	396	ASP	22.5
1	D	173	GLU	22.5
2	E	405	ASP	22.5
1	Q	159	ILE	22.5
2	R	417	ALA	22.5
2	R	277	LYS	22.5
1	D	194	ILE	22.4
2	R	140	GLN	22.4
3	C	345	ASN	22.4
2	R	220	LYS	22.4
3	C	53	LYS	22.3
2	R	123	GLN	22.3
2	R	260	GLN	22.3
3	F	325	ASN	22.2
3	S	179	LEU	22.2
2	O	400	GLN	22.1
3	S	97	GLU	22.1
2	B	109	ASN	22.1
3	F	93	ILE	22.1
2	R	357	GLY	22.1
3	F	312	PHE	22.1

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Mol	Chain	Res	Type	RSRZ
2	O	112	ASP	22.1
1	D	114	ILE	22.1
3	P	159	LYS	22.1
3	S	321	LYS	22.0
3	F	241	THR	22.0
2	E	315	THR	22.0
2	R	326	GLY	22.0
3	S	157	ALA	22.0
2	O	269	PHE	21.9
2	B	151	SER	21.9
2	B	106	ASP	21.9
3	F	243	PRO	21.9
3	S	232	LYS	21.9
2	R	134	GLY	21.9
3	P	375	ARG	21.9
3	S	185	ASP	21.9
2	R	382	PHE	21.9
2	R	284	ALA	21.9
2	R	102	LYS	21.8
3	P	179	LEU	21.8
2	O	420	ASN	21.8
3	C	27	ASP	21.8
3	P	49	GLN	21.8
2	E	342	ALA	21.8
2	E	440	ASP	21.7
3	P	329	GLN	21.7
2	O	122	PHE	21.7
2	R	180	GLU	21.7
3	S	333	GLY	21.7
3	C	63	ALA	21.6
3	S	111	GLN	21.6
3	S	268	THR	21.6
2	E	307	SER	21.6
2	R	402	SER	21.6
1	A	68	ARG	21.6
3	P	215	PHE	21.5
1	Q	195	ASN	21.5
3	C	303	PHE	21.5
3	S	295	PHE	21.5
3	F	257	THR	21.4
2	R	122	PHE	21.4
2	O	448	GLN	21.4

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Mol	Chain	Res	Type	RSRZ
1	D	195	ASN	21.4
2	E	371	ASN	21.4
2	B	388	ASP	21.4
2	O	373	THR	21.4
2	E	429	TYR	21.4
1	A	67	SER	21.4
2	O	375	THR	21.3
2	B	277	LYS	21.3
2	R	307	SER	21.3
3	P	151	ARG	21.3
2	R	119	SER	21.3
3	P	201	SER	21.3
2	R	132	TRP	21.3
3	P	53	LYS	21.3
2	E	320	GLU	21.2
2	O	143	GLU	21.2
2	R	438	THR	21.2
2	R	322	GLU	21.2
2	R	405	ASP	21.2
3	S	154	GLN	21.1
2	R	135	ARG	21.1
3	P	349	TYR	21.1
1	Q	174	HIS	21.1
3	S	334	TRP	21.1
2	O	405	ASP	21.1
2	B	311	ASN	21.1
3	S	188	GLY	21.0
3	C	123	ASN	21.0
3	P	272	ASP	21.0
3	S	388	PRO	21.0
3	F	253	TRP	20.9
3	S	375	ARG	20.9
3	P	295	PHE	20.9
3	C	272	ASP	20.9
1	Q	173	GLU	20.8
3	P	348	TYR	20.8
1	Q	192	ILE	20.8
2	E	177	SER	20.8
2	E	249	MET	20.8
3	C	365	ASN	20.8
3	F	271	ASN	20.7
3	C	325	ASN	20.7

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Mol	Chain	Res	Type	RSRZ
2	B	303	ASN	20.6
3	S	159	LYS	20.6
2	O	311	ASN	20.6
2	E	366	GLN	20.6
2	E	106	ASP	20.5
2	R	211	PRO	20.5
2	O	277	LYS	20.5
3	F	99	LEU	20.5
3	P	265	PHE	20.5
3	P	258	SER	20.5
2	E	296	PRO	20.5
2	B	315	THR	20.5
2	B	126	THR	20.4
3	P	284	GLY	20.4
1	D	125	LEU	20.4
2	R	232	TYR	20.4
2	B	418	ASN	20.2
2	R	104	ILE	20.2
2	R	410	TRP	20.2
3	P	278	TYR	20.2
2	R	449	GLY	20.1
3	F	155	ASP	20.1
3	F	358	SER	20.1
2	R	116	ARG	20.1
1	D	108	ASP	20.1
3	S	294	ASP	20.0
3	F	84	LYS	20.0
3	F	59	GLU	20.0
3	F	295	PHE	20.0
3	P	333	GLY	20.0
1	N	68	ARG	20.0
3	F	234	HIS	20.0
3	C	388	PRO	20.0
2	E	413	ARG	20.0
2	B	144	ASN	20.0
1	D	115	ASN	19.9
2	B	129	LYS	19.9
2	E	444	TRP	19.9
2	R	441	GLY	19.9
2	O	318	LEU	19.9
3	F	105	SER	19.9
1	N	212	THR	19.8

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Mol	Chain	Res	Type	RSRZ
2	R	238	ASP	19.8
2	B	383	SER	19.8
2	R	170	THR	19.8
1	A	163	SER	19.8
3	P	156	VAL	19.7
2	O	161	ASP	19.7
3	S	346	GLY	19.7
1	Q	113	GLN	19.7
2	E	253	LYS	19.7
2	O	308	GLN	19.7
3	C	306	SER	19.7
2	R	378	ASN	19.7
3	C	134	ASN	19.6
2	E	377	HIS	19.6
2	R	437	GLY	19.6
2	E	306	ILE	19.6
3	F	116	SER	19.6
2	R	397	PRO	19.6
2	B	444	TRP	19.6
2	R	249	MET	19.5
3	P	207	ASN	19.5
2	B	90	GLN	19.5
3	P	109	PHE	19.4
2	R	133	LYS	19.4
2	E	252	GLU	19.4
2	R	244	ARG	19.4
2	B	448	GLN	19.4
3	S	112	GLU	19.4
2	E	256	TRP	19.4
3	S	342	GLY	19.4
3	C	340	HIS	19.3
1	N	210	MET	19.3
3	S	161	ALA	19.3
2	O	99	PRO	19.3
2	R	408	GLY	19.3
1	Q	182	LYS	19.3
2	R	137	ASN	19.3
3	S	306	SER	19.3
2	E	248	ASP	19.3
2	E	423	TYR	19.3
2	R	183	ARG	19.2
2	R	455	LYS	19.2

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Mol	Chain	Res	Type	RSRZ
3	S	151	ARG	19.2
3	S	363	TYR	19.2
2	O	218	CYS	19.2
3	S	162	LYS	19.2
1	N	104	ALA	19.2
3	P	46	ILE	19.2
1	N	70	ASN	19.2
2	R	463	PRO	19.2
2	R	424	TYR	19.2
3	P	264	SER	19.1
2	R	430	THR	19.1
3	F	320	ASP	19.1
2	B	133	LYS	19.1
3	C	278	TYR	19.1
2	B	124	TYR	19.1
2	O	102	LYS	19.1
3	S	310	MET	19.1
2	O	382	PHE	19.1
3	C	342	GLY	19.1
3	S	251	GLU	19.1
3	P	279	ALA	19.0
2	E	297	GLY	19.0
3	P	118	SER	19.0
2	E	314	PRO	19.0
1	Q	99	GLY	19.0
2	B	266	SER	19.0
3	S	291	ASP	19.0
2	O	303	ASN	19.0
3	S	377	TYR	19.0
3	P	76	PRO	19.0
2	B	265	GLY	19.0
2	O	358	ASN	19.0
2	R	177	SER	18.9
2	E	341	GLU	18.9
2	E	143	GLU	18.9
3	P	219	SER	18.9
2	E	395	THR	18.9
3	P	198	LEU	18.8
2	R	192	ASP	18.8
2	B	218	CYS	18.8
2	R	114	VAL	18.8
2	E	326	GLY	18.8

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Mol	Chain	Res	Type	RSRZ
2	R	309	LEU	18.8
2	O	274	ASP	18.8
1	D	90	THR	18.8
3	F	95	LYS	18.8
2	O	240	SER	18.7
2	R	253	LYS	18.7
3	C	178	PHE	18.7
2	O	341	GLU	18.7
2	B	200	CYS	18.7
3	P	247	ARG	18.7
2	E	228	THR	18.7
2	E	270	GLY	18.6
2	R	333	TYR	18.6
3	C	44	GLU	18.6
3	S	102	THR	18.6
3	F	272	ASP	18.6
2	R	124	TYR	18.6
2	O	207	THR	18.6
3	S	327	ALA	18.6
2	O	223	ARG	18.6
2	R	409	TRP	18.5
3	S	108	ARG	18.5
2	O	357	GLY	18.5
2	R	224	ASN	18.5
2	R	298	GLU	18.4
3	C	105	SER	18.4
3	F	361	ASN	18.4
2	E	184	SER	18.4
3	P	254	ASN	18.4
2	O	117	THR	18.4
1	N	49	PRO	18.3
2	R	323	ASP	18.3
2	R	295	VAL	18.3
3	S	138	PRO	18.3
2	O	141	ASP	18.3
1	Q	196	LEU	18.3
2	E	170	THR	18.2
1	A	62	ASP	18.2
2	R	173	ARG	18.2
3	P	150	GLY	18.2
3	S	155	ASP	18.2
2	R	380	MET	18.2

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Mol	Chain	Res	Type	RSRZ
3	S	118	SER	18.2
2	E	394	THR	18.2
2	E	268	ASP	18.2
2	B	408	GLY	18.1
3	P	184	ILE	18.1
3	P	393	ALA	18.1
1	Q	189	GLU	18.1
3	C	358	SER	18.1
2	O	267	VAL	18.1
2	R	268	ASP	18.1
3	S	190	GLY	18.1
2	B	123	GLN	18.1
2	R	272	LYS	18.1
3	C	316	ASP	18.1
2	R	275	PRO	18.1
2	E	455	LYS	18.1
3	S	88	SER	18.1
2	E	457	MET	18.0
3	F	347	VAL	18.0
2	O	383	SER	18.0
3	P	327	ALA	18.0
3	C	158	ASN	18.0
2	O	352	TYR	18.0
1	A	189	GLU	18.0
2	B	414	CYS	18.0
2	O	466	PRO	18.0
2	O	107	LEU	17.9
3	P	221	THR	17.9
2	B	427	GLY	17.9
1	D	102	ALA	17.9
1	A	82	ASN	17.9
3	C	350	GLN	17.9
3	S	175	LYS	17.9
3	S	389	LEU	17.9
3	C	279	ALA	17.9
1	Q	94	VAL	17.9
3	C	284	GLY	17.9
3	P	303	PHE	17.9
3	C	135	CYS	17.8
3	F	214	GLY	17.8
2	R	329	VAL	17.8
3	F	174	ALA	17.8

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Mol	Chain	Res	Type	RSRZ
1	N	52	CYS	17.8
2	O	209	ASN	17.8
2	E	115	SER	17.8
2	R	181	ASN	17.8
3	F	357	THR	17.8
3	P	394	ILE	17.8
2	O	180	GLU	17.7
3	S	254	ASN	17.7
1	A	108	ASP	17.7
2	E	138	GLN	17.6
1	A	196	LEU	17.6
3	P	387	ILE	17.6
3	S	105	SER	17.6
3	C	321	LYS	17.6
2	R	160	ILE	17.6
1	D	111	PHE	17.6
2	R	337	THR	17.6
1	Q	105	ASN	17.6
3	S	142	THR	17.5
2	O	108	ARG	17.5
2	R	446	ASN	17.5
3	S	303	PHE	17.5
2	B	127	LEU	17.5
3	S	156	VAL	17.5
2	O	126	THR	17.5
2	B	134	GLY	17.5
2	O	398	ARG	17.4
2	R	403	LYS	17.4
3	F	160	GLY	17.4
3	F	173	LYS	17.4
1	Q	137	ASN	17.4
2	O	192	ASP	17.4
2	O	196	GLN	17.4
2	R	456	LYS	17.4
2	R	346	GLN	17.4
3	S	369	TRP	17.4
1	D	190	GLN	17.4
2	O	395	THR	17.4
3	C	153	CYS	17.3
2	R	363	GLY	17.3
2	B	269	PHE	17.3
3	F	343	HIS	17.3

