



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 15, 2017 – 06:30 am GMT

PDB ID : 3B5W
Title : Crystal Structure of Eschericia coli MsbA
Authors : Ward, A.; Reyes, C.L.; Yu, J.; Roth, C.B.; Chang, G.
Deposited on : 2007-10-26
Resolution : 5.30 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Xtriage (Phenix) : 1.9-1692
EDS : trunk28620
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
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) : recalc28949

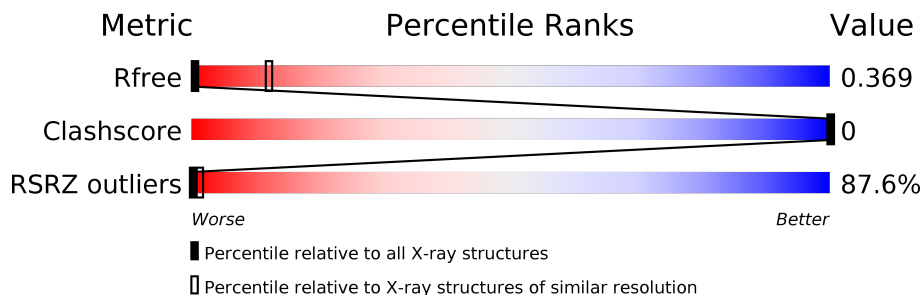
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 5.30 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}	100719	1024 (6.86-3.70)
Clashscore	112137	1009 (6.86-3.72)
RSRZ outliers	101464	1033 (6.86-3.70)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. 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	582	
1	B	582	
1	C	582	
1	D	582	
1	E	582	
1	F	582	
1	G	582	
1	H	582	

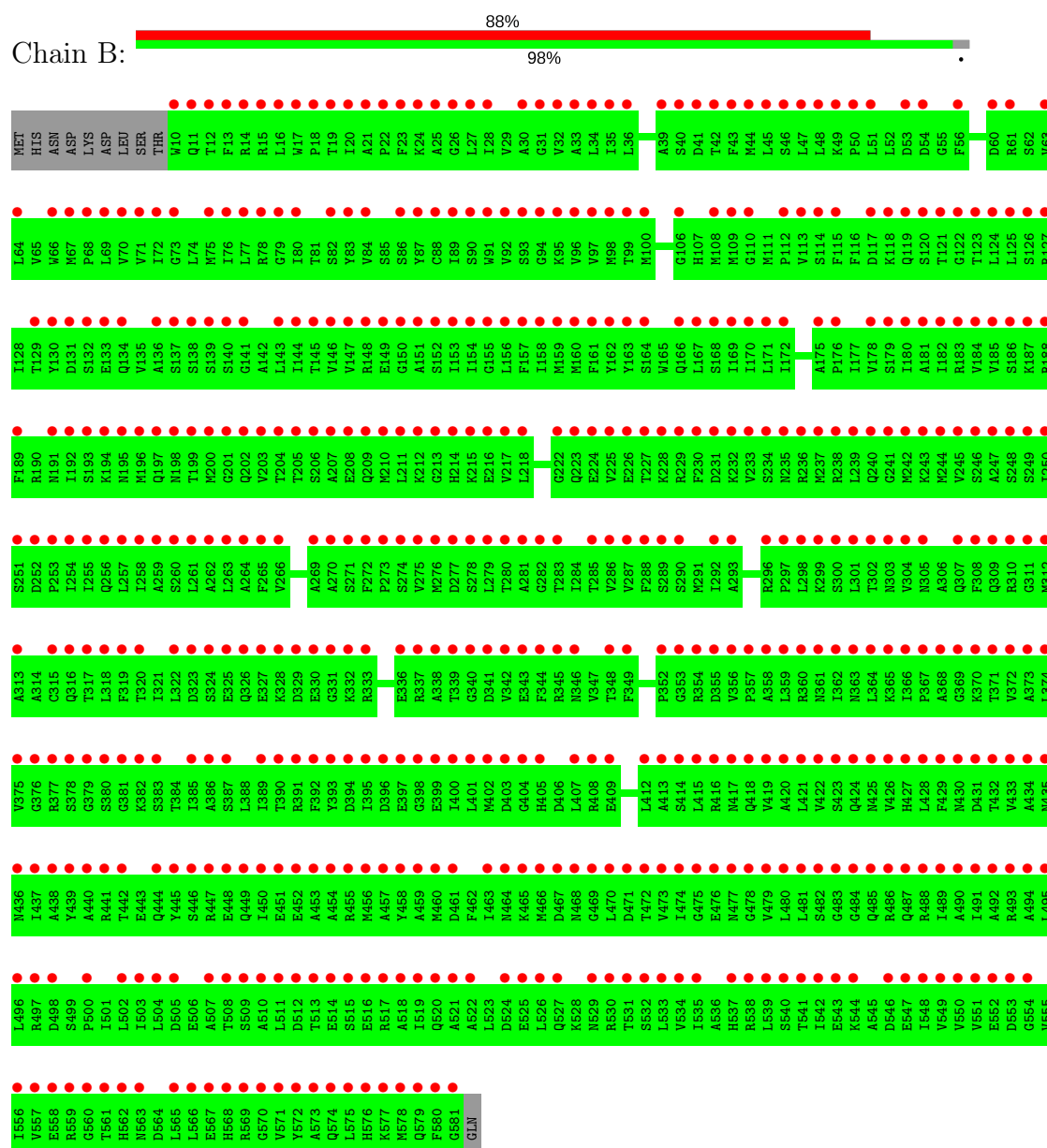
2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 4576 atoms, of which 0 are hydrogens and 0 are deuteriums.

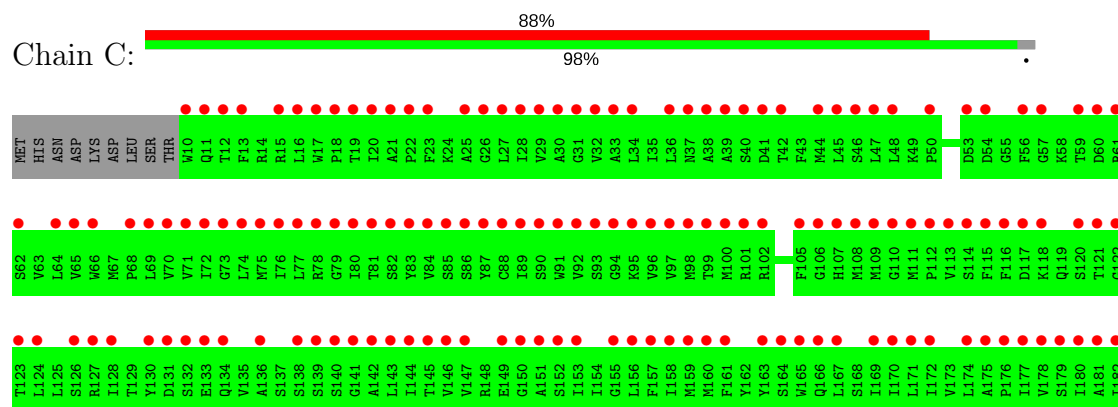
In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

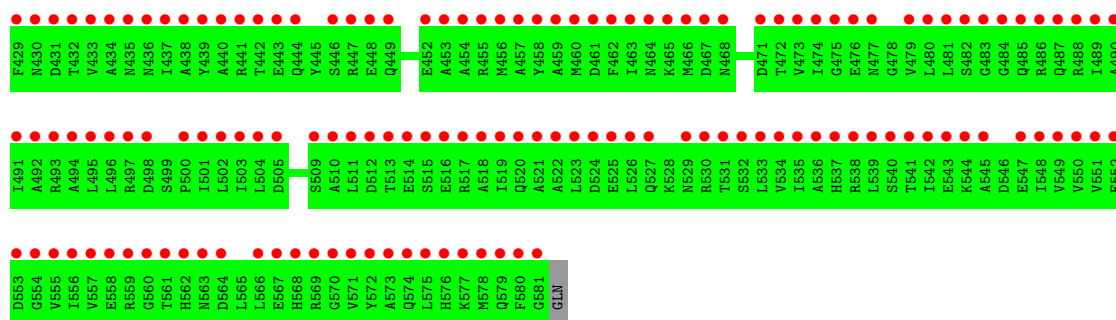
- Molecule 1 is a protein called Lipid A export ATP-binding/permease protein msbA.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf	Trace
1	A	572	Total	C	0	0	572
			572	572			
1	B	572	Total	C	0	0	572
			572	572			
1	C	572	Total	C	0	0	572
			572	572			
1	D	572	Total	C	0	0	572
			572	572			
1	E	572	Total	C	0	0	572
			572	572			
1	F	572	Total	C	0	0	572
			572	572			
1	G	572	Total	C	0	0	572
			572	572			
1	H	572	Total	C	0	0	572
			572	572			