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Mol	Chain	Res	Type	RSRZ
1	Q	145	ASP	17.3
2	O	136	GLN	17.3
2	R	282	ASN	17.3
2	O	396	ASP	17.3
2	E	442	VAL	17.3
3	S	119	GLN	17.3
3	F	330	ASP	17.3
3	F	365	ASN	17.3
3	P	189	ASN	17.3
2	B	350	SER	17.3
2	E	454	MET	17.2
2	E	273	TRP	17.2
2	E	319	ILE	17.2
3	F	106	THR	17.2
3	P	280	TYR	17.2
1	D	163	SER	17.2
2	E	274	ASP	17.2
3	P	162	LYS	17.2
3	P	355	SER	17.2
3	C	335	TRP	17.1
2	B	387	ARG	17.1
3	F	313	SER	17.1
2	R	428	ALA	17.1
2	R	420	ASN	17.1
2	E	358	ASN	17.0
3	F	31	ASN	17.0
2	B	191	SER	17.0
1	N	163	SER	17.0
3	S	220	PRO	17.0
2	R	280	PHE	17.0
2	E	200	CYS	17.0
3	C	263	ALA	17.0
2	E	382	PHE	17.0
3	C	330	ASP	17.0
2	E	311	ASN	16.9
3	P	385	LYS	16.9
1	A	199	SER	16.9
3	F	51	GLU	16.9
2	O	421	GLY	16.9
2	R	229	SER	16.9
3	C	151	ARG	16.9
1	Q	193	ALA	16.9

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Mol	Chain	Res	Type	RSRZ
2	E	226	GLY	16.8
2	R	392	TRP	16.8
2	R	387	ARG	16.8
2	R	99	PRO	16.8
1	N	170	ARG	16.8
2	E	396	ASP	16.8
2	E	119	SER	16.8
2	E	414	CYS	16.8
1	D	98	ARG	16.8
2	R	129	LYS	16.8
2	R	353	LYS	16.7
3	P	391	ARG	16.7
2	O	243	TYR	16.7
1	D	101	PHE	16.7
2	R	136	GLN	16.7
2	O	315	THR	16.7
2	O	139	VAL	16.7
2	O	280	PHE	16.6
1	D	112	LYS	16.6
2	R	293	CYS	16.6
2	R	339	GLN	16.6
3	S	201	SER	16.5
2	R	325	LYS	16.5
3	C	320	ASP	16.5
2	R	396	ASP	16.5
2	E	162	GLU	16.5
3	F	350	GLN	16.5
3	F	276	LEU	16.5
2	R	205	THR	16.5
2	R	367	LEU	16.5
1	N	214	THR	16.5
2	B	95	ARG	16.5
2	E	334	GLU	16.5
2	R	317	LEU	16.4
2	E	462	ARG	16.4
1	Q	97	MET	16.4
2	O	219	GLU	16.3
3	F	158	ASN	16.3
2	B	345	TYR	16.3
2	E	201	ARG	16.3
3	S	367	ILE	16.3
3	F	49	GLN	16.3

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Mol	Chain	Res	Type	RSRZ
2	R	281	GLY	16.3
2	O	414	CYS	16.3
3	P	45	GLY	16.3
3	S	34	THR	16.3
3	S	54	THR	16.2
1	A	185	GLN	16.2
2	R	121	THR	16.2
2	R	464	TYR	16.2
2	R	315	THR	16.2
2	O	177	SER	16.2
2	R	226	GLY	16.2
3	P	310	MET	16.2
2	E	348	SER	16.1
3	S	264	SER	16.1
3	P	346	GLY	16.1
2	O	343	ASN	16.1
3	F	229	GLY	16.1
2	R	246	TYR	16.1
3	P	350	GLN	16.1
2	R	176	ARG	16.1
2	R	264	ASP	16.1
3	F	270	GLU	16.1
3	P	197	ARG	16.1
2	R	395	THR	16.0
3	C	136	GLN	16.0
2	R	225	GLU	16.0
3	F	341	ALA	16.0
2	R	94	VAL	16.0
2	E	451	TRP	16.0
3	F	176	GLN	16.0
3	P	239	GLN	16.0
3	P	154	GLN	15.9
2	O	204	CYS	15.9
2	B	412	ASN	15.9
3	F	268	THR	15.9
2	E	139	VAL	15.9
3	S	174	ALA	15.9
1	N	51	GLY	15.9
2	E	420	ASN	15.9
2	B	226	GLY	15.9
2	B	405	ASP	15.9
1	N	172	LEU	15.9

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Mol	Chain	Res	Type	RSRZ
1	N	111	PHE	15.9
2	E	452	TYR	15.9
2	R	406	GLY	15.9
1	N	168	CYS	15.8
3	S	147	ASP	15.8
2	O	193	VAL	15.8
3	S	55	SER	15.8
2	O	263	GLN	15.8
3	P	234	HIS	15.8
1	N	57	LEU	15.8
2	R	223	ARG	15.8
1	N	107	ASN	15.8
3	S	131	LEU	15.7
3	P	165	GLY	15.7
3	P	37	ASP	15.7
1	A	110	THR	15.7
1	D	128	LYS	15.7
2	O	401	CYS	15.7
3	P	294	ASP	15.7
3	C	221	THR	15.7
2	E	417	ALA	15.7
3	F	279	ALA	15.7
1	Q	191	VAL	15.7
3	S	278	TYR	15.7
2	E	224	ASN	15.6
2	E	406	GLY	15.6
3	F	52	ASN	15.6
2	B	139	VAL	15.6
2	B	243	TYR	15.6
1	D	177	ASP	15.6
1	Q	114	ILE	15.6
2	E	148	GLU	15.6
2	B	421	GLY	15.6
2	E	355	THR	15.6
2	E	214	SER	15.6
3	S	150	GLY	15.6
3	F	327	ALA	15.6
3	C	33	GLN	15.6
2	B	441	GLY	15.6
1	N	187	GLN	15.6
2	E	197	MET	15.6
2	E	343	ASN	15.6

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Mol	Chain	Res	Type	RSRZ
2	O	365	SER	15.6
3	F	394	ILE	15.5
3	S	49	GLN	15.5
2	E	172	LEU	15.5
3	C	372	TRP	15.5
2	R	214	SER	15.5
2	E	459	LYS	15.5
1	Q	95	GLU	15.5
2	E	160	ILE	15.5
3	C	197	ARG	15.5
3	C	285	ASP	15.5
3	S	140	GLN	15.5
3	P	176	GLN	15.5
2	O	423	TYR	15.4
2	O	97	GLU	15.4
2	E	449	GLY	15.4
3	S	100	ILE	15.4
2	R	412	ASN	15.4
3	P	290	PHE	15.4
2	B	307	SER	15.4
3	F	109	PHE	15.4
2	E	127	LEU	15.4
2	B	389	ASN	15.4
2	E	199	TYR	15.3
2	O	195	THR	15.3
3	C	159	LYS	15.3
3	F	353	THR	15.3
2	O	251	THR	15.3
2	R	118	SER	15.3
2	R	365	SER	15.3
2	R	305	ARG	15.3
3	S	239	GLN	15.3
2	B	384	THR	15.3
1	A	126	ARG	15.3
2	O	242	PRO	15.2
2	E	240	SER	15.2
1	A	178	LEU	15.2
2	B	392	TRP	15.2
1	N	174	HIS	15.2
3	P	365	ASN	15.2
1	D	116	GLU	15.2
3	F	255	GLY	15.2

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
2	O	133	LYS	15.2
3	C	354	TYR	15.2
2	R	283	ILE	15.2
2	B	125	ILE	15.2
2	E	122	PHE	15.2
2	O	236	PRO	15.1
2	O	100	ILE	15.1
3	F	127	LYS	15.1
3	C	277	THR	15.1
2	R	217	GLU	15.1
2	R	429	TYR	15.1
3	P	208	TRP	15.1
2	B	382	PHE	15.1
2	R	350	SER	15.1
2	B	209	ASN	15.0
3	C	305	THR	15.0
3	C	390	ASN	15.0
2	B	199	TYR	15.0
2	R	186	ILE	15.0
3	S	339	CYS	15.0
2	B	404	GLU	15.0
3	S	173	LYS	15.0
3	F	50	VAL	15.0
3	F	236	ILE	15.0
1	N	211	SER	14.9
3	S	270	GLU	14.9
2	B	455	LYS	14.9
3	P	171	PRO	14.9
3	F	378	SER	14.9
2	R	451	TRP	14.9
1	Q	58	ILE	14.9
3	S	101	SER	14.9
1	D	196	LEU	14.9
3	S	381	LYS	14.9
1	A	64	ASP	14.9
2	R	297	GLY	14.9
2	E	374	MET	14.9
3	C	102	THR	14.9
1	A	77	PHE	14.9
2	B	132	TRP	14.9
1	Q	48	CYS	14.8
3	S	192	THR	14.8

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Mol	Chain	Res	Type	RSRZ
1	N	180	ASP	14.8
3	F	351	GLY	14.8
1	A	66	THR	14.8
3	S	368	ILE	14.7
2	O	91	ASP	14.7
2	R	195	THR	14.7
3	C	133	ALA	14.7
3	S	226	PHE	14.7
3	S	53	LYS	14.7
2	B	136	GLN	14.7
3	S	117	ASN	14.7
2	E	447	TRP	14.7
3	F	27	ASP	14.7
2	R	98	ARG	14.7
1	A	170	ARG	14.6
2	R	335	GLY	14.6
3	S	216	GLY	14.6
2	B	137	ASN	14.6
3	S	265	PHE	14.6
2	B	312	MET	14.6
1	A	193	ALA	14.6
2	O	229	SER	14.5
2	O	98	ARG	14.5
1	A	103	LYS	14.5
3	C	84	LYS	14.5
2	E	368	VAL	14.5
1	Q	180	ASP	14.5
3	C	222	GLY	14.5
3	S	374	SER	14.5
1	Q	82	ASN	14.5
2	B	398	ARG	14.5
2	B	278	GLN	14.4
3	C	35	SER	14.4
2	E	120	SER	14.4
3	C	295	PHE	14.4
1	Q	134	GLN	14.4
2	R	400	GLN	14.4
3	S	376	TRP	14.4
3	S	186	GLY	14.4
2	B	276	TYR	14.4
3	P	351	GLY	14.4
3	S	298	ASP	14.4

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
3	F	376	TRP	14.3
2	R	97	GLU	14.3
1	Q	83	SER	14.3
2	E	353	LYS	14.3
1	D	161	ILE	14.3
3	P	155	ASP	14.3
2	E	389	ASN	14.3
2	O	270	GLY	14.3
3	C	227	TRP	14.3
1	N	204	TYR	14.2
3	C	298	ASP	14.2
1	A	78	ASN	14.2
3	S	50	VAL	14.2
2	E	416	ALA	14.2
3	F	179	LEU	14.2
2	R	411	TYR	14.2
3	S	344	LEU	14.2
3	S	313	SER	14.2
1	D	134	GLN	14.2
2	B	135	ARG	14.2
3	P	315	TRP	14.2
2	O	163	THR	14.2
2	B	114	VAL	14.2
1	Q	132	GLN	14.2
2	O	94	VAL	14.1
2	O	115	SER	14.1
2	E	123	GLN	14.1
2	E	464	TYR	14.1
1	Q	168	CYS	14.1
2	E	105	GLU	14.1
2	E	305	ARG	14.0
2	O	252	GLU	14.0
3	S	314	THR	14.0
2	E	317	LEU	14.0
2	R	247	CYS	14.0
2	R	465	PHE	14.0
2	O	124	TYR	14.0
2	O	205	THR	14.0
2	O	323	ASP	14.0
3	P	287	GLY	14.0
3	S	311	GLN	14.0
2	B	423	TYR	14.0

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Mol	Chain	Res	Type	RSRZ
3	C	52	ASN	14.0
3	C	148	VAL	13.9
3	S	274	TYR	13.9
3	P	352	GLY	13.9
3	C	297	ASP	13.9
2	O	389	ASN	13.9
2	E	195	THR	13.9
1	Q	176	VAL	13.8
2	O	377	HIS	13.8
2	B	240	SER	13.8
2	E	212	VAL	13.8
3	S	132	GLU	13.8
3	S	204	PHE	13.8
1	A	83	SER	13.8
2	B	275	PRO	13.8
3	P	174	ALA	13.8
2	E	453	SER	13.8
3	F	92	GLU	13.8
3	P	368	ILE	13.8
3	S	370	ALA	13.7
2	O	392	TRP	13.7
3	F	170	ARG	13.7
3	S	348	TYR	13.7
3	P	178	PHE	13.7
3	S	358	SER	13.7
2	E	157	GLN	13.7
1	N	100	ASP	13.7
2	O	125	ILE	13.7
3	P	148	VAL	13.7
2	E	150	SER	13.7
3	S	386	ILE	13.6
2	R	193	VAL	13.6
1	Q	56	GLY	13.6
3	C	331	GLY	13.6
2	R	415	HIS	13.6
2	R	391	GLY	13.6
1	N	196	LEU	13.6
1	D	66	THR	13.5
1	Q	185	GLN	13.5
3	P	292	GLY	13.5
3	F	215	PHE	13.5
3	P	185	ASP	13.5

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
2	O	444	TRP	13.5
3	S	168	PHE	13.5
2	E	312	MET	13.5
2	O	310	THR	13.5
2	R	457	MET	13.5
2	B	128	LEU	13.4
3	S	366	GLY	13.4
3	P	360	PRO	13.4
1	D	164	CYS	13.4
3	S	359	THR	13.4
1	A	117	ASP	13.4
2	E	325	LYS	13.4
2	R	243	TYR	13.4
1	D	82	ASN	13.4
1	N	176	VAL	13.4
2	B	148	GLU	13.4
2	B	357	GLY	13.3
2	O	417	ALA	13.3
3	C	296	GLY	13.3
2	R	251	THR	13.3
3	F	395	GLY	13.3
3	S	207	ASN	13.3
2	O	255	GLY	13.3
3	P	62	LYS	13.3
3	S	290	PHE	13.3
1	N	123	GLU	13.3
2	R	462	ARG	13.3
3	P	240	SER	13.3
3	F	323	ASP	13.2
3	C	112	GLU	13.2
3	P	304	PHE	13.2
1	A	106	ASN	13.2
2	R	390	ASP	13.2
3	C	138	PRO	13.2
1	Q	175	LYS	13.2
2	E	400	GLN	13.2
1	D	193	ALA	13.2
3	S	194	PHE	13.2
3	F	322	TYR	13.2
1	Q	103	LYS	13.2
2	B	192	ASP	13.1
2	O	291	LYS	13.1

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
2	E	176	ARG	13.1
2	E	220	LYS	13.1
3	F	91	GLU	13.1
1	N	65	PHE	13.1
3	F	284	GLY	13.1
3	F	67	SER	13.1
2	B	119	SER	13.1
1	N	76	LEU	13.1
3	C	91	GLU	13.1
3	C	317	SER	13.1
3	C	309	GLY	13.1
1	A	131	GLU	13.1
2	B	409	TRP	13.0
2	E	179	LEU	13.0
2	B	447	TRP	13.0
3	S	27	ASP	13.0
3	P	339	CYS	13.0
3	C	257	THR	13.0
3	S	31	ASN	13.0
1	N	61	VAL	13.0
2	R	436	HIS	13.0
3	P	381	LYS	13.0
2	O	142	ASN	13.0
3	P	377	TYR	13.0
2	B	438	THR	13.0
3	C	337	ASN	13.0
2	R	194	SER	13.0
3	P	297	ASP	13.0
2	B	138	GLN	13.0
3	F	154	GLN	13.0
3	F	68	TYR	13.0
2	R	126	THR	13.0
2	B	270	GLY	13.0
1	D	133	VAL	13.0
1	Q	75	SER	12.9
3	C	361	ASN	12.9
2	R	199	TYR	12.9
3	C	200	GLY	12.9
2	O	257	THR	12.9
1	D	75	SER	12.9
2	E	427	GLY	12.9
2	O	220	LYS	12.9

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Mol	Chain	Res	Type	RSRZ
1	Q	178	LEU	12.9
1	N	126	ARG	12.9
1	Q	162	ARG	12.9
1	D	48	CYS	12.9
3	P	120	LYS	12.9
3	C	46	ILE	12.9
1	A	60	GLU	12.8
2	E	222	ILE	12.8
3	S	317	SER	12.8
3	S	379	MET	12.8
1	A	48	CYS	12.8
3	P	334	TRP	12.8
1	Q	116	GLU	12.8
3	C	173	LYS	12.8
2	O	135	ARG	12.7
2	E	181	ASN	12.7
2	B	187	GLN	12.7
2	O	106	ASP	12.7
2	O	408	GLY	12.7
3	P	173	LYS	12.7
3	F	352	GLY	12.7
2	R	344	LYS	12.7
2	O	116	ARG	12.7
2	B	235	GLN	12.7
3	F	336	MET	12.7
3	S	300	SER	12.6
3	C	347	VAL	12.6
2	E	92	THR	12.6
2	R	215	GLY	12.6
3	S	230	ASN	12.6
3	S	292	GLY	12.6
3	S	364	ASP	12.6
1	A	128	LYS	12.6
2	O	455	LYS	12.6
2	E	257	THR	12.6
2	E	418	ASN	12.6
3	C	130	GLN	12.6
3	S	229	GLY	12.6
1	Q	190	GLN	12.6
1	Q	139	LEU	12.6
2	B	283	ILE	12.5
3	F	70	PRO	12.5

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
3	P	68	TYR	12.5
3	S	394	ILE	12.5
2	B	348	SER	12.5
1	A	123	GLU	12.5
2	O	384	THR	12.5
3	C	98	THR	12.5
2	O	353	LYS	12.5
3	P	392	LEU	12.5
3	C	161	ALA	12.5
3	P	130	GLN	12.4
3	C	283	GLY	12.4
3	F	372	TRP	12.4
3	F	396	GLU	12.4
2	O	241	LYS	12.4
3	P	81	SER	12.4
3	F	71	ASP	12.4
2	B	195	THR	12.4
3	C	393	ALA	12.4
3	P	300	SER	12.3
3	S	170	ARG	12.3
2	E	461	ILE	12.3
3	F	213	GLU	12.3
3	F	240	SER	12.3
2	B	268	ASP	12.3
2	B	395	THR	12.3
3	F	165	GLY	12.3
3	S	116	SER	12.3
3	C	34	THR	12.3
3	P	305	THR	12.3
1	D	175	LYS	12.3
2	R	452	TYR	12.3
2	B	463	PRO	12.2
3	F	175	LYS	12.2
3	C	109	PHE	12.2
1	D	120	SER	12.2
2	E	381	PHE	12.2
1	N	193	ALA	12.2
2	R	442	VAL	12.2
1	D	130	ILE	12.2
3	S	169	ILE	12.2
2	B	385	TYR	12.2
2	R	342	ALA	12.2

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Mol	Chain	Res	Type	RSRZ
1	D	179	GLU	12.2
2	O	286	ASN	12.1
2	E	91	ASP	12.1
1	D	197	LEU	12.1
1	Q	106	ASN	12.1
3	C	89	MET	12.1
1	A	134	GLN	12.1
2	B	113	SER	12.1
2	R	212	VAL	12.1
3	F	171	PRO	12.1
1	N	185	GLN	12.1
2	B	146	VAL	12.1
2	E	310	THR	12.1
3	C	64	ILE	12.1
2	B	97	GLU	12.1
2	R	216	LYS	12.1
2	O	342	ALA	12.1
1	A	57	LEU	12.1
1	Q	87	ASN	12.1
2	R	355	THR	12.1
3	F	334	TRP	12.1
2	E	345	TYR	12.1
1	A	218	PRO	12.0
1	Q	123	GLU	12.0
2	O	439	ASP	12.0
3	S	30	ASN	12.0
3	C	313	SER	12.0
3	C	69	ASN	12.0
3	P	325	ASN	12.0
1	Q	77	PHE	12.0
2	R	381	PHE	12.0
2	R	269	PHE	12.0
2	E	276	TYR	12.0
2	E	207	THR	12.0
2	O	266	SER	12.0
1	Q	157	ILE	12.0
2	B	194	SER	12.0
2	E	244	ARG	12.0
3	S	71	ASP	12.0
2	R	388	ASP	11.9
3	S	316	ASP	11.9
2	E	131	MET	11.9

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Mol	Chain	Res	Type	RSRZ
3	P	378	SER	11.9
2	R	334	GLU	11.9
2	O	131	MET	11.9
3	P	180	VAL	11.9
1	N	189	GLU	11.9
1	N	50	SER	11.8
1	Q	78	ASN	11.8
2	B	332	LEU	11.8
2	R	92	THR	11.8
2	R	385	TYR	11.8
3	F	242	ILE	11.8
2	E	336	PHE	11.8
3	P	344	LEU	11.8
3	F	283	GLY	11.8
2	R	368	VAL	11.8
3	S	312	PHE	11.8
2	R	262	ARG	11.8
2	B	304	ASP	11.8
2	R	138	GLN	11.8
2	R	427	GLY	11.8
3	P	335	TRP	11.8
1	D	83	SER	11.8
3	P	169	ILE	11.8
2	B	450	SER	11.8
2	O	170	THR	11.8
3	P	244	TYR	11.8
1	N	213	ILE	11.8
2	E	152	HIS	11.7
2	R	306	ILE	11.7
2	O	118	SER	11.7
3	F	163	GLU	11.7
3	F	37	ASP	11.7
3	F	391	ARG	11.7
2	R	233	LEU	11.7
2	E	404	GLU	11.7
1	A	161	ILE	11.7
1	D	121	ARG	11.7
3	C	396	GLU	11.7
1	Q	86	SER	11.7
3	F	97	GLU	11.7
3	S	130	GLN	11.7
3	S	110	LEU	11.7

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Mol	Chain	Res	Type	RSRZ
1	A	198	PRO	11.6
3	P	386	ILE	11.6
2	B	169	PRO	11.6
1	Q	206	PRO	11.6
3	C	244	TYR	11.6
2	E	89	LEU	11.6
1	D	52	CYS	11.6
3	P	135	CYS	11.6
3	S	149	THR	11.6
3	C	38	LYS	11.6
1	Q	170	ARG	11.6
3	S	391	ARG	11.6
2	B	458	SER	11.5
3	C	346	GLY	11.5
1	N	215	GLY	11.5
2	E	426	GLY	11.5
3	S	357	THR	11.5
3	C	327	ALA	11.5
3	C	147	ASP	11.5
3	F	120	LYS	11.5
3	S	66	ILE	11.4
2	O	250	LYS	11.4
3	C	55	SER	11.4
2	R	459	LYS	11.4
3	F	368	ILE	11.4
1	D	88	THR	11.4
1	Q	179	GLU	11.4
2	O	317	LEU	11.4
1	D	123	GLU	11.4
2	B	306	ILE	11.4
3	C	215	PHE	11.4
3	C	250	LEU	11.4
1	D	78	ASN	11.4
3	C	68	TYR	11.4
3	F	387	ILE	11.3
1	D	198	PRO	11.3
3	F	349	TYR	11.3
2	R	444	TRP	11.3
2	E	384	THR	11.3
3	P	370	ALA	11.3
2	R	358	ASN	11.3
2	E	225	GLU	11.3