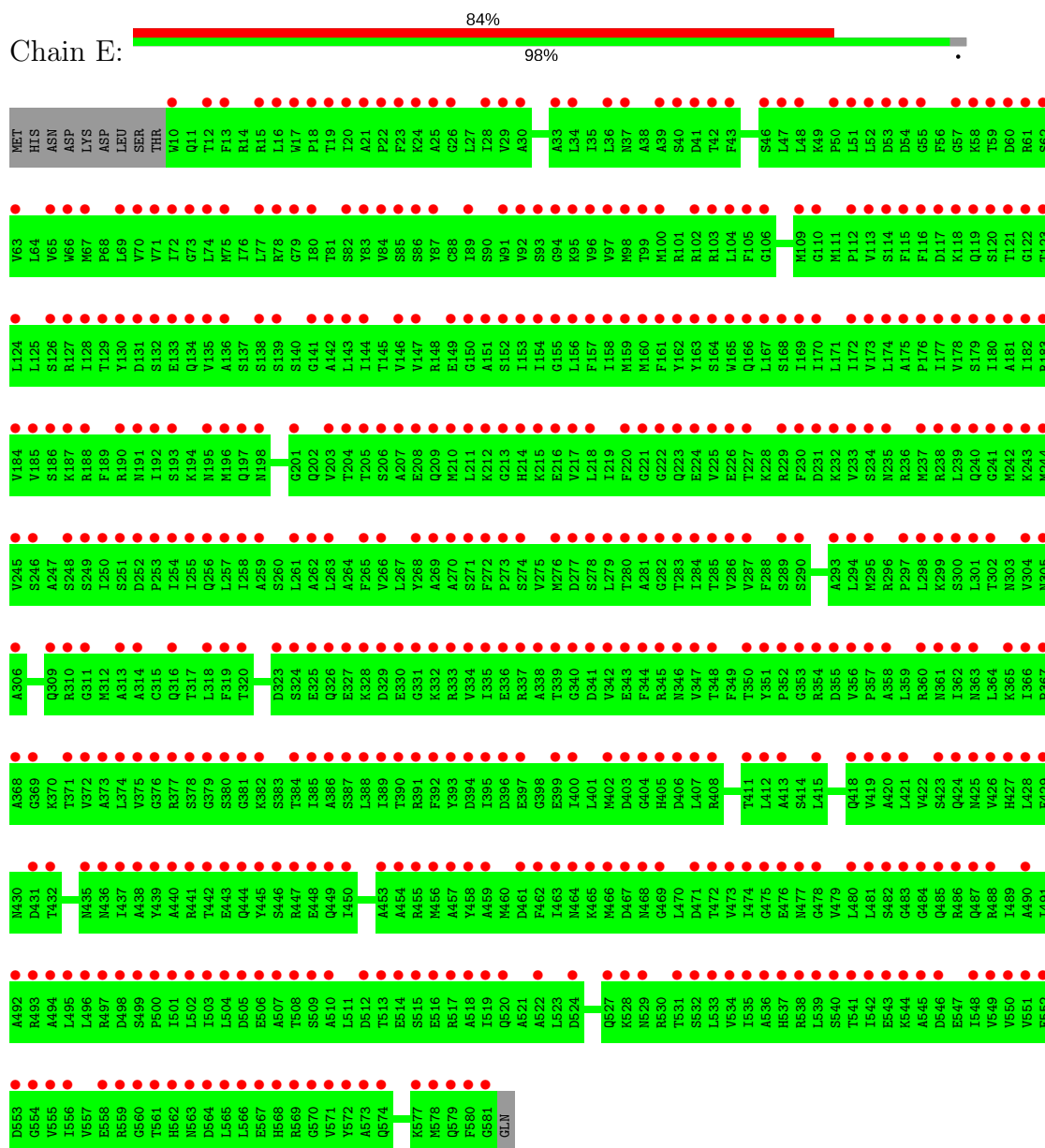


- Molecule 1: Lipid A export ATP-binding/permease protein msbA

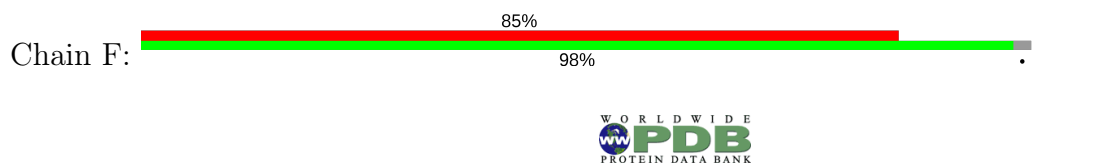


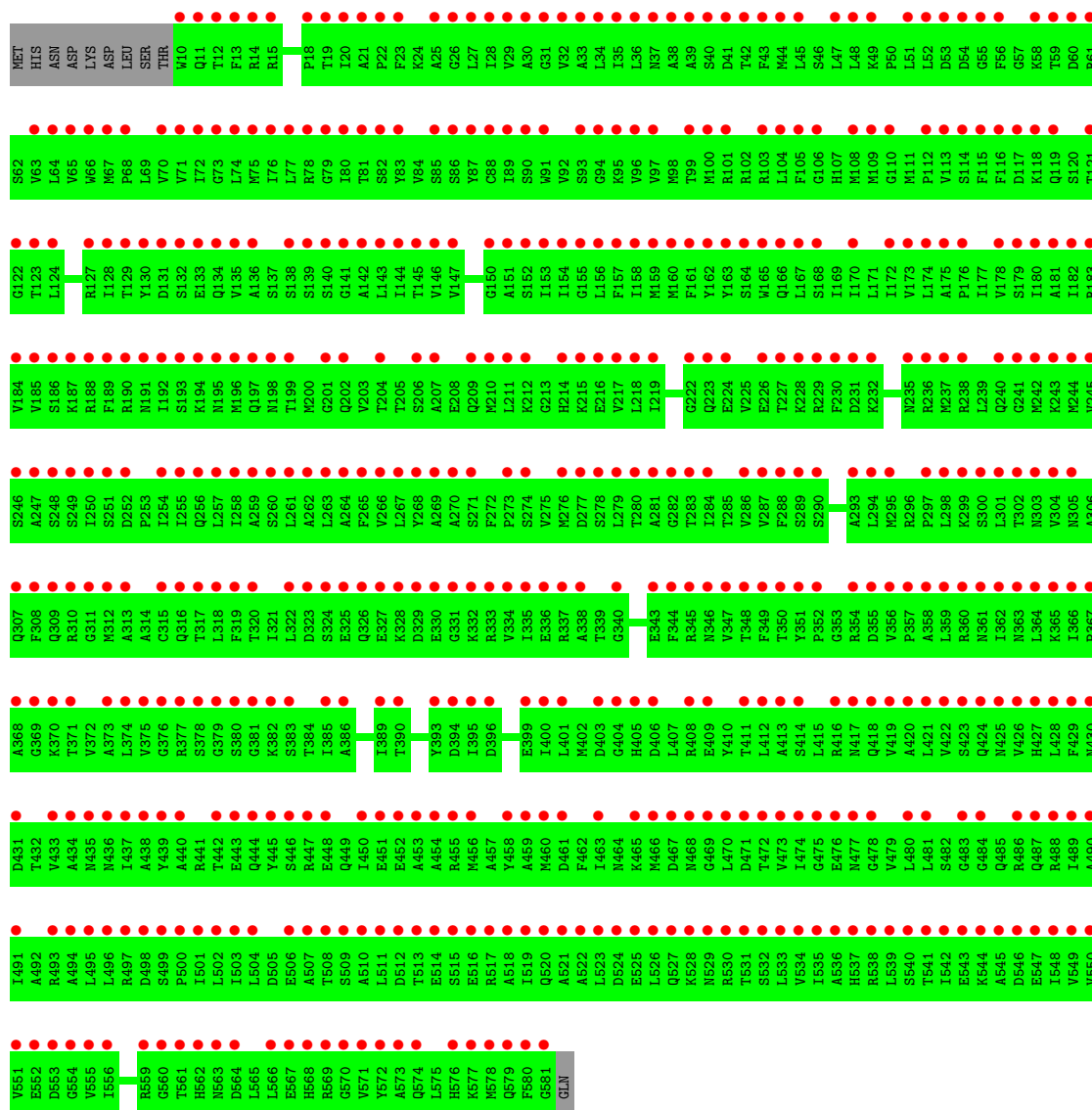


- Molecule 1: Lipid A export ATP-binding/permease protein msbA

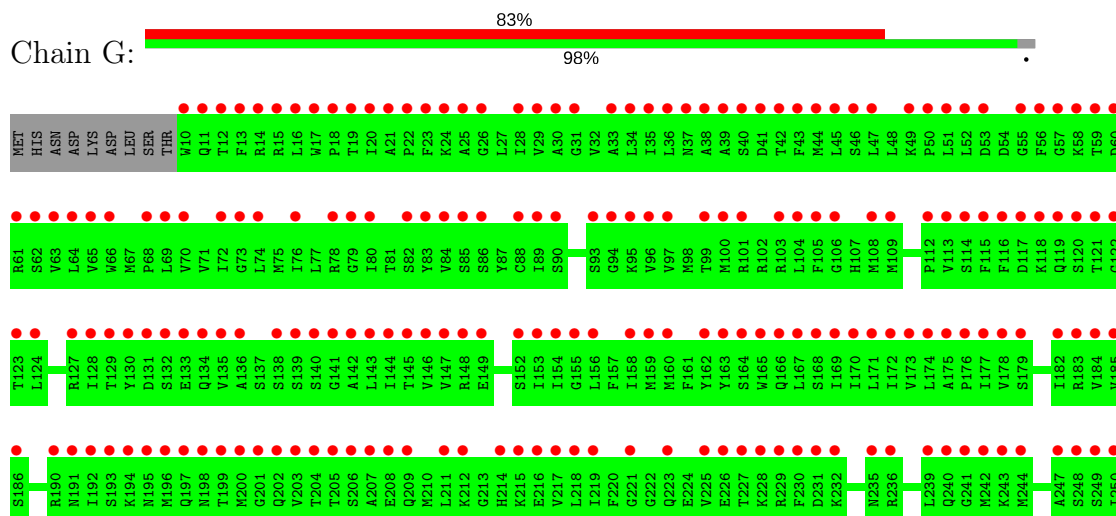


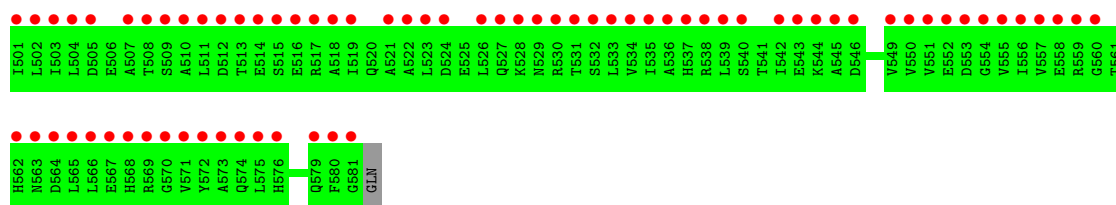
- Molecule 1: Lipid A export ATP-binding/permease protein msbA





• Molecule 1: Lipid A export ATP-binding/permease protein msbA





4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	107.79Å 126.07Å 206.56Å 83.47° 76.25° 84.07°	Depositor
Resolution (Å)	19.98 – 5.30 19.98 – 5.30	Depositor EDS
% Data completeness (in resolution range)	96.8 (19.98-5.30) 94.1 (19.98-5.30)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.05	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.08 (at 5.23Å)	Xtriage
Refinement program	CNS 1.2	Depositor
R, R_{free}	0.276 , 0.311 0.362 , 0.369	Depositor DCC
R_{free} test set	3663 reflections (10.18%)	DCC
Wilson B-factor (Å ²)	260.4	Xtriage
Anisotropy	0.114	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.40 , 74.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.85	EDS
Total number of atoms	4576	wwPDB-VP
Average B, all atoms (Å ²)	308.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.78% 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	572	0	0	0	0
1	B	572	0	0	0	0
1	C	572	0	0	0	0
1	D	572	0	0	0	0
1	E	572	0	0	0	0
1	F	572	0	0	0	0
1	G	572	0	0	0	0
1	H	572	0	0	0	0
All	All	4576	0	0	0	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 0.

There are no clashes within the asymmetric unit.

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, 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	572/582 (98%)	7.25	518 (90%) 0 1	223, 300, 343, 343	0
1	B	572/582 (98%)	7.76	510 (89%) 0 1	218, 299, 340, 343	0
1	C	572/582 (98%)	7.16	510 (89%) 0 1	227, 310, 343, 343	0
1	D	572/582 (98%)	7.14	515 (90%) 0 1	238, 308, 343, 343	0
1	E	572/582 (98%)	6.29	487 (85%) 0 1	243, 317, 343, 343	0
1	F	572/582 (98%)	6.19	497 (86%) 0 1	229, 311, 343, 343	0
1	G	572/582 (98%)	6.24	481 (84%) 0 1	245, 320, 343, 343	0
1	H	572/582 (98%)	6.17	492 (86%) 0 1	236, 317, 343, 343	0
All	All	4576/4656 (98%)	6.77	4010 (87%) 0 1	218, 311, 343, 343	0

All (4010) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	377	ARG	35.2
1	D	243	LYS	34.6
1	B	324	SER	33.2
1	C	236	ARG	33.1
1	B	524	ASP	31.7
1	B	360	ARG	30.4
1	D	299	LYS	29.2
1	B	193	SER	29.0
1	D	253	PRO	28.4
1	G	131	ASP	28.1
1	B	370	LYS	28.0
1	B	186	SER	27.5
1	H	483	GLY	27.4
1	H	300	SER	27.2
1	C	193	SER	25.7
1	C	473	VAL	25.6

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Mol	Chain	Res	Type	RSRZ
1	H	377	ARG	25.5
1	C	448	GLU	25.2
1	D	380	SER	25.1
1	H	482	SER	25.1
1	C	175	ALA	23.8
1	B	70	VAL	23.8
1	C	519	ILE	23.7
1	A	323	ASP	23.7
1	A	247	ALA	23.4
1	D	32	VAL	23.3
1	B	170	ILE	23.3
1	A	248	SER	23.2
1	C	520	GLN	22.9
1	G	295	MET	22.8
1	E	546	ASP	22.8
1	C	359	LEU	22.8
1	C	561	THR	22.7
1	H	34	LEU	22.5
1	F	170	ILE	22.4
1	A	468	ASN	22.4
1	B	323	ASP	22.3
1	A	563	ASN	22.3
1	C	191	ASN	22.2
1	F	44	MET	22.1
1	A	340	GLY	22.1
1	H	182	ILE	22.1
1	C	147	VAL	22.0
1	E	209	GLN	22.0
1	G	141	GLY	22.0
1	B	31	GLY	22.0
1	G	115	PHE	21.9
1	D	425	ASN	21.9
1	G	154	ILE	21.9
1	H	573	ALA	21.9
1	G	46	SER	21.8
1	F	317	THR	21.7
1	B	192	ILE	21.6
1	E	396	ASP	21.6
1	B	67	MET	21.6
1	H	425	ASN	21.5
1	C	32	VAL	21.5
1	A	80	ILE	21.5

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Mol	Chain	Res	Type	RSRZ
1	G	277	ASP	21.3
1	A	252	ASP	21.2
1	C	320	THR	21.2
1	H	78	ARG	21.2
1	G	556	ILE	20.9
1	B	171	LEU	20.8
1	C	563	ASN	20.6
1	B	25	ALA	20.6
1	A	166	GLN	20.5
1	H	450	ILE	20.4
1	G	563	ASN	20.3
1	G	425	ASN	20.2
1	D	20	ILE	20.2
1	D	90	SER	20.2
1	B	548	ILE	20.2
1	B	15	ARG	20.2
1	A	503	ILE	20.1
1	B	16	LEU	20.0
1	C	460	MET	20.0
1	A	383	SER	20.0
1	H	235	ASN	19.9
1	C	579	GLN	19.9
1	G	50	PRO	19.8
1	A	79	GLY	19.7
1	C	233	VAL	19.5
1	B	76	ILE	19.4
1	G	44	MET	19.4
1	B	558	GLU	19.4
1	C	417	ASN	19.3
1	H	467	ASP	19.3
1	D	301	LEU	19.2
1	D	515	SER	19.2
1	E	100	MET	19.1
1	H	164	SER	19.1
1	A	150	GLY	19.1
1	B	228	LYS	19.1
1	A	273	PRO	19.1
1	H	226	GLU	19.0
1	D	223	GLN	19.0
1	G	158	ILE	19.0
1	B	425	ASN	19.0
1	F	343	GLU	18.9

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Mol	Chain	Res	Type	RSRZ
1	F	544	LYS	18.9
1	G	164	SER	18.8
1	A	46	SER	18.7
1	B	559	ARG	18.7
1	D	559	ARG	18.7
1	B	525	GLU	18.7
1	C	247	ALA	18.7
1	G	249	SER	18.7
1	C	28	ILE	18.7
1	B	94	GLY	18.6
1	C	471	ASP	18.6
1	F	404	GLY	18.6
1	B	378	SER	18.5
1	D	93	SER	18.4
1	F	500	PRO	18.4
1	H	368	ALA	18.3
1	G	285	THR	18.3
1	F	519	ILE	18.3
1	H	181	ALA	18.2
1	D	326	GLN	18.2
1	D	576	HIS	18.2
1	A	341	ASP	18.1
1	C	79	GLY	18.1
1	E	285	THR	18.0
1	B	22	PRO	17.9
1	F	445	TYR	17.9
1	H	42	THR	17.9
1	D	31	GLY	17.9
1	C	262	ALA	17.7
1	G	291	MET	17.7
1	H	146	VAL	17.7
1	C	18	PRO	17.6
1	B	277	ASP	17.6
1	E	164	SER	17.6
1	F	158	ILE	17.6
1	B	95	LYS	17.6
1	C	445	TYR	17.5
1	F	327	GLU	17.5
1	C	170	ILE	17.5
1	D	566	LEU	17.4
1	A	125	LEU	17.4
1	D	577	LYS	17.4

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Mol	Chain	Res	Type	RSRZ
1	B	319	PHE	17.4
1	G	45	LEU	17.4
1	B	249	SER	17.4
1	D	181	ALA	17.3
1	H	355	ASP	17.3
1	D	304	VAL	17.3
1	B	122	GLY	17.3
1	B	508	THR	17.2
1	A	47	LEU	17.2
1	C	117	ASP	17.2
1	A	576	HIS	17.2
1	D	252	ASP	17.2
1	D	166	GLN	17.1
1	G	34	LEU	17.1
1	A	259	ALA	17.1
1	B	359	LEU	17.1
1	G	196	MET	17.1
1	A	249	SER	17.1
1	D	471	ASP	17.1
1	F	131	ASP	17.0
1	H	21	ALA	17.0
1	D	46	SER	17.0
1	E	23	PHE	17.0
1	B	182	ILE	17.0
1	A	163	TYR	17.0
1	A	400	ILE	17.0
1	C	324	SER	17.0
1	A	297	PRO	16.9
1	C	252	ASP	16.9
1	G	165	TRP	16.9
1	G	176	PRO	16.9
1	B	34	LEU	16.9
1	D	62	SER	16.9
1	E	146	VAL	16.8
1	G	25	ALA	16.8
1	C	134	GLN	16.8
1	A	147	VAL	16.8
1	E	159	MET	16.7
1	E	183	ARG	16.7
1	C	352	PRO	16.7
1	H	332	LYS	16.7
1	A	242	MET	16.7

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Mol	Chain	Res	Type	RSRZ
1	D	191	ASN	16.6
1	C	166	GLN	16.6
1	B	577	LYS	16.6
1	C	362	ILE	16.6
1	C	325	GLU	16.6
1	B	520	GLN	16.6
1	C	287	VAL	16.6
1	E	15	ARG	16.5
1	D	158	ILE	16.5
1	F	399	GLU	16.4
1	E	500	PRO	16.3
1	F	439	TYR	16.3
1	B	475	GLY	16.2
1	A	510	ALA	16.2
1	H	169	ILE	16.2
1	B	13	PHE	16.2
1	A	349	PHE	16.2
1	B	191	ASN	16.2
1	A	16	LEU	16.1
1	E	238	ARG	16.1
1	A	448	GLU	16.1
1	D	312	MET	16.1
1	H	80	ILE	16.1
1	B	36	LEU	16.1
1	D	324	SER	16.0
1	A	360	ARG	16.0
1	G	323	ASP	16.0
1	B	46	SER	16.0
1	B	35	ILE	16.0
1	A	309	GLN	16.0
1	A	175	ALA	15.9
1	G	334	VAL	15.9
1	A	127	ARG	15.9
1	H	448	GLU	15.9
1	B	261	LEU	15.9
1	A	167	LEU	15.9
1	C	259	ALA	15.9
1	H	327	GLU	15.9
1	A	524	ASP	15.9
1	A	172	ILE	15.8
1	H	64	LEU	15.8
1	D	313	ALA	15.8

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Mol	Chain	Res	Type	RSRZ
1	F	68	PRO	15.8
1	C	37	ASN	15.8
1	B	252	ASP	15.8
1	D	361	ASN	15.7
1	H	81	THR	15.7
1	A	103	ARG	15.7
1	E	512	ASP	15.7
1	E	141	GLY	15.7
1	F	378	SER	15.7
1	A	182	ILE	15.7
1	B	380	SER	15.7
1	H	277	ASP	15.7
1	C	378	SER	15.7
1	D	557	VAL	15.7
1	C	283	THR	15.6
1	F	248	SER	15.6
1	B	320	THR	15.6
1	F	543	GLU	15.6
1	G	148	ARG	15.6
1	B	187	LYS	15.5
1	A	337	ARG	15.5
1	G	272	PHE	15.5
1	D	468	ASN	15.5
1	C	31	GLY	15.5
1	B	68	PRO	15.5
1	D	224	GLU	15.5
1	G	467	ASP	15.5
1	H	86	SER	15.5
1	H	186	SER	15.4
1	H	468	ASN	15.4
1	A	467	ASP	15.4
1	B	299	LYS	15.4
1	F	134	GLN	15.4
1	C	461	ASP	15.4
1	E	82	SER	15.4
1	E	361	ASN	15.4
1	C	326	GLN	15.4
1	A	206	SER	15.4
1	D	333	ARG	15.4
1	C	121	THR	15.3
1	G	522	ALA	15.3
1	C	538	ARG	15.3

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Mol	Chain	Res	Type	RSRZ
1	A	62	SER	15.3
1	G	243	LYS	15.3
1	H	336	GLU	15.3
1	B	258	ILE	15.2
1	E	93	SER	15.2
1	E	475	GLY	15.2
1	D	262	ALA	15.2
1	A	90	SER	15.2
1	G	183	ARG	15.2
1	C	94	GLY	15.2
1	H	330	GLU	15.2
1	F	396	ASP	15.2
1	B	502	LEU	15.2
1	H	196	MET	15.1
1	A	367	PRO	15.1
1	D	467	ASP	15.1
1	E	371	THR	15.1
1	B	563	ASN	15.1
1	B	325	GLU	15.1
1	C	457	ALA	15.1
1	F	379	GLY	15.1
1	H	156	LEU	15.0
1	H	580	PHE	15.0
1	E	372	VAL	15.0
1	F	349	PHE	15.0
1	F	144	ILE	15.0
1	E	343	GLU	15.0
1	D	570	GLY	15.0
1	C	285	THR	15.0
1	C	223	GLN	14.9
1	E	178	VAL	14.9
1	A	261	LEU	14.9
1	D	58	LYS	14.9
1	F	80	ILE	14.9
1	C	454	ALA	14.9
1	A	136	ALA	14.9
1	B	243	LYS	14.9
1	B	529	ASN	14.9
1	G	562	HIS	14.8
1	F	305	ASN	14.8
1	A	128	ILE	14.8
1	E	573	ALA	14.8

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Mol	Chain	Res	Type	RSRZ
1	H	456	MET	14.8
1	C	549	VAL	14.8
1	G	510	ALA	14.8
1	B	246	SER	14.8
1	E	468	ASN	14.8
1	C	156	LEU	14.7
1	C	323	ASP	14.7
1	B	399	GLU	14.7
1	D	182	ILE	14.7
1	B	43	PHE	14.7
1	E	369	GLY	14.7
1	B	482	SER	14.7
1	G	519	ILE	14.6
1	A	368	ALA	14.6
1	B	20	ILE	14.6
1	B	511	LEU	14.6
1	C	240	GLN	14.6
1	A	193	SER	14.6
1	D	316	GLN	14.6
1	A	186	SER	14.6
1	G	381	GLY	14.6
1	C	423	SER	14.5
1	F	498	ASP	14.5
1	H	543	GLU	14.5
1	B	551	VAL	14.5
1	G	37	ASN	14.5
1	F	302	THR	14.5
1	E	249	SER	14.5
1	B	514	GLU	14.5
1	E	425	ASN	14.5
1	A	23	PHE	14.5
1	A	513	THR	14.5
1	D	556	ILE	14.5
1	C	116	PHE	14.4
1	G	169	ILE	14.4
1	D	369	GLY	14.4
1	B	79	GLY	14.3
1	B	423	SER	14.3
1	G	12	THR	14.3
1	F	185	VAL	14.3
1	E	204	THR	14.3
1	C	521	ALA	14.3

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Mol	Chain	Res	Type	RSRZ
1	E	98	MET	14.3
1	F	459	ALA	14.3
1	G	539	LEU	14.2
1	B	480	LEU	14.2
1	B	93	SER	14.1
1	A	262	ALA	14.1
1	E	92	VAL	14.1
1	A	253	PRO	14.1
1	E	133	GLU	14.0
1	H	387	SER	14.0
1	D	254	ILE	14.0
1	C	131	ASP	14.0
1	B	349	PHE	14.0
1	A	25	ALA	14.0
1	D	134	GLN	14.0
1	D	113	VAL	14.0
1	H	447	ARG	14.0
1	G	304	VAL	14.0
1	G	333	ARG	14.0
1	E	40	SER	14.0
1	D	101	ARG	13.9
1	A	530	ARG	13.9
1	F	444	GLN	13.9
1	F	559	ARG	13.9
1	D	143	LEU	13.9
1	E	235	ASN	13.9
1	E	439	TYR	13.8
1	H	252	ASP	13.8
1	F	142	ALA	13.8
1	C	560	GLY	13.8
1	H	191	ASN	13.8
1	C	398	GLY	13.8
1	A	169	ILE	13.8
1	F	79	GLY	13.8
1	A	22	PRO	13.8
1	D	214	HIS	13.8
1	G	140	SER	13.7
1	A	21	ALA	13.7
1	H	488	ARG	13.7
1	B	576	HIS	13.7
1	G	546	ASP	13.7
1	B	457	ALA	13.7

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Mol	Chain	Res	Type	RSRZ
1	C	425	ASN	13.6
1	C	150	GLY	13.6
1	A	479	VAL	13.6
1	A	192	ILE	13.6
1	A	246	SER	13.6
1	H	489	ILE	13.6
1	A	339	THR	13.6
1	D	366	ILE	13.6
1	D	352	PRO	13.6
1	E	283	THR	13.6
1	G	430	ASN	13.6
1	A	506	GLU	13.6
1	F	41	ASP	13.5
1	D	95	LYS	13.5
1	D	563	ASN	13.5
1	H	134	GLN	13.5
1	B	188	ARG	13.5
1	D	424	GLN	13.5
1	E	117	ASP	13.5
1	F	529	ASN	13.5
1	D	131	ASP	13.4
1	C	467	ASP	13.4
1	H	522	ALA	13.4
1	E	191	ASN	13.4
1	B	132	SER	13.4
1	C	566	LEU	13.4
1	C	158	ILE	13.4
1	C	91	TRP	13.4
1	C	145	THR	13.4
1	F	350	THR	13.4
1	D	196	MET	13.3
1	A	54	ASP	13.3
1	G	35	ILE	13.3
1	B	296	ARG	13.3
1	G	43	PHE	13.3
1	B	235	ASN	13.3
1	B	253	PRO	13.3
1	A	31	GLY	13.3
1	A	254	ILE	13.2
1	D	195	ASN	13.2
1	H	310	ARG	13.2
1	A	168	SER	13.2

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Mol	Chain	Res	Type	RSRZ
1	D	23	PHE	13.2
1	H	129	THR	13.2
1	B	526	LEU	13.2
1	C	349	PHE	13.2
1	B	195	ASN	13.2
1	A	116	PHE	13.2
1	B	71	VAL	13.2
1	A	235	ASN	13.2
1	B	546	ASP	13.2
1	E	226	GLU	13.2
1	H	453	ALA	13.2
1	E	363	ASN	13.1
1	F	115	PHE	13.1
1	F	204	THR	13.1
1	F	175	ALA	13.1
1	A	463	ILE	13.1
1	B	126	SER	13.1
1	B	230	PHE	13.1
1	H	43	PHE	13.1
1	A	204	THR	13.1
1	E	132	SER	13.1
1	A	24	LYS	13.0
1	D	242	MET	13.0
1	A	574	GLN	13.0
1	C	466	MET	13.0
1	C	256	GLN	13.0
1	G	317	THR	13.0
1	H	566	LEU	13.0
1	D	24	LYS	13.0
1	B	244	MET	13.0
1	G	64	LEU	13.0
1	B	166	GLN	12.9
1	D	192	ILE	12.9
1	F	510	ALA	12.9
1	D	466	MET	12.9
1	F	447	ARG	12.9
1	E	447	ARG	12.9
1	E	83	TYR	12.9
1	H	378	SER	12.9
1	F	265	PHE	12.9
1	B	227	THR	12.9
1	D	117	ASP	12.9

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Mol	Chain	Res	Type	RSRZ
1	B	466	MET	12.8
1	G	103	ARG	12.8
1	F	336	GLU	12.8
1	A	378	SER	12.8
1	E	287	VAL	12.8
1	F	289	SER	12.8
1	A	581	GLY	12.8
1	D	136	ALA	12.8
1	G	379	GLY	12.8
1	C	393	TYR	12.7
1	D	505	ASP	12.7
1	H	176	PRO	12.7
1	C	297	PRO	12.7
1	F	330	GLU	12.7
1	B	175	ALA	12.7
1	D	353	GLY	12.7
1	H	413	ALA	12.7
1	B	435	ASN	12.7
1	F	560	GLY	12.7
1	B	424	GLN	12.7
1	D	323	ASP	12.6
1	C	255	ILE	12.6
1	F	119	GLN	12.6
1	A	356	VAL	12.6
1	E	157	PHE	12.6
1	G	513	THR	12.6
1	E	458	TYR	12.6
1	G	156	LEU	12.6
1	C	332	LYS	12.6
1	G	544	LYS	12.6
1	D	57	GLY	12.6
1	B	248	SER	12.6
1	A	419	VAL	12.6
1	C	242	MET	12.6
1	C	391	ARG	12.6
1	F	332	LYS	12.5
1	E	421	LEU	12.5
1	F	143	LEU	12.5
1	B	245	VAL	12.5
1	C	480	LEU	12.5
1	C	249	SER	12.5
1	D	121	THR	12.5

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Mol	Chain	Res	Type	RSRZ
1	B	361	ASN	12.5
1	A	95	LYS	12.5
1	C	66	TRP	12.5
1	C	257	LEU	12.5
1	F	30	ALA	12.5
1	G	498	ASP	12.5
1	A	573	ALA	12.5
1	E	144	ILE	12.5
1	A	122	GLY	12.5
1	A	231	ASP	12.5
1	H	28	ILE	12.4
1	B	566	LEU	12.4
1	A	265	PHE	12.4
1	A	484	GLY	12.4
1	A	145	THR	12.4
1	A	366	ILE	12.4
1	D	142	ALA	12.4
1	G	311	GLY	12.4
1	F	377	ARG	12.4
1	B	279	LEU	12.4
1	D	444	GLN	12.4
1	E	187	LYS	12.4
1	F	301	LEU	12.4
1	B	455	ARG	12.4
1	F	52	LEU	12.4
1	E	190	ARG	12.4
1	C	73	GLY	12.3
1	H	94	GLY	12.3
1	E	354	ARG	12.3
1	E	514	GLU	12.3
1	A	325	GLU	12.3
1	G	411	THR	12.3
1	E	482	SER	12.3
1	E	379	GLY	12.3
1	A	301	LEU	12.3
1	G	29	VAL	12.3
1	B	215	LYS	12.3
1	B	541	THR	12.3
1	A	348	THR	12.3
1	G	116	PHE	12.2
1	G	325	GLU	12.2
1	D	367	PRO	12.2

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Mol	Chain	Res	Type	RSRZ
1	A	447	ARG	12.2
1	G	363	ASN	12.2
1	A	567	GLU	12.2
1	E	225	VAL	12.2
1	G	120	SER	12.2
1	A	357	PRO	12.2
1	F	230	PHE	12.2
1	A	19	THR	12.2
1	A	199	THR	12.2
1	A	480	LEU	12.2
1	C	251	SER	12.2
1	G	194	LYS	12.2
1	D	479	VAL	12.2
1	G	36	LEU	12.2
1	G	282	GLY	12.2
1	H	454	ALA	12.2
1	D	16	LEU	12.2
1	G	359	LEU	12.2
1	C	444	GLN	12.1
1	B	474	ILE	12.1
1	C	456	MET	12.1
1	F	130	TYR	12.1
1	B	301	LEU	12.1
1	C	482	SER	12.1
1	D	144	ILE	12.1
1	C	328	LYS	12.1
1	A	320	THR	12.1
1	H	431	ASP	12.1
1	D	156	LEU	12.1
1	G	579	GLN	12.1
1	B	532	SER	12.1
1	G	197	GLN	12.1
1	C	575	LEU	12.1
1	C	513	THR	12.1
1	D	300	SER	12.1
1	H	144	ILE	12.1
1	C	44	MET	12.1
1	F	277	ASP	12.0
1	D	514	GLU	12.0
1	G	567	GLU	12.0
1	A	559	ARG	12.0
1	A	32	VAL	12.0