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Mol	Chain	Res	Type	RSRZ
1	A	187	GLN	11.3
2	O	355	THR	11.3
1	Q	136	ILE	11.3
1	Q	161	ILE	11.3
2	B	379	SER	11.3
2	B	184	SER	11.3
2	O	208	CYS	11.3
1	A	92	ASN	11.3
2	E	425	TRP	11.3
2	E	407	GLY	11.2
3	C	37	ASP	11.2
2	O	181	ASN	11.2
3	C	328	GLU	11.2
1	D	87	ASN	11.2
2	E	109	ASN	11.2
2	R	467	GLU	11.2
2	B	116	ARG	11.2
3	C	291	ASP	11.2
3	S	211	TYR	11.2
3	F	237	SER	11.2
2	B	181	ASN	11.2
3	C	70	PRO	11.2
2	E	194	SER	11.2
3	P	255	GLY	11.2
3	P	291	ASP	11.2
2	R	366	GLN	11.1
1	N	130	ILE	11.1
1	N	102	ALA	11.1
3	C	47	LEU	11.1
1	D	46	THR	11.1
2	E	356	ALA	11.1
1	D	178	LEU	11.1
3	S	35	SER	11.1
3	F	278	TYR	11.1
3	F	212	LYS	11.1
2	B	336	PHE	11.1
1	A	70	ASN	11.0
3	C	171	PRO	11.0
1	A	208	LEU	11.0
3	S	360	PRO	11.0
3	S	347	VAL	11.0
2	E	369	GLY	11.0

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	N	113	GLN	11.0
1	A	197	LEU	11.0
3	C	240	SER	11.0
3	P	216	GLY	11.0
2	R	319	ILE	11.0
2	B	417	ALA	11.0
3	F	370	ALA	11.0
2	B	428	ALA	11.0
3	C	174	ALA	11.0
3	F	156	VAL	11.0
2	O	313	GLY	11.0
1	N	161	ILE	11.0
1	Q	52	CYS	11.0
3	S	178	PHE	11.0
2	B	355	THR	10.9
2	O	272	LYS	10.9
1	Q	194	ILE	10.9
2	R	236	PRO	10.9
3	F	35	SER	10.9
3	C	260	ALA	10.9
2	O	404	GLU	10.9
3	C	152	ASP	10.9
1	D	169	SER	10.9
2	R	458	SER	10.9
3	P	136	GLN	10.9
2	O	265	GLY	10.9
2	R	90	GLN	10.9
3	S	187	SER	10.9
1	D	96	LEU	10.9
3	C	300	SER	10.8
1	D	124	ILE	10.8
2	R	125	ILE	10.8
2	E	277	LYS	10.8
3	S	241	THR	10.8
2	B	433	MET	10.8
2	B	465	PHE	10.8
1	A	87	ASN	10.8
3	P	324	GLY	10.8
2	R	416	ALA	10.8
2	R	163	THR	10.8
3	C	157	ALA	10.8
2	E	103	SER	10.8

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
3	C	286	ALA	10.8
3	P	275	ARG	10.8
3	S	286	ALA	10.8
3	S	37	ASP	10.8
1	Q	74	ASP	10.7
2	R	413	ARG	10.7
1	D	81	LYS	10.7
3	S	167	TYR	10.7
2	E	322	GLU	10.7
3	C	142	THR	10.7
3	F	321	LYS	10.7
3	C	119	GLN	10.7
3	S	356	LYS	10.7
3	S	42	THR	10.7
3	C	234	HIS	10.7
3	S	77	ASN	10.6
3	C	30	ASN	10.6
2	O	307	SER	10.6
2	E	96	GLN	10.6
2	B	104	ILE	10.6
2	O	413	ARG	10.6
2	B	99	PRO	10.6
2	E	171	LYS	10.6
1	D	49	PRO	10.6
3	C	249	GLN	10.6
3	F	177	GLN	10.6
3	P	309	GLY	10.6
3	S	305	THR	10.6
2	O	409	TRP	10.6
3	S	380	LYS	10.6
1	N	98	ARG	10.6
2	B	301	LEU	10.6
3	C	165	GLY	10.6
2	R	448	GLN	10.6
3	C	308	ASN	10.6
1	N	101	PHE	10.6
3	S	362	GLY	10.6
3	F	316	ASP	10.6
1	A	121	ARG	10.6
1	Q	198	PRO	10.5
3	C	352	GLY	10.5
1	D	61	VAL	10.5

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
2	O	199	TYR	10.5
3	C	302	LYS	10.5
3	C	150	GLY	10.5
2	E	108	ARG	10.5
3	S	296	GLY	10.5
3	S	74	SER	10.5
1	Q	80	GLN	10.5
2	E	159	TYR	10.5
2	R	201	ARG	10.4
2	R	271	ARG	10.4
1	D	74	ASP	10.4
1	D	85	ASP	10.4
3	C	65	GLN	10.4
3	C	43	LEU	10.4
1	Q	47	LYS	10.4
2	E	304	ASP	10.4
3	S	81	SER	10.4
2	O	410	TRP	10.4
2	R	174	VAL	10.4
1	A	205	LEU	10.4
2	R	188	LYS	10.4
1	D	218	PRO	10.3
2	E	409	TRP	10.3
3	S	325	ASN	10.3
2	B	98	ARG	10.3
1	D	208	LEU	10.3
3	P	380	LYS	10.3
3	S	343	HIS	10.3
2	O	453	SER	10.3
3	P	249	GLN	10.3
3	P	147	ASP	10.3
3	P	395	GLY	10.3
3	S	137	GLU	10.3
1	N	66	THR	10.3
3	C	29	LEU	10.3
3	C	172	LEU	10.3
3	P	66	ILE	10.3
2	R	131	MET	10.3
1	D	54	MET	10.3
2	B	341	GLU	10.3
2	R	213	VAL	10.3
3	S	114	TYR	10.3

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Mol	Chain	Res	Type	RSRZ
2	B	329	VAL	10.2
2	B	220	LYS	10.2
2	O	371	ASN	10.2
3	S	353	THR	10.2
2	R	234	ILE	10.2
2	R	91	ASP	10.2
3	C	137	GLU	10.2
3	C	39	ASP	10.2
3	S	28	PHE	10.2
2	R	336	PHE	10.2
3	S	392	LEU	10.2
2	B	163	THR	10.2
3	F	310	MET	10.2
3	S	92	GLU	10.1
3	F	39	ASP	10.1
1	Q	120	SER	10.1
2	B	103	SER	10.1
2	E	266	SER	10.1
2	E	437	GLY	10.1
1	A	174	HIS	10.1
2	E	229	SER	10.1
2	E	174	VAL	10.1
2	O	127	LEU	10.1
3	F	148	VAL	10.1
2	E	147	ASN	10.1
3	P	342	GLY	10.1
3	S	69	ASN	10.1
1	D	80	GLN	10.1
2	R	310	THR	10.0
3	P	28	PHE	10.0
1	N	67	SER	10.0
2	R	203	PRO	10.0
1	Q	61	VAL	10.0
3	P	41	ARG	10.0
3	S	244	TYR	10.0
3	F	54	THR	10.0
1	A	94	VAL	10.0
1	Q	60	GLU	10.0
2	B	229	SER	10.0
2	O	458	SER	10.0
1	A	114	ILE	10.0
2	O	387	ARG	10.0

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Mol	Chain	Res	Type	RSRZ
2	E	166	ASN	10.0
1	D	93	ILE	9.9
3	C	381	LYS	9.9
3	C	389	LEU	9.9
2	R	466	PRO	9.9
2	B	223	ARG	9.9
3	P	321	LYS	9.9
2	O	215	GLY	9.9
1	D	185	GLN	9.9
2	R	422	ARG	9.9
2	O	224	ASN	9.9
3	S	51	GLU	9.9
3	F	34	THR	9.9
3	F	77	ASN	9.8
1	Q	76	LEU	9.8
3	P	133	ALA	9.8
2	B	407	GLY	9.8
3	P	131	LEU	9.8
1	D	62	ASP	9.8
2	E	466	PRO	9.8
3	C	353	THR	9.8
1	Q	117	ASP	9.8
2	R	361	ILE	9.8
1	N	78	ASN	9.8
1	Q	210	MET	9.8
3	S	213	GLU	9.8
2	E	243	TYR	9.8
3	F	132	GLU	9.8
2	E	99	PRO	9.8
3	F	30	ASN	9.8
3	C	395	GLY	9.8
3	S	95	LYS	9.8
3	F	345	ASN	9.7
3	P	51	GLU	9.7
3	S	148	VAL	9.7
2	E	398	ARG	9.7
2	B	354	GLY	9.7
3	P	347	VAL	9.7
1	Q	121	ARG	9.7
3	F	83	THR	9.7
1	N	206	PRO	9.7
3	F	359	THR	9.7

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Mol	Chain	Res	Type	RSRZ
1	Q	102	ALA	9.7
2	R	245	VAL	9.7
2	B	89	LEU	9.7
3	S	240	SER	9.7
3	C	204	PHE	9.7
3	F	379	MET	9.7
3	P	183	GLU	9.7
1	N	96	LEU	9.7
3	S	263	ALA	9.7
2	E	412	ASN	9.6
1	D	95	GLU	9.6
1	D	97	MET	9.6
3	C	201	SER	9.6
2	B	343	ASN	9.6
2	O	461	ILE	9.6
2	R	187	GLN	9.6
2	R	273	TRP	9.6
1	Q	88	THR	9.6
3	S	304	PHE	9.6
2	E	271	ARG	9.6
2	B	152	HIS	9.6
3	C	71	ASP	9.6
2	B	141	ASP	9.6
2	O	105	GLU	9.6
2	B	166	ASN	9.6
2	B	170	THR	9.6
1	A	52	CYS	9.5
1	A	113	GLN	9.5
2	R	228	THR	9.5
1	D	45	ASN	9.5
3	F	104	GLU	9.5
2	E	121	THR	9.5
2	O	376	ILE	9.5
1	A	206	PRO	9.5
3	P	84	LYS	9.5
1	N	116	GLU	9.5
3	P	57	ALA	9.5
2	O	329	VAL	9.5
2	O	278	GLN	9.5
1	N	63	GLN	9.4
3	F	157	ALA	9.4
2	E	215	GLY	9.4

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Mol	Chain	Res	Type	RSRZ
1	N	80	GLN	9.4
3	C	236	ILE	9.4
3	P	311	GLN	9.4
1	N	82	ASN	9.4
3	C	77	ASN	9.4
3	P	50	VAL	9.4
3	S	78	ASN	9.4
2	E	167	ASN	9.4
3	P	43	LEU	9.4
3	C	212	LYS	9.4
3	F	113	ILE	9.4
3	F	346	GLY	9.3
1	D	84	LYS	9.3
3	P	259	THR	9.3
3	F	96	TYR	9.3
3	F	60	LEU	9.3
2	B	334	GLU	9.3
2	B	255	GLY	9.3
2	O	271	ARG	9.3
1	A	130	ILE	9.3
2	R	110	THR	9.3
3	C	86	SER	9.3
2	O	462	ARG	9.3
2	O	237	GLU	9.3
3	S	396	GLU	9.3
2	O	407	GLY	9.3
2	B	164	VAL	9.3
2	E	392	TRP	9.3
1	Q	49	PRO	9.3
2	B	399	LYS	9.3
2	O	147	ASN	9.2
3	C	59	GLU	9.2
3	S	87	LYS	9.2
1	Q	199	SER	9.2
2	E	217	GLU	9.2
3	P	366	GLY	9.2
3	F	222	GLY	9.2
1	N	89	LEU	9.2
3	S	200	GLY	9.2
3	C	116	SER	9.2
3	F	69	ASN	9.2
3	S	39	ASP	9.2

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Mol	Chain	Res	Type	RSRZ
2	B	211	PRO	9.2
3	S	76	PRO	9.2
2	B	356	ALA	9.2
2	E	324	TRP	9.2
1	D	70	ASN	9.2
3	C	364	ASP	9.2
2	E	430	THR	9.2
3	S	171	PRO	9.2
3	P	27	ASP	9.2
2	R	100	ILE	9.1
3	F	38	LYS	9.1
1	A	89	LEU	9.1
1	Q	81	LYS	9.1
1	Q	46	THR	9.1
2	O	465	PHE	9.1
2	R	371	ASN	9.1
3	S	393	ALA	9.1
1	A	74	ASP	9.1
2	O	381	PHE	9.1
3	S	65	GLN	9.1
1	D	189	GLU	9.1
1	N	145	ASP	9.1
2	B	257	THR	9.1
2	R	432	ASP	9.1
1	A	45	ASN	9.1
1	N	216	PRO	9.1
3	F	318	ASP	9.1
1	N	150	MET	9.1
3	S	32	TYR	9.1
2	B	376	ILE	9.1
2	R	318	LEU	9.1
2	B	413	ARG	9.1
3	S	309	GLY	9.1
3	F	58	ARG	9.1
3	P	308	ASN	9.1
2	R	109	ASN	9.0
1	A	122	ILE	9.0
2	O	393	LYS	9.0
3	C	311	GLN	9.0
1	Q	218	PRO	9.0
2	E	344	LYS	9.0
2	O	302	GLY	9.0

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Mol	Chain	Res	Type	RSRZ
1	N	162	ARG	9.0
1	N	55	LYS	9.0
1	A	132	GLN	9.0
3	F	74	SER	9.0
3	F	266	LYS	9.0
1	Q	130	ILE	9.0
2	E	142	ASN	9.0
2	E	269	PHE	9.0
2	R	222	ILE	9.0
1	N	183	ASN	9.0
1	A	200	ARG	9.0
3	P	168	PHE	9.0
2	E	173	ARG	8.9
2	E	361	ILE	8.9
1	A	120	SER	8.9
2	O	441	GLY	8.9
3	P	114	TYR	8.9
1	D	168	CYS	8.9
3	C	216	GLY	8.9
2	R	112	ASP	8.9
3	F	324	GLY	8.9
2	E	438	THR	8.9
3	P	40	LEU	8.9
2	R	423	TYR	8.8
2	O	320	GLU	8.8
3	F	335	TRP	8.8
3	S	242	ILE	8.8
2	O	191	SER	8.8
1	A	88	THR	8.8
1	A	127	ARG	8.8
3	P	271	ASN	8.8
2	E	110	THR	8.8
2	O	333	TYR	8.8
1	D	213	ILE	8.8
1	A	90	THR	8.8
1	N	109	ASN	8.8
2	O	312	MET	8.8
3	P	121	ILE	8.8
2	O	463	PRO	8.8
1	A	75	SER	8.8
3	C	238	THR	8.7
3	C	368	ILE	8.7

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Mol	Chain	Res	Type	RSRZ
3	S	80	GLU	8.7
3	P	253	TRP	8.7
2	B	302	GLY	8.7
3	C	394	ILE	8.7
3	S	85	ASN	8.7
3	F	63	ALA	8.7
2	B	180	GLU	8.7
2	B	446	ASN	8.7
2	E	328	LYS	8.7
3	F	211	TYR	8.7
2	E	258	VAL	8.7
2	B	381	PHE	8.7
2	E	145	VAL	8.7
2	E	288	GLU	8.7
2	O	399	LYS	8.7
2	O	150	SER	8.7
2	E	98	ARG	8.7
3	F	390	ASN	8.6
1	Q	73	ARG	8.6
1	D	157	ILE	8.6
3	P	85	ASN	8.6
2	B	374	MET	8.6
2	E	112	ASP	8.6
3	F	124	LEU	8.6
2	R	184	SER	8.6
3	C	237	SER	8.6
3	F	61	VAL	8.6
1	Q	50	SER	8.6
2	E	357	GLY	8.6
1	A	80	GLN	8.6
2	R	254	GLY	8.6
2	E	90	GLN	8.6
3	S	335	TRP	8.5
1	D	211	SER	8.5
2	R	267	VAL	8.5
3	F	81	SER	8.5
2	O	185	LYS	8.5
3	C	385	LYS	8.5
3	S	289	ALA	8.5
1	D	50	SER	8.5
1	D	206	PRO	8.5
2	E	300	TRP	8.5

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Mol	Chain	Res	Type	RSRZ
3	F	78	ASN	8.5
2	E	202	THR	8.5
2	E	365	SER	8.5
2	B	237	GLU	8.5
3	C	67	SER	8.5
3	F	333	GLY	8.5
2	E	424	TYR	8.5
3	S	72	GLN	8.4
1	N	177	ASP	8.4
1	Q	166	GLY	8.4
3	C	32	TYR	8.4
3	C	93	ILE	8.4
3	S	373	LYS	8.4
3	F	65	GLN	8.4
2	O	234	ILE	8.4
3	P	31	ASN	8.4
1	Q	70	ASN	8.4
1	D	199	SER	8.4
1	Q	90	THR	8.4
2	B	205	THR	8.4
2	E	467	GLU	8.4
2	E	182	LEU	8.4
2	B	280	PHE	8.4
3	C	379	MET	8.4
1	N	84	LYS	8.4
1	A	159	ILE	8.3
3	C	344	LEU	8.3
1	A	49	PRO	8.3
1	D	214	THR	8.3
2	B	279	GLY	8.3
2	B	429	TYR	8.3
1	N	115	ASN	8.3
2	E	95	ARG	8.3
2	O	309	LEU	8.3
2	O	144	ASN	8.3
1	Q	93	ILE	8.3
2	B	217	GLU	8.3
3	C	275	ARG	8.3
1	Q	186	LYS	8.3
2	O	349	VAL	8.3
1	Q	109	ASN	8.3
1	D	203	GLN	8.3

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Mol	Chain	Res	Type	RSRZ
2	O	304	ASP	8.3
3	S	107	ILE	8.3
1	N	83	SER	8.3
3	S	33	GLN	8.3
1	A	164	CYS	8.2
3	C	253	TRP	8.2
2	B	176	ARG	8.2
3	S	164	SER	8.2
2	O	282	ASN	8.2
3	C	386	ILE	8.2
3	P	141	ASP	8.2
3	C	374	SER	8.2
3	C	370	ALA	8.2
2	R	107	LEU	8.2
3	C	125	ARG	8.2
3	F	62	LYS	8.2
1	Q	165	LYS	8.2
3	S	29	LEU	8.2
3	P	144	LYS	8.2
1	A	50	SER	8.2
1	Q	79	TYR	8.2
1	D	51	GLY	8.2
2	O	184	SER	8.2
2	O	419	PRO	8.2
1	Q	92	ASN	8.2
3	C	310	MET	8.2
3	F	72	GLN	8.1
3	S	205	LYS	8.1
2	O	288	GLU	8.1
1	A	216	PRO	8.1
1	Q	45	ASN	8.1
3	P	186	GLY	8.1
1	Q	197	LEU	8.1
1	D	58	ILE	8.1
3	S	307	HIS	8.1
3	S	75	LYS	8.1
3	F	337	ASN	8.1
1	A	72	LEU	8.1
3	C	60	LEU	8.1
3	S	196	LYS	8.1
2	E	399	LYS	8.1
3	S	299	SER	8.0

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Mol	Chain	Res	Type	RSRZ
1	A	93	ILE	8.0
2	B	373	THR	8.0
2	O	437	GLY	8.0
1	Q	211	SER	8.0
1	A	69	ILE	8.0
3	P	89	MET	8.0
3	S	125	ARG	8.0
1	Q	177	ASP	8.0
3	F	258	SER	8.0
3	C	72	GLN	8.0
1	A	211	SER	8.0
2	B	198	GLU	8.0
2	O	281	GLY	8.0
2	B	196	GLN	8.0
3	F	33	GLN	8.0
3	P	30	ASN	8.0
3	C	74	SER	8.0
3	S	67	SER	8.0
2	R	399	LYS	7.9
3	F	66	ILE	7.9
2	E	134	GLY	7.9
1	A	63	GLN	7.9
1	Q	146	GLN	7.9
1	D	135	ARG	7.9
2	E	111	VAL	7.9
2	E	332	LEU	7.9
3	S	47	LEU	7.9
3	C	42	THR	7.9
2	O	412	ASN	7.9
1	D	221	PHE	7.9
1	D	77	PHE	7.9
3	C	49	GLN	7.9
3	C	120	LYS	7.9
3	P	33	GLN	7.9
1	Q	51	GLY	7.9
1	Q	89	LEU	7.9
1	N	79	TYR	7.9
2	B	193	VAL	7.9
1	N	198	PRO	7.9
2	O	111	VAL	7.9
3	F	264	SER	7.9
3	P	59	GLU	7.9

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Mol	Chain	Res	Type	RSRZ
2	E	375	THR	7.8
3	S	121	ILE	7.8
3	C	129	VAL	7.8
3	S	64	ILE	7.8
2	E	97	GLU	7.8
3	P	70	PRO	7.8
2	B	259	ILE	7.8
2	E	456	LYS	7.8
1	A	212	THR	7.8
3	C	366	GLY	7.8
3	P	32	TYR	7.8
1	N	69	ILE	7.8
2	R	108	ARG	7.8
1	D	216	PRO	7.8
2	B	323	ASP	7.8
3	F	57	ALA	7.8
3	F	73	PRO	7.8
3	S	38	LYS	7.8
1	Q	127	ARG	7.8
2	B	386	ASP	7.7
3	C	341	ALA	7.7
1	Q	151	LYS	7.7
3	F	298	ASP	7.7
3	F	354	TYR	7.7
3	P	396	GLU	7.7
2	B	225	GLU	7.7
3	S	70	PRO	7.7
2	O	361	ILE	7.7
3	C	232	LYS	7.7
2	B	154	GLU	7.7
1	A	166	GLY	7.7
1	D	137	ASN	7.7
3	P	341	ALA	7.7
3	C	51	GLU	7.7
3	F	47	LEU	7.7
2	E	107	LEU	7.7
1	Q	216	PRO	7.7
3	S	354	TYR	7.7
3	F	309	GLY	7.6
1	Q	129	VAL	7.6
3	P	340	HIS	7.6
1	Q	126	ARG	7.6

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Mol	Chain	Res	Type	RSRZ
1	N	191	VAL	7.6
3	S	82	ALA	7.6
3	C	132	GLU	7.6
1	Q	214	THR	7.6
2	B	216	LYS	7.6
3	C	76	PRO	7.6
3	C	36	VAL	7.6
3	F	56	GLU	7.6
1	D	156	ASP	7.6
2	E	88	LYS	7.6
3	S	249	GLN	7.6
3	F	45	GLY	7.6
3	F	42	THR	7.6
3	S	73	PRO	7.6
3	P	86	SER	7.6
3	P	250	LEU	7.6
2	B	410	TRP	7.6
1	D	155	VAL	7.6
2	O	385	TYR	7.5
3	S	202	LEU	7.5
1	A	59	ASP	7.5
2	O	172	LEU	7.5
2	R	166	ASN	7.5
3	C	141	ASP	7.5
3	P	94	MET	7.5
1	D	220	GLU	7.5
3	P	44	GLU	7.5
1	Q	124	ILE	7.5
1	D	212	THR	7.5
3	S	68	TYR	7.5
2	B	319	ILE	7.5
3	S	36	VAL	7.5
3	S	45	GLY	7.5
2	R	276	TYR	7.5
1	N	179	GLU	7.5
1	N	166	GLY	7.5
3	S	83	THR	7.5
1	Q	220	GLU	7.5
2	R	270	GLY	7.5
3	S	146	HIS	7.5
2	B	339	GLN	7.5
3	C	359	THR	7.5