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Mol	Chain	Res	Type	RSRZ
1	C	218	LEU	12.0
1	D	530	ARG	12.0
1	D	457	ALA	12.0
1	F	363	ASN	11.9
1	B	549	VAL	11.9
1	D	60	ASP	11.9
1	G	159	MET	11.9
1	C	151	ALA	11.9
1	A	146	VAL	11.9
1	F	497	ARG	11.9
1	A	223	GLN	11.9
1	E	463	ILE	11.9
1	C	46	SER	11.8
1	F	311	GLY	11.8
1	G	338	ALA	11.8
1	B	273	PRO	11.8
1	D	145	THR	11.8
1	A	115	PHE	11.8
1	A	171	LEU	11.8
1	A	300	SER	11.8
1	F	283	THR	11.8
1	A	144	ILE	11.8
1	D	273	PRO	11.8
1	E	263	LEU	11.8
1	A	390	THR	11.8
1	B	401	LEU	11.8
1	D	245	VAL	11.8
1	F	548	ILE	11.8
1	A	483	GLY	11.7
1	C	118	LYS	11.7
1	H	171	LEU	11.7
1	F	123	THR	11.7
1	B	328	LYS	11.7
1	C	12	THR	11.7
1	E	50	PRO	11.7
1	D	303	ASN	11.7
1	D	139	SER	11.7
1	E	170	ILE	11.7
1	E	28	ILE	11.7
1	F	228	LYS	11.7
1	F	235	ASN	11.7
1	C	401	LEU	11.7

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Mol	Chain	Res	Type	RSRZ
1	B	242	MET	11.6
1	D	579	GLN	11.6
1	F	458	TYR	11.6
1	F	173	VAL	11.6
1	F	368	ALA	11.6
1	F	335	ILE	11.6
1	A	181	ALA	11.6
1	B	531	THR	11.6
1	D	358	ALA	11.6
1	E	265	PHE	11.6
1	B	231	ASP	11.6
1	D	170	ILE	11.6
1	E	487	GLN	11.6
1	E	66	TRP	11.6
1	D	357	PRO	11.6
1	C	182	ILE	11.6
1	H	170	ILE	11.5
1	A	96	VAL	11.5
1	D	474	ILE	11.5
1	B	358	ALA	11.5
1	B	367	PRO	11.5
1	B	355	ASP	11.5
1	C	443	GLU	11.5
1	C	301	LEU	11.4
1	C	48	LEU	11.4
1	G	76	ILE	11.4
1	F	155	GLY	11.4
1	C	47	LEU	11.4
1	G	559	ARG	11.4
1	H	498	ASP	11.4
1	B	144	ILE	11.4
1	B	473	VAL	11.4
1	D	265	PHE	11.4
1	B	330	GLU	11.4
1	F	426	VAL	11.4
1	B	329	ASP	11.4
1	A	205	THR	11.4
1	E	284	ILE	11.4
1	G	542	ILE	11.4
1	E	467	ASP	11.3
1	C	57	GLY	11.3
1	D	76	ILE	11.3

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Mol	Chain	Res	Type	RSRZ
1	B	197	GLN	11.3
1	H	386	ALA	11.3
1	F	201	GLY	11.3
1	B	223	GLN	11.3
1	G	463	ILE	11.3
1	C	369	GLY	11.3
1	C	424	GLN	11.3
1	D	197	GLN	11.3
1	C	99	THR	11.3
1	E	562	HIS	11.3
1	B	567	GLU	11.3
1	C	360	ARG	11.3
1	H	499	SER	11.3
1	E	278	SER	11.3
1	C	348	THR	11.3
1	H	476	GLU	11.3
1	B	131	ASP	11.2
1	B	121	THR	11.2
1	E	329	ASP	11.2
1	H	424	GLN	11.2
1	B	226	GLU	11.2
1	G	354	ARG	11.2
1	D	455	ARG	11.2
1	A	322	LEU	11.2
1	C	93	SER	11.2
1	A	94	GLY	11.2
1	E	163	TYR	11.2
1	E	407	LEU	11.2
1	F	67	MET	11.2
1	A	313	ALA	11.1
1	B	515	SER	11.1
1	G	456	MET	11.1
1	A	355	ASP	11.1
1	B	113	VAL	11.1
1	G	177	ILE	11.1
1	D	517	ARG	11.1
1	B	155	GLY	11.1
1	B	47	LEU	11.1
1	E	413	ALA	11.1
1	A	397	GLU	11.1
1	D	202	GLN	11.1
1	B	467	ASP	11.1

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Mol	Chain	Res	Type	RSRZ
1	B	477	ASN	11.0
1	B	280	THR	11.0
1	A	65	VAL	11.0
1	D	175	ALA	11.0
1	C	19	THR	11.0
1	C	76	ILE	11.0
1	B	21	ALA	11.0
1	F	10	TRP	11.0
1	D	417	ASN	11.0
1	B	259	ALA	11.0
1	B	453	ALA	11.0
1	F	135	VAL	11.0
1	D	355	ASP	11.0
1	A	380	SER	11.0
1	C	514	GLU	11.0
1	E	572	TYR	11.0
1	D	28	ILE	11.0
1	B	189	PHE	11.0
1	B	181	ALA	11.0
1	G	310	ARG	11.0
1	F	42	THR	11.0
1	A	418	GLN	10.9
1	G	337	ARG	10.9
1	E	471	ASP	10.9
1	H	371	THR	10.9
1	E	426	VAL	10.9
1	A	557	VAL	10.9
1	D	92	VAL	10.9
1	B	408	ARG	10.9
1	A	66	TRP	10.9
1	B	17	TRP	10.9
1	D	496	LEU	10.9
1	B	66	TRP	10.9
1	D	297	PRO	10.9
1	G	443	GLU	10.9
1	D	87	TYR	10.9
1	A	560	GLY	10.9
1	D	516	GLU	10.9
1	H	209	GLN	10.9
1	E	165	TRP	10.9
1	E	253	PRO	10.9
1	D	153	ILE	10.9

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Mol	Chain	Res	Type	RSRZ
1	H	512	ASP	10.9
1	E	537	HIS	10.9
1	G	426	VAL	10.9
1	F	188	ARG	10.8
1	D	452	GLU	10.8
1	F	318	LEU	10.8
1	F	167	LEU	10.8
1	C	568	HIS	10.8
1	C	95	LYS	10.8
1	C	200	MET	10.8
1	E	286	VAL	10.8
1	F	34	LEU	10.8
1	H	248	SER	10.8
1	E	184	VAL	10.8
1	D	513	THR	10.8
1	B	333	ARG	10.8
1	F	425	ASN	10.8
1	H	117	ASP	10.8
1	A	143	LEU	10.8
1	F	194	LYS	10.7
1	G	117	ASP	10.7
1	C	389	ILE	10.7
1	H	289	SER	10.7
1	B	14	ARG	10.7
1	B	356	VAL	10.7
1	B	571	VAL	10.7
1	B	348	THR	10.7
1	H	486	ARG	10.7
1	F	11	GLN	10.7
1	B	112	PRO	10.7
1	D	338	ALA	10.7
1	F	261	LEU	10.7
1	H	337	ARG	10.7
1	F	118	LYS	10.7
1	H	39	ALA	10.6
1	F	326	GLN	10.6
1	F	416	ARG	10.6
1	C	115	PHE	10.6
1	E	353	GLY	10.6
1	G	457	ALA	10.6
1	H	579	GLN	10.6
1	D	157	PHE	10.6

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Mol	Chain	Res	Type	RSRZ
1	C	260	SER	10.6
1	H	343	GLU	10.6
1	F	180	ILE	10.6
1	D	155	GLY	10.6
1	G	271	SER	10.6
1	H	255	ILE	10.6
1	F	461	ASP	10.6
1	C	106	GLY	10.6
1	F	352	PRO	10.6
1	A	497	ARG	10.6
1	C	329	ASP	10.6
1	C	356	VAL	10.6
1	D	33	ALA	10.6
1	E	47	LEU	10.6
1	E	301	LEU	10.6
1	D	571	VAL	10.5
1	B	547	GLU	10.5
1	D	331	GLY	10.5
1	G	572	TYR	10.5
1	B	134	GLN	10.5
1	E	248	SER	10.5
1	H	230	PHE	10.5
1	H	72	ILE	10.5
1	H	41	ASP	10.5
1	F	212	LYS	10.5
1	C	479	VAL	10.5
1	A	91	TRP	10.5
1	C	284	ILE	10.5
1	F	281	ALA	10.5
1	E	110	GLY	10.5
1	G	409	GLU	10.5
1	H	419	VAL	10.4
1	E	337	ARG	10.4
1	D	394	ASP	10.4
1	B	383	SER	10.4
1	G	168	SER	10.4
1	H	363	ASN	10.4
1	G	60	ASP	10.4
1	E	403	ASP	10.4
1	B	167	LEU	10.4
1	D	449	GLN	10.4
1	A	329	ASP	10.4

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Mol	Chain	Res	Type	RSRZ
1	D	164	SER	10.4
1	C	316	GLN	10.4
1	H	518	ALA	10.4
1	G	413	ALA	10.4
1	D	120	SER	10.4
1	H	565	LEU	10.4
1	B	185	VAL	10.4
1	C	45	LEU	10.4
1	G	42	THR	10.4
1	D	150	GLY	10.3
1	C	163	TYR	10.3
1	F	76	ILE	10.3
1	H	276	MET	10.3
1	B	276	MET	10.3
1	A	42	THR	10.3
1	H	35	ILE	10.3
1	A	333	ARG	10.3
1	B	362	ILE	10.3
1	H	66	TRP	10.3
1	D	305	ASN	10.3
1	D	122	GLY	10.3
1	A	512	ASP	10.3
1	B	459	ALA	10.3
1	F	351	TYR	10.2
1	G	147	VAL	10.2
1	B	30	ALA	10.2
1	B	293	ALA	10.2
1	E	70	VAL	10.2
1	B	196	MET	10.2
1	C	15	ARG	10.2
1	A	377	ARG	10.2
1	E	22	PRO	10.2
1	G	152	SER	10.2
1	G	142	ALA	10.2
1	H	304	VAL	10.2
1	B	418	GLN	10.2
1	B	400	ILE	10.2
1	A	304	VAL	10.2
1	C	293	ALA	10.2
1	G	38	ALA	10.2
1	D	447	ARG	10.2
1	C	228	LYS	10.2

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Mol	Chain	Res	Type	RSRZ
1	F	383	SER	10.2
1	G	361	ASN	10.2
1	C	394	ASP	10.2
1	B	229	ARG	10.2
1	B	251	SER	10.2
1	B	569	ARG	10.2
1	C	511	LEU	10.2
1	E	186	SER	10.2
1	G	182	ILE	10.2
1	H	204	THR	10.2
1	D	217	VAL	10.2
1	G	580	PHE	10.1
1	H	102	ARG	10.1
1	G	378	SER	10.1
1	H	460	MET	10.1
1	D	548	ILE	10.1
1	E	207	ALA	10.1
1	A	78	ARG	10.1
1	C	258	ILE	10.1
1	D	359	LEU	10.1
1	F	23	PHE	10.1
1	D	482	SER	10.1
1	A	226	GLU	10.1
1	F	231	ASP	10.1
1	D	461	ASP	10.1
1	E	568	HIS	10.1
1	F	245	VAL	10.1
1	D	569	ARG	10.1
1	A	426	VAL	10.1
1	D	137	SER	10.1
1	A	188	ARG	10.1
1	D	340	GLY	10.1
1	B	64	LEU	10.1
1	D	454	ALA	10.1
1	B	316	GLN	10.1
1	C	485	GLN	10.1
1	D	111	MET	10.1
1	C	338	ALA	10.1
1	B	96	VAL	10.0
1	B	138	SER	10.0
1	D	61	ARG	10.0
1	C	580	PHE	10.0

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Mol	Chain	Res	Type	RSRZ
1	F	274	SER	10.0
1	D	74	LEU	10.0
1	B	136	ALA	10.0
1	E	560	GLY	10.0
1	C	572	TYR	10.0
1	E	355	ASP	10.0
1	B	99	THR	10.0
1	D	91	TRP	10.0
1	G	239	LEU	10.0
1	E	36	LEU	10.0
1	F	312	MET	10.0
1	C	261	LEU	10.0
1	E	564	ASP	10.0
1	H	225	VAL	10.0
1	G	574	GLN	10.0
1	A	35	ILE	10.0
1	D	503	ILE	10.0
1	A	55	GLY	10.0
1	A	303	ASN	10.0
1	B	24	LYS	10.0
1	D	52	LEU	10.0
1	A	516	GLU	9.9
1	D	558	GLU	9.9
1	E	302	THR	9.9
1	E	480	LEU	9.9
1	D	413	ALA	9.9
1	E	212	LYS	9.9
1	C	570	GLY	9.9
1	A	137	SER	9.9
1	F	146	VAL	9.9
1	C	459	ALA	9.9
1	F	214	HIS	9.9
1	E	356	VAL	9.9
1	E	59	THR	9.9
1	E	127	ARG	9.9
1	A	258	ILE	9.9
1	F	153	ILE	9.9
1	H	544	LYS	9.9
1	D	53	ASP	9.9
1	A	177	ILE	9.9
1	A	556	ILE	9.9
1	H	22	PRO	9.9

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Mol	Chain	Res	Type	RSRZ
1	E	255	ILE	9.9
1	B	336	GLU	9.9
1	E	325	GLU	9.9
1	D	198	ASN	9.9
1	C	186	SER	9.9
1	D	511	LEU	9.9
1	F	218	LEU	9.9
1	B	446	SER	9.9
1	C	122	GLY	9.9
1	A	558	GLU	9.8
1	D	329	ASP	9.8
1	G	534	VAL	9.8
1	A	482	SER	9.8
1	G	179	SER	9.8
1	E	338	ALA	9.8
1	H	445	TYR	9.8
1	G	235	ASN	9.8
1	G	391	ARG	9.8
1	C	484	GLY	9.8
1	E	449	GLN	9.8
1	F	184	VAL	9.8
1	G	446	SER	9.8
1	H	423	SER	9.8
1	G	483	GLY	9.8
1	H	323	ASP	9.8
1	B	570	GLY	9.8
1	A	68	PRO	9.8
1	B	503	ILE	9.8
1	B	426	VAL	9.8
1	C	180	ILE	9.8
1	D	200	MET	9.8
1	C	498	ASP	9.8
1	F	150	GLY	9.8
1	E	152	SER	9.8
1	B	287	VAL	9.8
1	G	254	ILE	9.8
1	A	236	ARG	9.8
1	B	11	GLN	9.8
1	B	90	SER	9.8
1	F	154	ILE	9.8
1	H	485	GLN	9.8
1	D	138	SER	9.7

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Mol	Chain	Res	Type	RSRZ
1	F	63	VAL	9.7
1	B	581	GLY	9.7
1	E	570	GLY	9.7
1	E	229	ARG	9.7
1	A	215	LYS	9.7
1	H	199	THR	9.7
1	B	150	GLY	9.7
1	H	147	VAL	9.7
1	D	443	GLU	9.7
1	B	23	PHE	9.7
1	E	386	ALA	9.7
1	D	337	ARG	9.7
1	E	368	ALA	9.7
1	D	260	SER	9.7
1	C	96	VAL	9.7
1	B	75	MET	9.7
1	F	346	ASN	9.7
1	C	559	ARG	9.7
1	C	383	SER	9.7
1	F	476	GLU	9.7
1	C	447	ARG	9.7
1	H	338	ALA	9.7
1	H	418	GLN	9.7
1	C	408	ARG	9.7
1	G	231	ASP	9.7
1	A	185	VAL	9.7
1	F	117	ASP	9.7
1	G	368	ALA	9.7
1	H	313	ALA	9.7
1	D	10	TRP	9.6
1	E	509	SER	9.6
1	E	333	ARG	9.6
1	C	87	TYR	9.6
1	D	351	TYR	9.6
1	B	483	GLY	9.6
1	A	255	ILE	9.6
1	H	559	ARG	9.6
1	B	214	HIS	9.6
1	G	70	VAL	9.6
1	F	340	GLY	9.6
1	D	226	GLU	9.6
1	F	540	SER	9.6

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Mol	Chain	Res	Type	RSRZ
1	G	298	LEU	9.6
1	G	452	GLU	9.6
1	E	510	ALA	9.6
1	B	278	SER	9.6
1	G	497	ARG	9.6
1	B	247	ALA	9.6
1	A	289	SER	9.6
1	H	60	ASP	9.6
1	F	122	GLY	9.6
1	D	348	THR	9.6
1	E	540	SER	9.6
1	C	355	ASP	9.5
1	D	581	GLY	9.5
1	A	161	PHE	9.5
1	G	554	GLY	9.5
1	B	199	THR	9.5
1	C	34	LEU	9.5
1	A	113	VAL	9.5
1	B	326	GLN	9.5
1	E	408	ARG	9.5
1	F	174	LEU	9.5
1	G	286	VAL	9.5
1	G	153	ILE	9.5
1	H	166	GLN	9.5
1	B	28	ILE	9.5
1	C	164	SER	9.4
1	E	280	THR	9.4
1	B	114	SER	9.4
1	D	350	THR	9.4
1	H	227	THR	9.4
1	D	456	MET	9.4
1	A	287	VAL	9.4
1	A	481	LEU	9.4
1	B	338	ALA	9.4
1	D	538	ARG	9.4
1	E	277	ASP	9.4
1	H	59	THR	9.4
1	G	322	LEU	9.4
1	A	392	PHE	9.4
1	H	444	GLN	9.4
1	A	72	ILE	9.4
1	B	497	ARG	9.4

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Mol	Chain	Res	Type	RSRZ
1	C	176	PRO	9.4
1	C	464	ASN	9.4
1	E	420	ALA	9.4
1	G	517	ARG	9.4
1	H	214	HIS	9.4
1	A	425	ASN	9.3
1	B	262	ALA	9.3
1	A	119	GLN	9.3
1	D	286	VAL	9.3
1	A	328	LYS	9.3
1	C	472	THR	9.3
1	D	99	THR	9.3
1	B	39	ALA	9.3
1	B	300	SER	9.3
1	E	435	ASN	9.3
1	D	401	LEU	9.3
1	D	328	LYS	9.3
1	E	266	VAL	9.3
1	A	153	ILE	9.3
1	D	541	THR	9.3
1	E	180	ILE	9.3
1	B	417	ASN	9.3
1	G	527	GLN	9.3
1	B	54	ASP	9.3
1	C	62	SER	9.3
1	A	580	PHE	9.3
1	F	556	ILE	9.3
1	A	176	PRO	9.3
1	D	94	GLY	9.3
1	F	72	ILE	9.3
1	F	295	MET	9.3
1	D	239	LEU	9.3
1	G	294	LEU	9.3
1	E	503	ILE	9.2
1	A	218	LEU	9.2
1	B	396	ASP	9.2
1	E	412	LEU	9.2
1	G	248	SER	9.2
1	C	209	GLN	9.2
1	C	181	ALA	9.2
1	D	405	HIS	9.2
1	D	152	SER	9.2

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Mol	Chain	Res	Type	RSRZ
1	A	439	TYR	9.2
1	A	438	ALA	9.2
1	B	19	THR	9.2
1	C	80	ILE	9.2
1	G	186	SER	9.2
1	F	574	GLN	9.2
1	G	444	GLN	9.2
1	E	519	ILE	9.2
1	H	79	GLY	9.2
1	A	331	GLY	9.2
1	H	121	THR	9.2
1	A	416	ARG	9.2
1	F	522	ALA	9.2
1	C	27	LEU	9.2
1	C	418	GLN	9.2
1	A	424	GLN	9.1
1	G	305	ASN	9.1
1	F	27	LEU	9.1
1	A	164	SER	9.1
1	D	248	SER	9.1
1	D	373	ALA	9.1
1	F	337	ARG	9.1
1	H	135	VAL	9.1
1	A	454	ALA	9.1
1	D	473	VAL	9.1
1	F	282	GLY	9.1
1	E	158	ILE	9.1
1	C	335	ILE	9.1
1	F	406	ASP	9.1
1	D	453	ALA	9.1
1	E	176	PRO	9.1
1	H	568	HIS	9.1
1	F	215	LYS	9.1
1	G	266	VAL	9.1
1	D	463	ILE	9.1
1	E	404	GLY	9.1
1	A	58	LYS	9.1
1	C	432	THR	9.1
1	F	569	ARG	9.1
1	H	118	LYS	9.1
1	H	430	ASN	9.1
1	C	581	GLY	9.1

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Mol	Chain	Res	Type	RSRZ
1	D	59	THR	9.1
1	G	350	THR	9.1
1	E	97	VAL	9.1
1	G	134	GLN	9.0
1	F	12	THR	9.0
1	E	222	GLY	9.0
1	D	259	ALA	9.0
1	G	358	ALA	9.0
1	G	303	ASN	9.0
1	G	30	ALA	9.0
1	F	552	GLU	9.0
1	B	332	LYS	9.0
1	D	400	ILE	9.0
1	D	341	ASP	9.0
1	F	570	GLY	9.0
1	C	358	ALA	9.0
1	C	160	MET	9.0
1	A	445	TYR	9.0
1	H	333	ARG	9.0
1	F	159	MET	9.0
1	C	196	MET	9.0
1	E	328	LYS	9.0
1	H	238	ARG	9.0
1	H	399	GLU	9.0
1	D	535	ILE	9.0
1	E	495	LEU	9.0
1	B	441	ARG	9.0
1	H	297	PRO	9.0
1	G	209	GLN	8.9
1	C	529	ASN	8.9
1	B	60	ASP	8.9
1	E	166	GLN	8.9
1	D	112	PRO	8.9
1	D	480	LEU	8.9
1	D	315	CYS	8.9
1	E	528	LYS	8.9
1	F	329	ASP	8.9
1	G	215	LYS	8.9
1	H	497	ARG	8.9
1	E	84	VAL	8.9
1	C	330	GLU	8.9
1	G	448	GLU	8.9

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Mol	Chain	Res	Type	RSRZ
1	B	580	PHE	8.9
1	H	127	ARG	8.9
1	A	12	THR	8.9
1	F	535	ILE	8.9
1	H	379	GLY	8.9
1	F	534	VAL	8.9
1	A	76	ILE	8.8
1	C	299	LYS	8.8
1	F	551	VAL	8.8
1	F	33	ALA	8.8
1	E	529	ASN	8.8
1	G	242	MET	8.8
1	C	10	TRP	8.8
1	A	444	GLN	8.8
1	B	430	ASN	8.8
1	C	199	THR	8.8
1	D	540	SER	8.8
1	B	163	TYR	8.8
1	B	427	HIS	8.8
1	B	106	GLY	8.8
1	D	83	TYR	8.8
1	A	123	THR	8.8
1	H	427	HIS	8.8
1	H	295	MET	8.8
1	B	481	LEU	8.8
1	B	391	ARG	8.8
1	D	123	THR	8.8
1	D	285	THR	8.8
1	A	196	MET	8.8
1	D	459	ALA	8.8
1	D	539	LEU	8.8
1	C	253	PRO	8.8
1	E	103	ARG	8.8
1	E	488	ARG	8.8
1	D	332	LYS	8.8
1	C	244	MET	8.8
1	E	42	THR	8.8
1	D	393	TYR	8.8
1	D	489	ILE	8.8
1	H	435	ASN	8.8
1	C	202	GLN	8.8
1	F	48	LEU	8.8

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Mol	Chain	Res	Type	RSRZ
1	C	576	HIS	8.8
1	D	103	ARG	8.8
1	F	95	LYS	8.8
1	A	336	GLU	8.7
1	A	83	TYR	8.7
1	B	461	ASP	8.7
1	F	528	LYS	8.7
1	B	436	ASN	8.7
1	B	225	VAL	8.7
1	B	460	MET	8.7
1	B	232	LYS	8.7
1	A	464	ASN	8.7
1	C	399	GLU	8.7
1	C	390	THR	8.7
1	D	572	TYR	8.7
1	E	46	SER	8.7
1	E	341	ASP	8.7
1	H	15	ARG	8.7
1	F	456	MET	8.7
1	C	248	SER	8.7
1	A	389	ILE	8.7
1	D	376	GLY	8.7
1	B	100	MET	8.7
1	A	441	ARG	8.7
1	C	571	VAL	8.7
1	B	484	GLY	8.7
1	F	467	ASP	8.7
1	E	397	GLU	8.6
1	D	51	LEU	8.6
1	G	474	ILE	8.6
1	H	150	GLY	8.6
1	D	518	ALA	8.6
1	E	245	VAL	8.6
1	H	328	LYS	8.6
1	B	432	THR	8.6
1	D	210	MET	8.6
1	E	169	ILE	8.6
1	H	244	MET	8.6
1	A	420	ALA	8.6
1	H	249	SER	8.6
1	D	485	GLN	8.6
1	G	227	THR	8.6

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Mol	Chain	Res	Type	RSRZ
1	H	210	MET	8.6
1	E	555	VAL	8.6
1	F	181	ALA	8.6
1	A	53	ASP	8.6
1	G	202	GLN	8.6
1	A	151	ALA	8.6
1	C	30	ALA	8.6
1	C	463	ILE	8.6
1	B	178	VAL	8.6
1	E	538	ARG	8.6
1	C	427	HIS	8.6
1	F	223	GLN	8.6
1	C	26	GLY	8.6
1	D	560	GLY	8.6
1	E	61	ARG	8.6
1	G	357	PRO	8.6
1	H	155	GLY	8.6
1	A	61	ARG	8.6
1	D	567	GLU	8.5
1	A	191	ASN	8.5
1	B	289	SER	8.5
1	E	290	SER	8.5
1	D	370	LYS	8.5
1	F	290	SER	8.5
1	F	229	ARG	8.5
1	G	447	ARG	8.5
1	G	540	SER	8.5
1	A	334	VAL	8.5
1	A	532	SER	8.5
1	D	193	SER	8.5
1	D	549	VAL	8.5
1	G	302	THR	8.5
1	D	167	LEU	8.5
1	E	10	TRP	8.5
1	B	505	ASP	8.5
1	D	402	MET	8.5
1	D	365	LYS	8.5
1	B	393	TYR	8.5
1	G	573	ALA	8.5
1	B	87	TYR	8.5
1	B	27	LEU	8.5
1	G	73	GLY	8.5

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Mol	Chain	Res	Type	RSRZ
1	A	277	ASP	8.4
1	E	390	THR	8.4
1	G	128	ILE	8.4
1	A	310	ARG	8.4
1	B	307	GLN	8.4
1	G	471	ASP	8.4
1	A	577	LYS	8.4
1	B	130	TYR	8.4
1	G	431	ASP	8.4
1	B	285	THR	8.4
1	H	421	LEU	8.4
1	C	558	GLU	8.4
1	H	546	ASP	8.4
1	A	511	LEU	8.4
1	H	515	SER	8.4
1	C	169	ILE	8.4
1	E	332	LYS	8.4
1	C	230	PHE	8.4
1	C	405	HIS	8.4
1	D	446	SER	8.4
1	A	63	VAL	8.4
1	H	329	ASP	8.4
1	A	381	GLY	8.4
1	G	250	ILE	8.4
1	F	86	SER	8.4
1	F	567	GLU	8.4
1	A	207	ALA	8.4
1	B	308	PHE	8.4
1	A	26	GLY	8.4
1	H	335	ILE	8.4
1	C	59	THR	8.4
1	C	380	SER	8.4
1	A	229	ARG	8.4
1	C	235	ASN	8.4
1	E	259	ALA	8.4
1	F	74	LEU	8.4
1	G	80	ILE	8.4
1	C	382	LYS	8.3
1	A	209	GLN	8.3
1	E	113	VAL	8.3
1	C	552	GLU	8.3
1	H	412	LEU	8.3