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Mol	Chain	Res	Type	RSRZ
3	C	348	TYR	7.5
1	D	223	SER	7.5
1	D	79	TYR	7.4
1	Q	96	LEU	7.4
2	E	294	GLY	7.4
1	D	201	ASP	7.4
3	P	29	LEU	7.4
3	F	107	ILE	7.4
3	C	131	LEU	7.4
2	B	406	GLY	7.4
2	R	95	ARG	7.4
2	E	221	ILE	7.4
3	P	71	ASP	7.4
3	C	41	ARG	7.4
3	C	351	GLY	7.4
2	O	467	GLU	7.4
3	S	224	THR	7.4
2	O	345	TYR	7.4
2	O	427	GLY	7.3
3	F	76	PRO	7.3
3	S	267	VAL	7.3
1	A	79	TYR	7.3
3	C	376	TRP	7.3
2	E	349	VAL	7.3
1	D	55	LYS	7.3
3	S	255	GLY	7.3
3	C	255	GLY	7.3
2	B	342	ALA	7.3
3	S	198	LEU	7.3
3	P	123	ASN	7.3
1	Q	201	ASP	7.3
3	F	186	GLY	7.3
3	F	230	ASN	7.3
3	C	127	LYS	7.3
1	N	132	GLN	7.2
2	O	350	SER	7.2
3	F	64	ILE	7.2
2	E	428	ALA	7.2
3	F	392	LEU	7.2
2	R	88	LYS	7.2
2	R	185	LYS	7.2
3	F	227	TRP	7.2

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Mol	Chain	Res	Type	RSRZ
1	A	73	ARG	7.2
1	Q	212	THR	7.2
2	B	393	LYS	7.2
2	E	102	LYS	7.2
1	Q	53	ARG	7.2
3	C	307	HIS	7.2
2	R	364	ALA	7.2
1	D	209	LYS	7.2
1	A	210	MET	7.2
1	Q	215	GLY	7.2
3	F	87	LYS	7.2
3	S	59	GLU	7.2
2	E	94	VAL	7.2
2	O	197	MET	7.1
3	F	46	ILE	7.1
3	C	114	TYR	7.1
1	Q	148	VAL	7.1
3	C	73	PRO	7.1
3	C	85	ASN	7.1
1	Q	140	GLN	7.1
1	Q	203	GLN	7.1
3	C	45	GLY	7.1
1	A	190	GLN	7.1
2	E	100	ILE	7.1
2	E	104	ILE	7.1
1	A	105	ASN	7.1
1	N	164	CYS	7.1
1	N	219	ARG	7.1
2	O	262	ARG	7.1
1	D	217	VAL	7.0
3	S	44	GLU	7.0
3	P	252	ASP	7.0
1	D	140	GLN	7.0
2	E	458	SER	7.0
2	R	313	GLY	7.0
3	F	28	PHE	7.0
2	B	461	ILE	7.0
3	S	60	LEU	7.0
2	R	89	LEU	7.0
3	P	263	ALA	7.0
1	D	215	GLY	7.0
1	Q	208	LEU	7.0

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Mol	Chain	Res	Type	RSRZ
3	S	40	LEU	7.0
3	F	80	GLU	7.0
2	R	324	TRP	7.0
2	E	403	LYS	7.0
3	C	355	SER	7.0
1	A	203	GLN	7.0
2	O	121	THR	7.0
3	P	191	TRP	7.0
1	Q	101	PHE	7.0
3	P	72	GLN	7.0
1	N	218	PRO	7.0
1	N	110	THR	7.0
2	E	372	ARG	7.0
3	S	180	VAL	7.0
3	F	164	SER	6.9
3	C	202	LEU	6.9
1	N	192	ILE	6.9
1	D	67	SER	6.9
2	R	113	SER	6.9
1	A	220	GLU	6.9
3	S	63	ALA	6.9
3	F	178	PHE	6.9
2	O	305	ARG	6.9
3	P	306	SER	6.9
1	Q	84	LYS	6.9
1	A	209	LYS	6.9
1	D	69	ILE	6.9
2	B	422	ARG	6.8
3	F	311	GLN	6.8
3	F	40	LEU	6.8
3	F	123	ASN	6.8
3	C	292	GLY	6.8
3	F	82	ALA	6.8
2	R	111	VAL	6.8
1	N	221	PHE	6.8
2	O	128	LEU	6.8
1	Q	104	ALA	6.8
1	D	76	LEU	6.8
2	B	430	THR	6.8
3	F	252	ASP	6.8
2	B	188	LYS	6.8
1	D	72	LEU	6.8

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Mol	Chain	Res	Type	RSRZ
1	Q	150	MET	6.8
3	S	371	THR	6.8
2	O	244	ARG	6.8
2	O	160	ILE	6.8
3	F	366	GLY	6.8
2	E	338	VAL	6.7
3	F	288	ASP	6.7
1	N	91	LYS	6.7
3	F	32	TYR	6.7
3	S	324	GLY	6.7
3	S	57	ALA	6.7
1	Q	188	LEU	6.7
2	B	201	ARG	6.7
3	P	246	LEU	6.7
1	D	207	ILE	6.7
1	A	76	LEU	6.7
3	F	344	LEU	6.7
2	B	327	ASP	6.7
3	C	61	VAL	6.6
3	F	103	HIS	6.6
2	R	239	SER	6.6
3	S	62	LYS	6.6
1	A	51	GLY	6.6
3	C	57	ALA	6.6
3	S	283	GLY	6.6
1	N	223	SER	6.6
3	C	58	ARG	6.6
2	B	317	LEU	6.6
3	C	56	GLU	6.6
2	B	93	LEU	6.6
3	F	254	ASN	6.6
2	O	194	SER	6.6
3	F	209	ILE	6.6
3	F	36	VAL	6.6
3	P	73	PRO	6.6
1	D	202	ILE	6.6
3	C	281	PHE	6.6
3	C	349	TYR	6.6
2	R	261	ASN	6.6
2	B	281	GLY	6.6
2	B	437	GLY	6.6
1	A	215	GLY	6.6

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Mol	Chain	Res	Type	RSRZ
1	Q	163	SER	6.6
1	Q	54	MET	6.6
3	C	78	ASN	6.6
3	P	119	GLN	6.5
3	S	56	GLU	6.5
1	Q	100	ASP	6.5
2	R	101	ARG	6.5
3	C	199	ASP	6.5
2	R	316	LYS	6.5
3	C	179	LEU	6.5
2	O	415	HIS	6.5
3	C	229	GLY	6.5
2	B	286	ASN	6.5
1	Q	200	ARG	6.5
2	E	281	GLY	6.5
2	B	88	LYS	6.5
1	Q	207	ILE	6.5
1	Q	55	LYS	6.5
3	C	377	TYR	6.5
2	B	333	TYR	6.5
1	D	210	MET	6.5
1	A	124	ILE	6.4
2	E	192	ASP	6.4
2	E	373	THR	6.4
1	A	214	THR	6.4
2	E	93	LEU	6.4
3	P	60	LEU	6.4
2	O	226	GLY	6.4
2	E	101	ARG	6.4
3	F	377	TYR	6.4
1	A	85	ASP	6.4
1	D	47	LYS	6.4
2	E	205	THR	6.4
2	E	125	ILE	6.4
2	O	386	ASP	6.4
1	A	55	LYS	6.4
3	P	175	LYS	6.4
3	S	227	TRP	6.4
1	D	191	VAL	6.4
3	S	41	ARG	6.4
3	C	66	ILE	6.4
3	C	266	LYS	6.4

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	D	224	GLN	6.4
3	C	75	LYS	6.4
3	S	355	SER	6.3
1	D	94	VAL	6.3
1	A	54	MET	6.3
2	B	403	LYS	6.3
2	E	282	ASN	6.3
3	F	29	LEU	6.3
3	P	382	THR	6.3
1	N	208	LEU	6.3
1	Q	221	PHE	6.3
3	C	62	LYS	6.3
2	B	377	HIS	6.3
3	F	269	GLY	6.3
2	R	460	MET	6.3
2	O	449	GLY	6.3
1	D	71	LYS	6.3
1	N	220	GLU	6.3
1	Q	115	ASN	6.3
2	O	109	ASN	6.3
2	E	187	GLN	6.3
2	E	376	ILE	6.3
1	N	202	ILE	6.3
1	A	213	ILE	6.3
1	A	91	LYS	6.2
3	F	101	SER	6.2
3	C	103	HIS	6.2
1	D	222	LYS	6.2
3	P	373	LYS	6.2
3	C	186	GLY	6.2
1	D	73	ARG	6.2
1	N	222	LYS	6.2
2	R	235	GLN	6.2
1	Q	149	ASP	6.2
3	F	75	LYS	6.2
2	B	264	ASP	6.2
3	P	61	VAL	6.2
2	R	206	VAL	6.2
1	D	219	ARG	6.2
1	A	125	LEU	6.2
3	S	129	VAL	6.2
3	S	79	ILE	6.2

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Mol	Chain	Res	Type	RSRZ
3	C	97	GLU	6.2
3	C	382	THR	6.1
3	S	351	GLY	6.1
1	A	71	LYS	6.1
2	O	403	LYS	6.1
3	C	40	LEU	6.1
2	B	361	ILE	6.1
1	D	176	VAL	6.1
2	B	415	HIS	6.1
1	Q	217	VAL	6.1
3	P	58	ARG	6.1
3	F	375	ARG	6.1
2	B	368	VAL	6.1
3	S	61	VAL	6.1
1	N	171	ALA	6.1
1	D	113	GLN	6.1
1	D	204	TYR	6.1
2	R	419	PRO	6.1
3	F	139	CYS	6.1
3	S	197	ARG	6.1
2	B	215	GLY	6.0
3	S	217	HIS	6.0
3	F	55	SER	6.0
3	P	127	LYS	6.0
1	Q	57	LEU	6.0
2	R	338	VAL	6.0
3	F	291	ASP	6.0
3	P	293	TYR	6.0
3	C	329	GLN	6.0
3	F	277	THR	6.0
3	C	94	MET	6.0
3	P	82	ALA	6.0
1	N	224	GLN	6.0
1	Q	112	LYS	6.0
3	F	119	GLN	6.0
1	N	217	VAL	6.0
1	Q	222	LYS	6.0
1	D	154	GLU	6.0
1	Q	205	LEU	6.0
3	F	79	ILE	6.0
2	R	175	LEU	6.0
1	A	207	ILE	6.0

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Mol	Chain	Res	Type	RSRZ
1	D	122	ILE	6.0
3	F	147	ASP	6.0
3	S	266	LYS	6.0
3	C	156	VAL	5.9
3	F	130	GLN	5.9
3	S	58	ARG	5.9
1	D	53	ARG	5.9
3	S	340	HIS	5.9
2	O	217	GLU	5.9
1	N	199	SER	5.9
2	O	212	VAL	5.9
3	F	369	TRP	5.9
2	E	250	LYS	5.9
2	B	344	LYS	5.9
1	A	102	ALA	5.9
2	B	284	ALA	5.9
3	S	189	ASN	5.9
2	B	204	CYS	5.9
2	O	173	ARG	5.9
1	N	120	SER	5.9
3	F	342	GLY	5.8
3	C	115	ASN	5.8
1	Q	202	ILE	5.8
2	B	212	VAL	5.8
1	D	139	LEU	5.8
1	Q	167	SER	5.8
1	N	74	ASP	5.8
3	S	250	LEU	5.8
3	F	362	GLY	5.8
1	Q	219	ARG	5.8
3	P	106	THR	5.8
2	B	296	PRO	5.8
3	P	166	LEU	5.8
1	N	58	ILE	5.8
3	C	128	VAL	5.8
3	F	220	PRO	5.8
3	P	223	ASN	5.8
3	S	183	GLU	5.8
3	F	355	SER	5.8
1	A	176	VAL	5.8
2	E	378	ASN	5.7
2	R	301	LEU	5.7