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Mol	Chain	Res	Type	RSRZ
1	G	399	GLU	8.3
1	G	230	PHE	8.3
1	E	91	TRP	8.3
1	F	470	LEU	8.3
1	E	340	GLY	8.3
1	E	501	ILE	8.3
1	F	99	THR	8.3
1	F	333	ARG	8.3
1	F	571	VAL	8.3
1	H	487	GLN	8.3
1	A	393	TYR	8.3
1	D	165	TRP	8.3
1	G	328	LYS	8.3
1	E	389	ILE	8.3
1	B	539	LEU	8.3
1	C	376	GLY	8.3
1	E	279	LEU	8.3
1	G	280	THR	8.3
1	E	450	ILE	8.3
1	G	509	SER	8.3
1	H	194	LYS	8.3
1	D	261	LEU	8.2
1	F	319	PHE	8.2
1	F	403	ASP	8.2
1	H	85	SER	8.2
1	F	325	GLU	8.2
1	C	439	TYR	8.2
1	B	397	GLU	8.2
1	F	578	MET	8.2
1	G	514	GLU	8.2
1	G	397	GLU	8.2
1	G	503	ILE	8.2
1	H	446	SER	8.2
1	G	459	ALA	8.2
1	C	133	GLU	8.2
1	D	231	ASP	8.2
1	G	424	GLN	8.2
1	B	154	ILE	8.2
1	A	455	ARG	8.2
1	H	481	LEU	8.2
1	D	419	VAL	8.2
1	G	112	PRO	8.2

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Mol	Chain	Res	Type	RSRZ
1	H	90	SER	8.2
1	C	569	ARG	8.2
1	B	517	ARG	8.2
1	F	417	ASN	8.2
1	F	294	LEU	8.2
1	B	540	SER	8.2
1	D	362	ILE	8.2
1	F	165	TRP	8.2
1	G	571	VAL	8.1
1	D	442	THR	8.1
1	D	249	SER	8.1
1	F	316	GLN	8.1
1	B	303	ASN	8.1
1	E	230	PHE	8.1
1	H	314	ALA	8.1
1	E	357	PRO	8.1
1	C	477	ASN	8.1
1	E	289	SER	8.1
1	G	529	ASN	8.1
1	A	200	MET	8.1
1	C	72	ILE	8.1
1	D	230	PHE	8.1
1	B	69	LEU	8.1
1	G	207	ALA	8.1
1	E	237	MET	8.1
1	B	448	GLU	8.1
1	G	396	ASP	8.1
1	A	399	GLU	8.1
1	D	349	PHE	8.1
1	F	112	PRO	8.1
1	C	167	LEU	8.1
1	F	568	HIS	8.0
1	G	485	GLN	8.0
1	E	423	SER	8.0
1	F	511	LEU	8.0
1	G	133	GLU	8.0
1	H	14	ARG	8.0
1	B	151	ALA	8.0
1	D	66	TRP	8.0
1	F	106	GLY	8.0
1	G	427	HIS	8.0
1	C	319	PHE	8.0

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Mol	Chain	Res	Type	RSRZ
1	H	536	ALA	8.0
1	D	391	ARG	8.0
1	C	368	ALA	8.0
1	A	129	THR	8.0
1	A	561	THR	8.0
1	H	303	ASN	8.0
1	F	273	PRO	8.0
1	D	55	GLY	8.0
1	C	535	ILE	8.0
1	F	499	SER	8.0
1	E	536	ALA	8.0
1	A	427	HIS	8.0
1	C	453	ALA	8.0
1	D	552	GLU	8.0
1	A	430	ASN	8.0
1	G	568	HIS	8.0
1	H	278	SER	8.0
1	D	30	ALA	7.9
1	A	502	LEU	7.9
1	F	471	ASP	7.9
1	E	313	ALA	7.9
1	C	333	ARG	7.9
1	A	462	PHE	7.9
1	A	148	ARG	7.9
1	G	558	GLU	7.9
1	A	330	GLU	7.9
1	F	400	ILE	7.9
1	E	122	GLY	7.9
1	A	155	GLY	7.9
1	A	282	GLY	7.9
1	F	209	GLN	7.9
1	H	443	GLU	7.9
1	G	41	ASP	7.9
1	G	343	GLU	7.9
1	A	460	MET	7.9
1	B	451	GLU	7.9
1	C	468	ASN	7.9
1	D	431	ASP	7.9
1	B	92	VAL	7.9
1	G	229	ARG	7.9
1	B	342	VAL	7.9
1	D	330	GLU	7.9

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Mol	Chain	Res	Type	RSRZ
1	E	399	GLU	7.9
1	F	308	PHE	7.9
1	B	478	GLY	7.9
1	F	222	GLY	7.9
1	H	501	ILE	7.9
1	H	93	SER	7.9
1	A	93	SER	7.9
1	E	131	ASP	7.8
1	E	431	ASP	7.8
1	F	537	HIS	7.8
1	H	37	ASN	7.8
1	C	211	LEU	7.8
1	E	210	MET	7.8
1	F	563	ASN	7.8
1	H	509	SER	7.8
1	D	410	TYR	7.8
1	G	520	GLN	7.8
1	H	222	GLY	7.8
1	G	405	HIS	7.8
1	A	212	LYS	7.8
1	E	18	PRO	7.8
1	B	404	GLY	7.8
1	F	51	LEU	7.8
1	F	424	GLN	7.8
1	B	516	GLU	7.8
1	E	558	GLU	7.8
1	F	26	GLY	7.8
1	G	228	LYS	7.8
1	G	219	ILE	7.8
1	B	572	TYR	7.8
1	E	432	THR	7.8
1	D	35	ILE	7.8
1	E	326	GLN	7.8
1	A	472	THR	7.8
1	C	138	SER	7.8
1	G	570	GLY	7.8
1	G	501	ILE	7.8
1	C	426	VAL	7.8
1	F	78	ARG	7.8
1	E	300	SER	7.7
1	E	311	GLY	7.7
1	C	109	MET	7.7

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Mol	Chain	Res	Type	RSRZ
1	E	443	GLU	7.7
1	E	72	ILE	7.7
1	B	354	ARG	7.7
1	F	359	LEU	7.7
1	F	32	VAL	7.7
1	H	131	ASP	7.7
1	B	48	LEU	7.7
1	A	190	ARG	7.7
1	B	440	ALA	7.7
1	F	190	ARG	7.7
1	G	461	ASP	7.7
1	B	575	LEU	7.7
1	B	156	LEU	7.7
1	F	140	SER	7.7
1	C	39	ALA	7.7
1	B	471	ASP	7.7
1	D	212	LYS	7.7
1	A	566	LEU	7.7
1	D	307	GLN	7.7
1	A	417	ASN	7.7
1	H	190	ARG	7.7
1	E	385	ILE	7.7
1	C	100	MET	7.7
1	E	419	VAL	7.7
1	E	262	ALA	7.7
1	F	94	GLY	7.7
1	F	494	ALA	7.7
1	E	336	GLU	7.7
1	C	273	PRO	7.7
1	G	113	VAL	7.7
1	B	125	LEU	7.7
1	B	91	TRP	7.7
1	C	225	VAL	7.7
1	D	70	VAL	7.7
1	B	77	LEU	7.7
1	D	163	TYR	7.7
1	F	28	ILE	7.6
1	C	327	GLU	7.6
1	D	545	ALA	7.6
1	H	395	ILE	7.6
1	D	36	LEU	7.6
1	D	298	LEU	7.6

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Mol	Chain	Res	Type	RSRZ
1	C	185	VAL	7.6
1	G	329	ASP	7.6
1	G	564	ASP	7.6
1	H	408	ARG	7.6
1	A	523	LEU	7.6
1	A	121	THR	7.6
1	E	571	VAL	7.6
1	C	136	ALA	7.6
1	E	580	PHE	7.6
1	C	548	ILE	7.6
1	B	264	ALA	7.6
1	C	69	LEU	7.6
1	E	527	GLN	7.6
1	G	13	PHE	7.6
1	H	436	ASN	7.6
1	H	556	ILE	7.6
1	E	185	VAL	7.6
1	F	240	GLN	7.6
1	G	214	HIS	7.6
1	G	451	GLU	7.6
1	H	245	VAL	7.6
1	B	139	SER	7.6
1	E	181	ALA	7.6
1	G	454	ALA	7.6
1	G	47	LEU	7.6
1	E	306	ALA	7.6
1	E	138	SER	7.6
1	E	517	ARG	7.6
1	G	491	ILE	7.6
1	E	376	GLY	7.6
1	A	501	ILE	7.6
1	A	452	GLU	7.5
1	H	394	ASP	7.5
1	H	535	ILE	7.5
1	G	146	VAL	7.5
1	G	267	LEU	7.5
1	A	201	GLY	7.5
1	E	106	GLY	7.5
1	C	516	GLU	7.5
1	B	369	GLY	7.5
1	H	315	CYS	7.5
1	F	58	LYS	7.5

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Mol	Chain	Res	Type	RSRZ
1	D	427	HIS	7.5
1	E	559	ARG	7.5
1	D	580	PHE	7.5
1	D	73	GLY	7.5
1	E	208	GLU	7.5
1	H	55	GLY	7.5
1	B	179	SER	7.5
1	F	287	VAL	7.5
1	F	307	GLN	7.5
1	B	530	ARG	7.5
1	D	258	ILE	7.5
1	C	38	ALA	7.5
1	H	572	TYR	7.5
1	H	411	THR	7.5
1	A	211	LEU	7.5
1	B	216	GLU	7.5
1	D	390	THR	7.5
1	H	48	LEU	7.5
1	C	404	GLY	7.4
1	H	108	MET	7.4
1	C	363	ASN	7.4
1	E	147	VAL	7.4
1	D	255	ILE	7.4
1	H	115	PHE	7.4
1	A	30	ALA	7.4
1	H	461	ASP	7.4
1	B	392	PHE	7.4
1	H	496	LEU	7.4
1	E	224	GLU	7.4
1	A	213	GLY	7.4
1	F	347	VAL	7.4
1	A	17	TRP	7.4
1	A	401	LEU	7.4
1	H	139	SER	7.4
1	D	553	ASP	7.4
1	C	65	VAL	7.4
1	G	289	SER	7.4
1	G	170	ILE	7.4
1	G	450	ILE	7.4
1	D	488	ARG	7.4
1	E	378	SER	7.4
1	F	448	GLU	7.4

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Mol	Chain	Res	Type	RSRZ
1	A	370	LYS	7.4
1	F	483	GLY	7.4
1	A	131	ASP	7.4
1	E	520	GLN	7.4
1	A	106	GLY	7.4
1	B	183	ARG	7.4
1	B	486	ARG	7.4
1	G	208	GLU	7.4
1	F	328	LYS	7.4
1	F	454	ALA	7.4
1	B	452	GLU	7.4
1	E	394	ASP	7.4
1	D	102	ARG	7.4
1	D	207	ALA	7.4
1	H	538	ARG	7.4
1	G	336	GLU	7.4
1	C	161	PHE	7.4
1	A	41	ASP	7.4
1	F	376	GLY	7.4
1	G	163	TYR	7.4
1	B	133	GLU	7.4
1	A	290	SER	7.3
1	B	553	ASP	7.3
1	F	547	GLU	7.3
1	A	326	GLN	7.3
1	F	538	ARG	7.3
1	C	305	ASN	7.3
1	D	82	SER	7.3
1	E	448	GLU	7.3
1	E	274	SER	7.3
1	G	543	GLU	7.3
1	G	547	GLU	7.3
1	A	20	ILE	7.3
1	E	344	PHE	7.3
1	C	157	PHE	7.3
1	C	488	ARG	7.3
1	H	283	THR	7.3
1	E	496	LEU	7.3
1	E	542	ILE	7.3
1	D	356	VAL	7.3
1	F	344	PHE	7.3
1	C	442	THR	7.3

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Mol	Chain	Res	Type	RSRZ
1	A	110	GLY	7.3
1	E	174	LEU	7.3
1	A	197	GLN	7.3
1	G	114	SER	7.2
1	E	124	LEU	7.2
1	E	462	PHE	7.2
1	C	396	ASP	7.2
1	D	39	ALA	7.2
1	A	84	VAL	7.2
1	D	19	THR	7.2
1	B	444	GLN	7.2
1	C	567	GLU	7.2
1	A	553	ASP	7.2
1	A	276	MET	7.2
1	E	193	SER	7.2
1	F	100	MET	7.2
1	A	294	LEU	7.2
1	G	284	ILE	7.2
1	B	260	SER	7.2
1	F	440	ALA	7.2
1	G	204	THR	7.2
1	H	68	PRO	7.2
1	B	117	ASP	7.2
1	F	61	ARG	7.2
1	D	428	LEU	7.2
1	H	291	MET	7.2
1	C	144	ILE	7.2
1	B	454	ALA	7.2
1	D	69	LEU	7.2
1	A	224	GLU	7.2
1	C	78	ARG	7.1
1	E	323	ASP	7.1
1	G	458	TYR	7.1
1	A	572	TYR	7.1
1	G	226	GLU	7.1
1	D	336	GLU	7.1
1	H	380	SER	7.1
1	F	323	ASP	7.1
1	G	283	THR	7.1
1	H	163	TYR	7.1
1	F	386	ALA	7.1
1	G	394	ASP	7.1

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Mol	Chain	Res	Type	RSRZ
1	D	189	PHE	7.1
1	B	72	ILE	7.1
1	A	319	PHE	7.1
1	F	555	VAL	7.1
1	E	574	GLN	7.1
1	A	489	ILE	7.1
1	C	274	SER	7.1
1	A	505	ASP	7.1
1	H	280	THR	7.1
1	E	490	ALA	7.1
1	F	390	THR	7.1
1	B	337	ARG	7.1
1	G	538	ARG	7.1
1	D	45	LEU	7.1
1	B	120	SER	7.1
1	B	211	LEU	7.1
1	A	435	ASN	7.1
1	H	75	MET	7.1
1	F	331	GLY	7.1
1	B	390	THR	7.1
1	H	361	ASN	7.1
1	E	51	LEU	7.1
1	E	168	SER	7.1
1	H	95	LYS	7.1
1	C	446	SER	7.0
1	G	439	TYR	7.0
1	A	11	GLN	7.0
1	A	473	VAL	7.0
1	G	488	ARG	7.0
1	G	123	THR	7.0
1	G	145	THR	7.0
1	H	574	GLN	7.0
1	G	541	THR	7.0
1	B	398	GLY	7.0
1	A	391	ARG	7.0
1	B	80	ILE	7.0
1	C	400	ILE	7.0
1	D	151	ALA	7.0
1	F	53	ASP	7.0
1	B	217	VAL	7.0
1	E	213	GLY	7.0
1	A	465	LYS	7.0

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Mol	Chain	Res	Type	RSRZ
1	D	203	VAL	7.0
1	H	87	TYR	7.0
1	E	544	LYS	7.0
1	C	553	ASP	7.0
1	F	322	LEU	7.0
1	F	21	ALA	7.0
1	E	543	GLU	7.0
1	H	311	GLY	7.0
1	A	75	MET	7.0
1	D	490	ALA	7.0
1	A	514	GLU	7.0
1	A	112	PRO	7.0
1	C	317	THR	7.0
1	E	20	ILE	7.0
1	G	495	LEU	7.0
1	G	418	GLN	7.0
1	A	105	PHE	6.9
1	C	420	ALA	6.9
1	B	496	LEU	6.9
1	C	455	ARG	6.9
1	C	237	MET	6.9
1	C	515	SER	6.9
1	E	115	PHE	6.9
1	A	203	VAL	6.9
1	C	413	ALA	6.9
1	D	465	LYS	6.9
1	B	317	THR	6.9
1	B	339	THR	6.9
1	D	42	THR	6.9
1	C	430	ASN	6.9
1	D	363	ASN	6.9
1	G	130	TYR	6.9
1	D	100	MET	6.9
1	E	53	ASP	6.9
1	A	477	ASN	6.9
1	B	78	ARG	6.9
1	B	256	GLN	6.9
1	C	336	GLU	6.9
1	E	246	SER	6.9
1	F	164	SER	6.9
1	A	507	ALA	6.9
1	C	370	LYS	6.9

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Mol	Chain	Res	Type	RSRZ
1	H	563	ASN	6.9
1	A	173	VAL	6.9
1	A	488	ARG	6.9
1	B	63	VAL	6.9
1	D	244	MET	6.9
1	B	561	THR	6.9
1	G	262	ALA	6.9
1	B	352	PRO	6.9
1	C	407	LEU	6.9
1	C	20	ILE	6.9
1	E	486	ARG	6.9
1	G	555	VAL	6.9
1	G	74	LEU	6.9
1	B	374	LEU	6.9
1	D	407	LEU	6.9
1	E	472	THR	6.8
1	G	78	ARG	6.8
1	H	10	TRP	6.8
1	B	509	SER	6.8
1	D	421	LEU	6.8
1	F	463	ILE	6.8
1	F	401	LEU	6.8
1	H	534	VAL	6.8
1	B	357	PRO	6.8
1	B	447	ARG	6.8
1	B	109	MET	6.8
1	H	562	HIS	6.8
1	A	394	ASP	6.8
1	A	519	ILE	6.8
1	G	101	ARG	6.8
1	B	363	ASN	6.8
1	A	70	VAL	6.8
1	B	534	VAL	6.8
1	G	332	LYS	6.8
1	G	480	LEU	6.8
1	D	17	TRP	6.8
1	F	549	VAL	6.8
1	D	186	SER	6.8
1	D	96	VAL	6.8
1	D	106	GLY	6.8
1	A	139	SER	6.8
1	D	132	SER	6.8

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Mol	Chain	Res	Type	RSRZ
1	E	74	LEU	6.8
1	E	153	ILE	6.8
1	E	19	THR	6.8
1	H	38	ALA	6.8
1	F	64	LEU	6.8
1	E	387	SER	6.8
1	B	420	ALA	6.8
1	E	552	GLU	6.8
1	H	529	ASN	6.8
1	H	172	ILE	6.8
1	B	201	GLY	6.7
1	E	120	SER	6.7
1	F	422	VAL	6.7
1	F	355	ASP	6.7
1	D	289	SER	6.7
1	E	67	MET	6.7
1	E	418	GLN	6.7
1	G	278	SER	6.7
1	B	172	ILE	6.7
1	B	10	TRP	6.7
1	B	127	ARG	6.7
1	B	402	MET	6.7
1	D	14	ARG	6.7
1	E	567	GLU	6.7
1	F	211	LEU	6.7
1	C	532	SER	6.7
1	G	193	SER	6.7
1	A	338	ALA	6.7
1	H	459	ALA	6.7
1	B	140	SER	6.7
1	E	217	VAL	6.7
1	H	491	ILE	6.7
1	B	309	GLN	6.7
1	H	103	ARG	6.7
1	H	551	VAL	6.7
1	E	350	THR	6.7
1	C	124	LEU	6.7
1	C	392	PHE	6.7
1	F	539	LEU	6.7
1	A	499	SER	6.7
1	C	41	ASP	6.7
1	F	147	VAL	6.7

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Mol	Chain	Res	Type	RSRZ
1	C	300	SER	6.7
1	H	352	PRO	6.7
1	H	469	GLY	6.7
1	C	510	ALA	6.7
1	C	542	ILE	6.7
1	G	185	VAL	6.7
1	H	31	GLY	6.7
1	B	468	ASN	6.6
1	E	270	ALA	6.6
1	F	413	ALA	6.6
1	F	176	PRO	6.6
1	E	78	ARG	6.6
1	F	446	SER	6.6
1	G	26	GLY	6.6
1	A	431	ASP	6.6
1	B	431	ASP	6.6
1	A	36	LEU	6.6
1	B	554	GLY	6.6
1	F	421	LEU	6.6
1	G	318	LEU	6.6
1	H	484	GLY	6.6
1	F	83	TYR	6.6
1	A	165	TRP	6.6
1	H	128	ILE	6.6
1	C	562	HIS	6.6
1	D	484	GLY	6.6
1	E	223	GLN	6.6
1	A	421	LEU	6.6
1	A	241	GLY	6.6
1	C	110	GLY	6.6
1	D	509	SER	6.6
1	G	200	MET	6.6
1	H	193	SER	6.6
1	B	488	ARG	6.6
1	D	408	ARG	6.6
1	B	373	ALA	6.6
1	C	434	ALA	6.6
1	E	41	ASP	6.6
1	E	539	LEU	6.5
1	F	216	GLU	6.6
1	F	526	LEU	6.5
1	H	426	VAL	6.5

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Mol	Chain	Res	Type	RSRZ
1	H	414	SER	6.5
1	E	71	VAL	6.5
1	C	270	ALA	6.5
1	D	37	ASN	6.5
1	G	93	SER	6.5
1	A	174	LEU	6.5
1	F	39	ALA	6.5
1	H	123	THR	6.5
1	G	393	TYR	6.5
1	H	160	MET	6.5
1	H	466	MET	6.5
1	E	34	LEU	6.5
1	H	23	PHE	6.5
1	H	116	PHE	6.5
1	G	61	ARG	6.5
1	F	65	VAL	6.5
1	H	308	PHE	6.5
1	G	436	ASN	6.5
1	H	223	GLN	6.5
1	B	394	ASP	6.5
1	C	263	LEU	6.5
1	C	481	LEU	6.5
1	E	177	ILE	6.5
1	B	286	VAL	6.5
1	B	537	HIS	6.5
1	F	430	ASN	6.5
1	H	492	ALA	6.5
1	D	414	SER	6.5
1	H	517	ARG	6.5
1	B	343	GLU	6.5
1	F	527	GLN	6.5
1	H	306	ALA	6.5
1	G	408	ARG	6.5
1	C	88	CYS	6.5
1	F	93	SER	6.5
1	E	466	MET	6.5
1	F	113	VAL	6.5
1	F	405	HIS	6.5
1	H	56	PHE	6.4
1	H	183	ARG	6.4
1	F	256	GLN	6.4
1	A	156	LEU	6.4

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Mol	Chain	Res	Type	RSRZ
1	E	515	SER	6.4
1	B	297	PRO	6.4
1	H	434	ALA	6.4
1	B	331	GLY	6.4
1	B	542	ILE	6.4
1	B	169	ILE	6.4
1	B	198	ASN	6.4
1	F	259	ALA	6.4
1	E	243	LYS	6.4
1	D	114	SER	6.4
1	B	377	ARG	6.4
1	G	33	ALA	6.4
1	A	466	MET	6.4
1	D	256	GLN	6.4
1	H	555	VAL	6.4
1	A	104	LEU	6.4
1	G	195	ASN	6.4
1	B	164	SER	6.4
1	G	155	GLY	6.4
1	G	316	GLN	6.4
1	B	345	ARG	6.4
1	E	167	LEU	6.4
1	C	86	SER	6.4
1	E	381	GLY	6.4
1	D	215	LYS	6.4
1	D	487	GLN	6.4
1	F	136	ALA	6.4
1	G	475	GLY	6.4
1	G	553	ASP	6.4
1	G	419	VAL	6.4
1	H	324	SER	6.4
1	F	310	ARG	6.4
1	B	255	ILE	6.4
1	C	410	TYR	6.4
1	C	351	TYR	6.4
1	E	250	ILE	6.3
1	A	227	THR	6.3
1	H	420	ALA	6.3
1	G	40	SER	6.3
1	C	551	VAL	6.3
1	A	361	ASN	6.3
1	D	238	ARG	6.3

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Mol	Chain	Res	Type	RSRZ
1	E	551	VAL	6.3
1	H	317	THR	6.3
1	A	37	ASN	6.3
1	F	243	LYS	6.3
1	F	514	GLU	6.3
1	F	357	PRO	6.3
1	F	249	SER	6.3
1	B	209	GLN	6.3
1	D	290	SER	6.3
1	D	325	GLU	6.3
1	F	516	GLU	6.3
1	A	109	MET	6.3
1	B	552	GLU	6.3
1	B	311	GLY	6.3
1	B	168	SER	6.3
1	D	426	VAL	6.3
1	D	334	VAL	6.3
1	C	487	GLN	6.3
1	H	293	ALA	6.3
1	G	86	SER	6.3
1	B	419	VAL	6.3
1	D	531	THR	6.3
1	B	124	LEU	6.3
1	D	236	ARG	6.3
1	C	201	GLY	6.3
1	A	71	VAL	6.3
1	E	96	VAL	6.3
1	F	380	SER	6.3
1	G	528	LYS	6.3
1	D	75	MET	6.3
1	C	337	ARG	6.3
1	A	312	MET	6.2
1	C	492	ALA	6.2
1	F	496	LEU	6.2
1	H	215	LYS	6.2
1	E	73	GLY	6.2
1	D	284	ILE	6.2
1	G	550	VAL	6.2
1	E	395	ILE	6.2
1	H	437	ILE	6.2
1	F	129	THR	6.2
1	A	291	MET	6.2

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Mol	Chain	Res	Type	RSRZ
1	B	490	ALA	6.2
1	H	99	THR	6.2
1	H	393	TYR	6.2
1	D	173	VAL	6.2
1	E	305	ASN	6.2
1	C	114	SER	6.2
1	E	294	LEU	6.2
1	G	132	SER	6.2
1	H	396	ASP	6.2
1	E	198	ASN	6.2
1	B	495	LEU	6.2
1	D	204	THR	6.2
1	C	419	VAL	6.2
1	B	42	THR	6.2
1	G	174	LEU	6.2
1	G	62	SER	6.2
1	B	519	ILE	6.2
1	C	385	ILE	6.2
1	F	487	GLN	6.2
1	G	581	GLY	6.2
1	B	304	VAL	6.2
1	D	397	GLU	6.2
1	E	57	GLY	6.2
1	B	494	ALA	6.1
1	G	490	ALA	6.1
1	A	214	HIS	6.1
1	B	456	MET	6.1
1	A	414	SER	6.1
1	E	273	PRO	6.1
1	B	153	ILE	6.1
1	C	132	SER	6.1
1	E	550	VAL	6.1
1	G	171	LEU	6.1
1	D	162	TYR	6.1
1	F	91	TRP	6.1
1	D	524	ASP	6.1
1	B	340	GLY	6.1
1	G	535	ILE	6.1
1	C	232	LYS	6.1
1	C	36	LEU	6.1
1	A	449	GLN	6.1
1	F	443	GLU	6.1

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Mol	Chain	Res	Type	RSRZ
1	D	177	ILE	6.1
1	D	263	LEU	6.1
1	A	533	LEU	6.1
1	G	24	LYS	6.1
1	B	403	ASP	6.1
1	C	77	LEU	6.1
1	E	241	GLY	6.1
1	A	15	ARG	6.1
1	E	256	GLN	6.1
1	F	300	SER	6.1
1	E	99	THR	6.1
1	E	271	SER	6.1
1	C	489	ILE	6.0
1	C	517	ARG	6.0
1	H	510	ALA	6.0
1	H	138	SER	6.0
1	B	375	VAL	6.0
1	H	270	ALA	6.0
1	H	224	GLU	6.0
1	F	20	ILE	6.0
1	H	205	THR	6.0
1	H	465	LYS	6.0
1	B	180	ILE	6.0
1	H	581	GLY	6.0
1	E	346	ASN	6.0
1	C	241	GLY	6.0
1	C	291	MET	6.0
1	C	126	SER	6.0
1	D	418	GLN	6.0
1	E	556	ILE	6.0
1	D	551	VAL	6.0
1	H	391	ARG	6.0
1	D	126	SER	6.0
1	D	360	ARG	6.0
1	G	236	ARG	6.0
1	H	570	GLY	6.0
1	B	274	SER	6.0
1	F	504	LEU	6.0
1	A	374	LEU	6.0
1	G	79	GLY	6.0
1	H	360	ARG	6.0
1	A	382	LYS	6.0