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Mol	Chain	Res	Type	RSRZ
3	P	172	LEU	5.7
1	A	111	PHE	5.7
2	E	191	SER	5.7
1	Q	91	LYS	5.7
1	Q	122	ILE	5.7
2	B	147	ASN	5.7
1	D	56	GLY	5.7
3	C	194	PHE	5.7
3	C	149	THR	5.7
2	O	182	LEU	5.7
1	A	53	ARG	5.7
1	Q	204	TYR	5.7
2	O	428	ALA	5.7
3	S	46	ILE	5.7
3	F	380	LYS	5.6
3	S	258	SER	5.6
3	S	191	TRP	5.6
1	D	205	LEU	5.6
2	R	285	THR	5.6
3	C	168	PHE	5.6
3	S	122	VAL	5.6
1	D	91	LYS	5.6
3	C	169	ILE	5.6
3	P	139	CYS	5.6
1	A	217	VAL	5.6
2	O	335	GLY	5.6
3	C	50	VAL	5.6
2	B	251	THR	5.6
3	F	317	SER	5.6
1	Q	65	PHE	5.6
2	O	362	GLU	5.6
2	R	237	GLU	5.6
2	R	204	CYS	5.6
1	Q	209	LYS	5.5
1	N	122	ILE	5.5
2	E	198	GLU	5.5
2	R	128	LEU	5.5
2	B	349	VAL	5.5
1	N	195	ASN	5.5
2	E	203	PRO	5.5
3	F	188	GLY	5.5
2	R	157	GLN	5.5

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Mol	Chain	Res	Type	RSRZ
2	B	267	VAL	5.5
2	B	236	PRO	5.5
2	O	166	ASN	5.5
3	P	227	TRP	5.5
2	R	259	ILE	5.5
1	D	68	ARG	5.5
2	B	149	TYR	5.4
3	C	126	ASP	5.4
1	N	134	GLN	5.4
2	O	459	LYS	5.4
2	B	252	GLU	5.4
2	O	424	TYR	5.4
2	R	191	SER	5.4
2	R	279	GLY	5.4
3	S	89	MET	5.4
2	E	275	PRO	5.4
3	P	79	ILE	5.4
2	O	292	TYR	5.4
1	D	187	GLN	5.4
1	Q	71	LYS	5.4
3	C	223	ASN	5.4
3	C	264	SER	5.4
3	C	367	ILE	5.4
3	P	229	GLY	5.4
1	Q	213	ILE	5.4
2	O	433	MET	5.3
2	B	160	ILE	5.3
2	O	275	PRO	5.3
3	F	290	PHE	5.3
3	C	195	GLN	5.3
2	O	447	TRP	5.3
1	A	112	LYS	5.3
2	B	291	LYS	5.3
3	P	266	LYS	5.3
3	P	112	GLU	5.3
1	Q	223	SER	5.3
2	O	411	TYR	5.3
1	Q	62	ASP	5.3
3	C	155	ASP	5.3
1	A	224	GLN	5.3
2	B	258	VAL	5.2
2	O	372	ARG	5.2

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Mol	Chain	Res	Type	RSRZ
2	B	102	LYS	5.2
2	R	242	PRO	5.2
2	R	209	ASN	5.2
2	B	366	GLN	5.2
3	C	265	PHE	5.2
2	O	258	VAL	5.2
3	C	360	PRO	5.2
3	F	117	ASN	5.2
1	N	125	LEU	5.2
1	N	205	LEU	5.2
3	F	168	PHE	5.2
3	P	170	ARG	5.2
3	S	277	THR	5.2
2	E	114	VAL	5.2
2	O	406	GLY	5.2
3	P	52	ASN	5.2
2	B	346	GLN	5.2
2	R	302	GLY	5.2
1	N	148	VAL	5.2
2	E	168	ILE	5.1
2	R	321	MET	5.1
2	O	203	PRO	5.1
1	A	160	LYS	5.1
3	C	362	GLY	5.1
1	A	192	ILE	5.1
1	A	98	ARG	5.1
1	Q	125	LEU	5.1
2	B	338	VAL	5.1
2	E	301	LEU	5.1
3	P	232	LYS	5.1
1	A	86	SER	5.1
3	P	177	GLN	5.0
1	Q	153	LEU	5.0
2	B	94	VAL	5.0
2	E	446	ASN	5.0
3	S	332	SER	5.0
1	N	124	ILE	5.0
2	E	359	ALA	5.0
2	O	325	LYS	5.0
1	D	200	ARG	5.0
3	F	267	VAL	5.0
1	D	167	SER	5.0

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Mol	Chain	Res	Type	RSRZ
3	P	262	TYR	5.0
2	R	348	SER	5.0
1	Q	143	VAL	4.9
3	C	192	THR	4.9
1	N	94	VAL	4.9
1	A	158	ASP	4.9
2	B	115	SER	4.9
3	S	284	GLY	4.9
3	P	338	LYS	4.9
3	C	245	VAL	4.9
3	P	276	LEU	4.9
1	D	182	LYS	4.9
3	S	84	LYS	4.9
2	R	231	MET	4.9
1	D	131	GLU	4.9
2	B	282	ASN	4.8
3	C	83	THR	4.8
2	E	209	ASN	4.8
3	C	187	SER	4.8
2	O	152	HIS	4.8
2	R	379	SER	4.8
1	Q	147	LEU	4.8
2	B	308	GLN	4.8
2	O	246	TYR	4.8
2	R	289	GLY	4.8
2	E	333	TYR	4.8
1	A	165	LYS	4.8
3	C	322	TYR	4.8
3	F	115	ASN	4.8
1	D	165	LYS	4.8
3	S	301	ASP	4.8
1	A	118	LEU	4.8
3	S	115	ASN	4.8
3	P	289	ALA	4.8
2	O	418	ASN	4.8
3	F	328	GLU	4.8
3	F	326	CYS	4.8
2	B	375	THR	4.7
3	C	79	ILE	4.7
1	N	157	ILE	4.7
2	B	172	LEU	4.7
2	O	187	GLN	4.7

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Mol	Chain	Res	Type	RSRZ
3	P	277	THR	4.7
1	A	84	LYS	4.7
1	A	169	SER	4.7
1	A	47	LYS	4.7
3	F	196	LYS	4.7
2	B	105	GLU	4.7
2	E	246	TYR	4.7
3	F	145	ILE	4.7
1	N	93	ILE	4.7
1	Q	128	LYS	4.7
2	B	459	LYS	4.7
2	E	124	TYR	4.7
3	C	196	LYS	4.6
2	B	456	LYS	4.6
2	B	370	GLU	4.6
3	F	275	ARG	4.6
2	O	336	PHE	4.6
2	O	256	TRP	4.6
1	D	57	LEU	4.6
2	R	159	TYR	4.6
1	A	143	VAL	4.6
3	P	268	THR	4.6
1	N	77	PHE	4.6
1	N	159	ILE	4.6
3	C	251	GLU	4.6
3	C	154	GLN	4.6
1	N	152	ARG	4.5
3	P	101	SER	4.5
3	C	181	TYR	4.5
1	A	219	ARG	4.5
2	E	408	GLY	4.5
3	S	219	SER	4.5
1	A	101	PHE	4.5
2	R	146	VAL	4.5
3	F	221	THR	4.5
3	C	146	HIS	4.5
3	C	118	SER	4.5
2	B	309	LEU	4.5
1	A	167	SER	4.5
2	E	259	ILE	4.5
2	E	164	VAL	4.5
3	P	200	GLY	4.5

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
2	R	435	LYS	4.4
1	A	183	ASN	4.4
1	N	119	ARG	4.4
2	B	445	MET	4.4
1	Q	152	ARG	4.4
2	B	182	LEU	4.4
2	O	146	VAL	4.4
3	S	271	ASN	4.4
2	R	328	LYS	4.4
3	S	145	ILE	4.4
2	B	203	PRO	4.4
1	D	100	ASP	4.4
3	F	134	ASN	4.4
2	E	155	LYS	4.4
3	C	139	CYS	4.4
3	C	96	TYR	4.4
1	Q	160	LYS	4.3
2	R	144	ASN	4.3
2	R	362	GLU	4.3
3	F	204	PHE	4.3
2	O	422	ARG	4.3
2	E	443	VAL	4.3
1	Q	224	GLN	4.3
1	N	117	ASP	4.3
2	B	118	SER	4.3
2	O	464	TYR	4.3
1	A	137	ASN	4.3
2	B	300	TRP	4.3
3	C	375	ARG	4.3
2	O	110	THR	4.3
3	P	231	GLU	4.3
2	O	326	GLY	4.3
3	P	369	TRP	4.3
3	S	256	ARG	4.3
2	E	153	LEU	4.3
2	E	272	LYS	4.3
3	F	48	TYR	4.3
1	A	150	MET	4.3
2	O	450	SER	4.3
3	P	54	THR	4.3
3	P	343	HIS	4.3
3	S	223	ASN	4.3

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Mol	Chain	Res	Type	RSRZ
2	B	467	GLU	4.2
3	F	143	VAL	4.2
2	B	234	ILE	4.2
1	N	155	VAL	4.2
3	C	287	GLY	4.2
2	E	186	ILE	4.2
3	P	108	ARG	4.2
2	O	394	THR	4.2
3	P	314	THR	4.2
2	O	334	GLU	4.2
2	E	247	CYS	4.2
3	C	198	LEU	4.2
3	F	233	ILE	4.2
1	D	158	ASP	4.2
2	O	438	THR	4.2
1	D	118	LEU	4.2
2	E	289	GLY	4.2
2	E	208	CYS	4.2
1	A	152	ARG	4.2
2	E	178	ILE	4.1
1	N	181	TYR	4.1
2	O	306	ILE	4.1
3	F	207	ASN	4.1
3	F	183	GLU	4.1
1	Q	68	ARG	4.1
3	C	378	SER	4.1
3	F	367	ILE	4.1
1	D	148	VAL	4.1
1	N	60	GLU	4.1
2	O	186	ILE	4.1
3	F	192	THR	4.1
2	E	117	THR	4.1
3	C	280	TYR	4.1
3	C	28	PHE	4.1
3	P	102	THR	4.1
2	R	425	TRP	4.1
3	P	122	VAL	4.1
3	S	166	LEU	4.1
2	B	362	GLU	4.1
3	C	299	SER	4.1
1	D	126	ARG	4.1
1	A	182	LYS	4.1

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Mol	Chain	Res	Type	RSRZ
3	P	204	PHE	4.1
1	Q	63	GLN	4.1
1	A	140	GLN	4.1
1	A	162	ARG	4.0
2	O	354	GLY	4.0
2	E	309	LEU	4.0
2	E	130	ASN	4.0
3	P	48	TYR	4.0
3	C	290	PHE	4.0
3	F	182	CYS	4.0
3	S	302	LYS	4.0
2	B	185	LYS	4.0
3	S	273	LYS	4.0
1	A	221	PHE	4.0
3	S	236	ILE	4.0
2	E	284	ALA	4.0
3	C	246	LEU	4.0
1	Q	98	ARG	4.0
3	C	369	TRP	4.0
1	Q	69	ILE	4.0
2	B	178	ILE	4.0
1	A	223	SER	4.0
2	B	271	ARG	4.0
2	O	221	ILE	4.0
3	S	182	CYS	4.0
2	B	340	ASN	4.0
3	P	195	GLN	4.0
1	A	115	ASN	3.9
1	N	103	LYS	3.9
1	A	144	ARG	3.9
2	O	319	ILE	3.9
2	O	232	TYR	3.9
1	D	159	ILE	3.9
2	B	432	ASP	3.9
3	F	381	LYS	3.9
3	F	251	GLU	3.9
2	E	154	GLU	3.9
2	O	132	TRP	3.9
3	P	98	THR	3.9
2	B	358	ASN	3.9
1	A	149	ASP	3.9
1	A	135	ARG	3.9

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Mol	Chain	Res	Type	RSRZ
1	A	181	TYR	3.9
3	S	143	VAL	3.9
3	P	281	PHE	3.9
2	B	174	VAL	3.8
1	D	145	ASP	3.8
2	O	430	THR	3.8
1	Q	119	ARG	3.8
1	A	95	GLU	3.8
1	N	71	LYS	3.8
3	P	116	SER	3.8
3	F	41	ARG	3.8
2	B	186	ILE	3.8
1	N	165	LYS	3.8
2	E	298	GLU	3.8
2	O	155	LYS	3.8
2	B	318	LEU	3.8
1	N	140	GLN	3.8
1	N	73	ARG	3.8
2	B	228	THR	3.8
2	R	156	HIS	3.8
2	E	185	LYS	3.8
2	O	297	GLY	3.8
3	C	231	GLU	3.7
3	F	166	LEU	3.7
1	Q	66	THR	3.7
3	C	276	LEU	3.7
3	F	162	LYS	3.7
2	O	296	PRO	3.7
2	O	211	PRO	3.7
2	B	434	ALA	3.7
3	P	129	VAL	3.7
3	F	169	ILE	3.7
3	S	352	GLY	3.7
1	A	136	ILE	3.7
2	B	466	PRO	3.7
1	Q	131	GLU	3.7
2	E	135	ARG	3.7
1	N	158	ASP	3.6
2	B	351	LYS	3.6
2	E	137	ASN	3.6
3	P	196	LYS	3.6
3	S	247	ARG	3.6

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Mol	Chain	Res	Type	RSRZ
2	E	136	GLN	3.6
2	R	347	LEU	3.6
3	C	203	ASP	3.6
3	C	207	ASN	3.6
1	D	127	ARG	3.6
3	C	259	THR	3.6
1	D	138	LEU	3.5
3	S	43	LEU	3.5
1	D	119	ARG	3.5
2	R	356	ALA	3.5
3	P	65	GLN	3.5
1	N	62	ASP	3.5
1	A	157	ILE	3.5
2	O	235	GLN	3.5
3	C	100	ILE	3.5
1	N	108	ASP	3.5
3	F	111	GLN	3.5
2	E	433	MET	3.5
3	F	374	SER	3.5
2	E	339	GLN	3.5
3	S	260	ALA	3.5
1	A	145	ASP	3.5
1	N	92	ASN	3.5
3	F	307	HIS	3.5
2	B	189	LEU	3.4
3	F	363	TYR	3.4
3	P	374	SER	3.4
2	B	111	VAL	3.4
2	E	347	LEU	3.4
2	O	148	GLU	3.4
3	C	336	MET	3.4
1	Q	72	LEU	3.4
2	O	338	VAL	3.4
1	N	81	LYS	3.4
1	N	156	ASP	3.4
1	N	95	GLU	3.4
3	S	177	GLN	3.4
1	Q	59	ASP	3.4
3	C	274	TYR	3.4
3	P	181	TYR	3.4
2	E	260	GLN	3.3
3	C	208	TRP	3.3

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Mol	Chain	Res	Type	RSRZ
2	R	141	ASP	3.3
3	S	181	TYR	3.3
3	C	387	ILE	3.3
3	C	304	PHE	3.3
3	F	273	LYS	3.3
2	R	300	TRP	3.3
3	P	125	ARG	3.3
1	D	143	VAL	3.3
1	A	173	GLU	3.3
1	D	129	VAL	3.3
2	O	332	LEU	3.3
3	C	188	GLY	3.3
2	E	285	THR	3.2
2	E	360	LEU	3.2
2	O	114	VAL	3.2
1	N	127	ARG	3.2
2	B	292	TYR	3.2
3	S	269	GLY	3.2
3	P	203	ASP	3.2
2	B	219	GLU	3.2
2	O	378	ASN	3.2
2	B	314	PRO	3.2
2	E	279	GLY	3.2
3	S	285	ASP	3.2
2	O	293	CYS	3.2
1	N	141	LYS	3.2
2	E	149	TYR	3.2
2	O	260	GLN	3.2
3	S	139	CYS	3.2
2	B	443	VAL	3.1
3	F	319	ASN	3.1
3	C	262	TYR	3.1
3	P	282	ILE	3.1
2	E	321	MET	3.1
2	O	359	ALA	3.1
3	C	252	ASP	3.1
2	E	141	ASP	3.1
2	R	431	TRP	3.1
3	P	323	ASP	3.1
2	B	242	PRO	3.1
1	N	154	GLU	3.1
3	C	99	LEU	3.1

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Mol	Chain	Res	Type	RSRZ
3	C	106	THR	3.1
2	E	292	TYR	3.1
2	B	305	ARG	3.1
3	S	210	GLN	3.0
2	O	178	ILE	3.0
3	P	193	VAL	3.0
2	B	155	LYS	3.0
1	A	171	ALA	3.0
1	Q	156	ASP	3.0
1	A	202	ILE	3.0
3	F	210	GLN	3.0
1	D	60	GLU	3.0
2	E	335	GLY	3.0
1	N	186	LYS	3.0
3	C	332	SER	3.0
3	P	145	ILE	3.0
3	S	144	LYS	3.0
1	Q	172	LEU	3.0
3	F	373	LYS	3.0
2	E	262	ARG	3.0
2	O	416	ALA	3.0
2	O	145	VAL	3.0
1	A	109	ASN	3.0
3	P	107	ILE	3.0
1	D	92	ASN	2.9
1	Q	111	PHE	2.9
2	E	183	ARG	2.9
3	P	128	VAL	2.9
1	A	168	CYS	2.9
2	O	429	TYR	2.9
3	C	326	CYS	2.9
1	A	201	ASP	2.9
2	R	227	GLU	2.9
2	O	222	ILE	2.9
2	B	378	ASN	2.9
3	F	112	GLU	2.9
3	S	193	VAL	2.9
3	S	383	THR	2.9
2	R	152	HIS	2.9
3	C	205	LYS	2.9
1	A	154	GLU	2.9
3	S	208	TRP	2.9

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Mol	Chain	Res	Type	RSRZ
2	B	197	MET	2.9
2	E	133	LYS	2.9
3	C	233	ILE	2.9
2	E	263	GLN	2.8
3	C	288	ASP	2.8
3	F	371	THR	2.8
3	P	103	HIS	2.8
3	C	211	TYR	2.8
2	O	445	MET	2.8
1	D	146	GLN	2.8
2	R	349	VAL	2.8
2	O	460	MET	2.8
1	N	90	THR	2.8
2	O	451	TRP	2.8
3	F	133	ALA	2.8
1	A	96	LEU	2.8
2	R	147	ASN	2.8
2	B	232	TYR	2.8
3	C	90	MET	2.8
2	R	171	LYS	2.8
2	O	151	SER	2.8
2	O	284	ALA	2.8
3	S	222	GLY	2.8
1	D	183	ASN	2.8
2	R	263	GLN	2.8
3	F	292	GLY	2.8
2	O	327	ASP	2.8
3	P	209	ILE	2.7
3	P	224	THR	2.7
3	S	245	VAL	2.7
3	S	338	LYS	2.7
3	C	31	ASN	2.7
2	E	227	GLU	2.7
1	Q	133	VAL	2.7
1	N	146	GLN	2.7
2	E	280	PHE	2.7
2	E	233	LEU	2.7
3	F	296	GLY	2.7
1	N	112	LYS	2.7
3	S	93	ILE	2.7
2	B	464	TYR	2.7
2	O	457	MET	2.7

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Mol	Chain	Res	Type	RSRZ
2	R	240	SER	2.7
3	P	47	LEU	2.6
1	N	169	SER	2.6
3	S	228	LEU	2.6
1	A	99	GLY	2.6
2	B	380	MET	2.6
3	C	117	ASN	2.6
1	D	65	PHE	2.6
3	S	253	TRP	2.6
2	E	386	ASP	2.6
1	N	87	ASN	2.6
2	E	267	VAL	2.6
3	C	271	ASN	2.6
3	S	238	THR	2.6
2	O	201	ARG	2.6
3	C	256	ARG	2.6
2	R	290	LYS	2.6
2	B	253	LYS	2.6
3	F	197	ARG	2.6
2	E	354	GLY	2.6
2	R	210	ILE	2.5
3	F	181	TYR	2.5
3	P	288	ASP	2.5
3	F	161	ALA	2.5
2	B	462	ARG	2.5
2	O	248	ASP	2.5
3	C	113	ILE	2.5
3	S	90	MET	2.5
2	B	272	LYS	2.5
2	B	426	GLY	2.5
1	Q	67	SER	2.5
2	E	379	SER	2.5
3	S	331	GLY	2.5
3	P	205	LYS	2.5
1	A	97	MET	2.5
2	B	177	SER	2.5
2	O	154	GLU	2.5
3	C	363	TYR	2.5
1	N	178	LEU	2.5
2	O	176	ARG	2.5
3	F	281	PHE	2.5
2	R	207	THR	2.5

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Mol	Chain	Res	Type	RSRZ
2	B	101	ARG	2.5
3	F	224	THR	2.5
1	D	192	ILE	2.4
3	F	146	HIS	2.4
2	B	337	THR	2.4
1	D	149	ASP	2.4
1	Q	110	THR	2.4
3	C	289	ALA	2.4
1	N	136	ILE	2.4
1	D	170	ARG	2.4
2	O	174	VAL	2.4
3	S	91	GLU	2.4
3	S	233	ILE	2.4
2	O	276	TYR	2.4
2	B	419	PRO	2.4
2	E	387	ARG	2.4
3	S	252	ASP	2.4
1	N	153	LEU	2.4
3	C	101	SER	2.4
2	E	293	CYS	2.4
1	D	141	LYS	2.3
2	R	426	GLY	2.3
2	B	224	ASN	2.3
2	B	244	ARG	2.3
3	P	214	GLY	2.3
2	B	222	ILE	2.3
3	P	111	GLN	2.3
2	B	246	TYR	2.3
3	F	329	GLN	2.3
1	D	160	LYS	2.3
3	F	108	ARG	2.3
3	F	265	PHE	2.3
2	R	155	LYS	2.2
2	B	320	GLU	2.2
3	C	170	ARG	2.2
2	B	440	ASP	2.2
3	F	144	LYS	2.2
3	F	249	GLN	2.2
1	D	144	ARG	2.2
3	S	336	MET	2.2
2	B	290	LYS	2.2
1	N	201	ASP	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	129	VAL	2.2
2	O	370	GLU	2.2
2	R	372	ARG	2.2
3	F	142	THR	2.2
1	D	162	ARG	2.2
3	P	235	LEU	2.1
1	N	143	VAL	2.1
1	Q	158	ASP	2.1
2	E	299	TYR	2.1
1	N	86	SER	2.1
2	B	328	LYS	2.1
2	E	302	GLY	2.1
3	F	216	GLY	2.1
2	E	380	MET	2.1
1	N	105	ASN	2.1
2	E	363	GLY	2.1
3	C	182	CYS	2.1
2	R	331	ALA	2.1
1	Q	108	ASP	2.1
3	P	88	SER	2.1
1	A	81	LYS	2.1
1	N	88	THR	2.1
2	B	167	ASN	2.1
2	E	261	ASN	2.1
2	E	291	LYS	2.1
2	E	445	MET	2.1
1	D	59	ASP	2.1
2	R	286	ASN	2.1
1	Q	144	ARG	2.1
3	S	315	TRP	2.1
2	B	221	ILE	2.1
3	S	235	LEU	2.0
1	N	182	LYS	2.0
2	E	331	ALA	2.0
3	S	203	ASP	2.0
2	B	207	THR	2.0
3	F	356	LYS	2.0
3	F	194	PHE	2.0
3	P	194	PHE	2.0
3	F	260	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 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.