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Mol	Chain	Res	Type	RSRZ
1	C	357	PRO	6.0
1	A	158	ILE	6.0
1	C	71	VAL	6.0
1	A	88	CYS	6.0
1	C	82	SER	6.0
1	E	79	GLY	6.0
1	F	19	THR	6.0
1	B	176	PRO	6.0
1	B	442	THR	6.0
1	E	498	ASP	6.0
1	F	267	LEU	6.0
1	H	273	PRO	6.0
1	A	527	GLN	6.0
1	C	406	ASP	6.0
1	C	90	SER	6.0
1	C	512	ASP	6.0
1	H	514	GLU	6.0
1	E	121	THR	6.0
1	A	415	LEU	6.0
1	A	117	ASP	6.0
1	H	228	LYS	6.0
1	F	419	VAL	6.0
1	C	483	GLY	6.0
1	G	340	GLY	5.9
1	C	346	ASN	5.9
1	G	403	ASP	5.9
1	E	533	LEU	5.9
1	G	533	LEU	5.9
1	D	201	GLY	5.9
1	A	487	GLN	5.9
1	G	121	THR	5.9
1	E	179	SER	5.9
1	B	257	LEU	5.9
1	F	103	ARG	5.9
1	F	232	LYS	5.9
1	A	554	GLY	5.9
1	B	379	GLY	5.9
1	C	123	THR	5.9
1	G	51	LEU	5.9
1	G	326	GLN	5.9
1	A	321	ILE	5.9
1	H	349	PHE	5.9

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Mol	Chain	Res	Type	RSRZ
1	C	172	ILE	5.9
1	G	412	LEU	5.9
1	E	295	MET	5.9
1	A	369	GLY	5.9
1	G	345	ARG	5.9
1	H	11	GLN	5.9
1	F	288	PHE	5.9
1	G	324	SER	5.9
1	B	464	ASN	5.9
1	A	230	PHE	5.9
1	A	353	GLY	5.9
1	F	518	ALA	5.9
1	H	132	SER	5.9
1	F	252	ASP	5.9
1	A	187	LYS	5.8
1	B	206	SER	5.9
1	H	242	MET	5.8
1	A	509	SER	5.8
1	E	85	SER	5.8
1	D	235	ASN	5.8
1	E	535	ILE	5.8
1	G	312	MET	5.8
1	A	234	SER	5.8
1	D	532	SER	5.8
1	F	104	LEU	5.8
1	F	280	THR	5.8
1	H	185	VAL	5.8
1	B	476	GLU	5.8
1	H	221	GLY	5.8
1	E	392	PHE	5.8
1	B	83	TYR	5.8
1	G	212	LYS	5.8
1	G	276	MET	5.8
1	D	154	ILE	5.8
1	D	320	THR	5.8
1	C	298	LEU	5.8
1	E	216	GLU	5.8
1	F	541	THR	5.8
1	G	523	LEU	5.8
1	D	13	PHE	5.8
1	H	44	MET	5.8
1	D	79	GLY	5.8

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Mol	Chain	Res	Type	RSRZ
1	D	448	GLU	5.8
1	A	542	ILE	5.8
1	F	206	SER	5.8
1	G	518	ALA	5.8
1	F	37	ASN	5.8
1	C	476	GLU	5.8
1	A	498	ASP	5.8
1	F	428	LEU	5.8
1	E	95	LYS	5.8
1	H	51	LEU	5.8
1	D	148	ARG	5.8
1	F	577	LYS	5.8
1	A	549	VAL	5.7
1	D	128	ILE	5.7
1	A	376	GLY	5.7
1	B	438	ALA	5.7
1	G	369	GLY	5.7
1	A	179	SER	5.7
1	F	179	SER	5.7
1	C	499	SER	5.7
1	E	29	VAL	5.7
1	H	197	GLN	5.7
1	C	279	LEU	5.7
1	G	327	GLU	5.7
1	C	486	ARG	5.7
1	G	205	THR	5.7
1	F	268	TYR	5.7
1	A	451	GLU	5.7
1	F	512	ASP	5.7
1	A	494	ALA	5.7
1	G	281	ALA	5.7
1	A	504	LEU	5.7
1	B	560	GLY	5.7
1	D	246	SER	5.7
1	A	335	ILE	5.7
1	D	104	LEU	5.7
1	C	449	GLN	5.7
1	D	149	GLU	5.7
1	H	554	GLY	5.7
1	G	99	THR	5.7
1	H	198	ASN	5.7
1	B	498	ASP	5.7

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Mol	Chain	Res	Type	RSRZ
1	H	464	ASN	5.7
1	C	557	VAL	5.7
1	A	140	SER	5.7
1	D	174	LEU	5.7
1	A	564	ASP	5.7
1	A	10	TRP	5.7
1	D	441	ARG	5.7
1	A	352	PRO	5.7
1	G	395	ILE	5.7
1	H	347	VAL	5.6
1	C	526	LEU	5.6
1	B	269	ALA	5.6
1	E	197	GLN	5.6
1	G	499	SER	5.6
1	G	515	SER	5.6
1	C	219	ILE	5.6
1	H	30	ALA	5.6
1	B	413	ALA	5.6
1	F	434	ALA	5.6
1	C	375	VAL	5.6
1	F	573	ALA	5.6
1	A	434	ALA	5.6
1	H	390	THR	5.6
1	B	472	THR	5.6
1	F	22	PRO	5.6
1	D	494	ALA	5.6
1	G	314	ALA	5.6
1	H	359	LEU	5.6
1	C	286	VAL	5.6
1	E	309	GLN	5.6
1	H	239	LEU	5.6
1	G	85	SER	5.6
1	E	276	MET	5.6
1	B	550	VAL	5.6
1	F	491	ILE	5.6
1	A	251	SER	5.6
1	F	345	ARG	5.6
1	B	213	GLY	5.6
1	D	542	ILE	5.6
1	C	179	SER	5.6
1	D	529	ASN	5.6
1	E	203	VAL	5.6

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Mol	Chain	Res	Type	RSRZ
1	G	551	VAL	5.6
1	H	452	GLU	5.6
1	G	299	LYS	5.6
1	E	268	TYR	5.6
1	D	398	GLY	5.6
1	G	375	VAL	5.5
1	F	195	ASN	5.5
1	H	325	GLU	5.5
1	E	155	GLY	5.5
1	A	133	GLU	5.5
1	D	67	MET	5.5
1	G	72	ILE	5.5
1	E	513	THR	5.5
1	A	315	CYS	5.5
1	C	227	THR	5.5
1	D	190	ARG	5.5
1	A	245	VAL	5.5
1	C	421	LEU	5.5
1	E	52	LEU	5.5
1	F	141	GLY	5.5
1	F	579	GLN	5.5
1	G	149	GLU	5.5
1	D	209	GLN	5.5
1	E	554	GLY	5.5
1	H	219	ILE	5.5
1	E	553	ASP	5.5
1	A	412	LEU	5.5
1	F	70	VAL	5.5
1	G	421	LEU	5.5
1	D	216	GLU	5.5
1	F	572	TYR	5.5
1	G	390	THR	5.5
1	F	217	VAL	5.5
1	A	457	ALA	5.5
1	E	327	GLU	5.5
1	E	134	GLN	5.5
1	F	166	GLN	5.5
1	E	54	ASP	5.5
1	G	355	ASP	5.5
1	B	366	ILE	5.5
1	G	484	GLY	5.5
1	G	377	ARG	5.5

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Mol	Chain	Res	Type	RSRZ
1	G	557	VAL	5.5
1	C	128	ILE	5.5
1	A	162	TYR	5.5
1	C	50	PRO	5.5
1	D	234	SER	5.5
1	G	96	VAL	5.5
1	C	42	THR	5.5
1	G	172	ILE	5.5
1	D	498	ASP	5.5
1	H	326	GLN	5.5
1	H	442	THR	5.5
1	B	33	ALA	5.5
1	C	68	PRO	5.5
1	C	490	ALA	5.5
1	F	431	ASP	5.5
1	B	485	GLN	5.5
1	E	269	ALA	5.5
1	H	422	VAL	5.5
1	G	166	GLN	5.5
1	A	217	VAL	5.5
1	C	276	MET	5.5
1	C	314	ALA	5.4
1	D	510	ALA	5.4
1	A	100	MET	5.4
1	A	152	SER	5.4
1	A	453	ALA	5.4
1	B	557	VAL	5.4
1	D	472	THR	5.4
1	D	347	VAL	5.4
1	A	496	LEU	5.4
1	C	207	ALA	5.4
1	E	63	VAL	5.4
1	G	389	ILE	5.4
1	H	409	GLU	5.4
1	H	339	THR	5.4
1	A	413	ALA	5.4
1	D	544	LYS	5.4
1	H	126	SER	5.4
1	C	101	ARG	5.4
1	D	84	VAL	5.4
1	B	353	GLY	5.4
1	C	11	GLN	5.4

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Mol	Chain	Res	Type	RSRZ
1	E	494	ALA	5.4
1	C	289	SER	5.4
1	E	427	HIS	5.4
1	C	190	ARG	5.4
1	E	441	ARG	5.4
1	A	456	MET	5.4
1	D	208	GLU	5.4
1	F	524	ASP	5.4
1	A	87	TYR	5.4
1	H	350	THR	5.4
1	H	184	VAL	5.4
1	D	314	ALA	5.4
1	C	278	SER	5.4
1	F	96	VAL	5.4
1	G	530	ARG	5.4
1	C	189	PHE	5.4
1	D	247	ALA	5.4
1	E	242	MET	5.4
1	H	388	LEU	5.4
1	B	147	VAL	5.4
1	E	339	THR	5.4
1	D	77	LEU	5.4
1	F	128	ILE	5.4
1	D	502	LEU	5.4
1	E	502	LEU	5.4
1	E	114	SER	5.4
1	E	578	MET	5.4
1	H	480	LEU	5.4
1	B	518	ALA	5.4
1	G	508	THR	5.3
1	C	435	ASN	5.3
1	H	109	MET	5.3
1	H	557	VAL	5.3
1	C	61	ARG	5.3
1	F	145	THR	5.3
1	A	296	ARG	5.3
1	D	48	LEU	5.3
1	D	342	VAL	5.3
1	C	141	GLY	5.3
1	E	457	ALA	5.3
1	D	133	GLU	5.3
1	E	342	VAL	5.3

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Mol	Chain	Res	Type	RSRZ
1	C	497	ARG	5.3
1	A	568	HIS	5.3
1	A	216	GLU	5.3
1	D	497	ARG	5.3
1	H	58	LYS	5.3
1	D	266	VAL	5.3
1	A	396	ASP	5.3
1	B	365	LYS	5.3
1	D	25	ALA	5.3
1	B	12	THR	5.3
1	C	25	ALA	5.3
1	G	360	ARG	5.3
1	A	13	PHE	5.3
1	G	468	ASN	5.3
1	E	123	THR	5.3
1	H	366	ILE	5.3
1	A	373	ALA	5.3
1	C	294	LEU	5.3
1	B	382	LYS	5.2
1	B	385	ILE	5.2
1	D	80	ILE	5.2
1	E	391	ARG	5.2
1	A	27	LEU	5.2
1	E	65	VAL	5.2
1	B	479	VAL	5.2
1	C	318	LEU	5.2
1	D	537	HIS	5.2
1	D	477	ASN	5.2
1	D	110	GLY	5.2
1	D	412	LEU	5.2
1	E	367	PRO	5.2
1	D	368	ALA	5.2
1	C	302	THR	5.2
1	H	550	VAL	5.2
1	G	315	CYS	5.2
1	H	457	ALA	5.2
1	A	57	GLY	5.2
1	A	225	VAL	5.2
1	C	171	LEU	5.2
1	H	168	SER	5.2
1	F	550	VAL	5.2
1	B	73	GLY	5.2

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Mol	Chain	Res	Type	RSRZ
1	H	213	GLY	5.2
1	C	452	GLU	5.2
1	B	389	ILE	5.2
1	E	105	PHE	5.2
1	B	51	LEU	5.2
1	H	18	PRO	5.2
1	C	205	THR	5.2
1	H	334	VAL	5.2
1	B	463	ILE	5.2
1	B	489	ILE	5.2
1	C	234	SER	5.2
1	F	266	VAL	5.2
1	B	344	PHE	5.2
1	G	273	PRO	5.2
1	C	89	ILE	5.2
1	D	318	LEU	5.2
1	H	73	GLY	5.2
1	C	142	ALA	5.2
1	G	432	THR	5.2
1	C	149	GLU	5.2
1	G	384	THR	5.2
1	F	262	ALA	5.2
1	H	367	PRO	5.2
1	B	533	LEU	5.1
1	D	272	PHE	5.1
1	C	531	THR	5.1
1	G	259	ALA	5.1
1	C	367	PRO	5.1
1	A	40	SER	5.1
1	F	338	ALA	5.1
1	B	203	VAL	5.1
1	F	298	LEU	5.1
1	H	47	LEU	5.1
1	H	279	LEU	5.1
1	A	114	SER	5.1
1	E	215	LYS	5.1
1	A	471	ASP	5.1
1	B	89	ILE	5.1
1	C	518	ALA	5.1
1	A	555	VAL	5.1
1	D	500	PRO	5.1
1	B	233	VAL	5.1

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Mol	Chain	Res	Type	RSRZ
1	D	211	LEU	5.1
1	A	286	VAL	5.1
1	A	375	VAL	5.1
1	B	386	ALA	5.1
1	D	379	GLY	5.1
1	F	237	MET	5.1
1	B	315	CYS	5.1
1	D	521	ALA	5.1
1	B	224	GLU	5.1
1	H	567	GLU	5.1
1	F	576	HIS	5.1
1	C	462	PHE	5.1
1	A	189	PHE	5.1
1	E	30	ALA	5.1
1	H	50	PRO	5.1
1	H	65	VAL	5.1
1	D	206	SER	5.1
1	D	389	ILE	5.1
1	F	364	LEU	5.1
1	C	525	GLU	5.1
1	F	324	SER	5.0
1	B	265	PHE	5.0
1	D	277	ASP	5.0
1	E	429	PHE	5.0
1	A	263	LEU	5.0
1	A	428	LEU	5.0
1	D	274	SER	5.0
1	E	473	VAL	5.0
1	G	127	ARG	5.0
1	E	17	TRP	5.0
1	A	29	VAL	5.0
1	A	99	THR	5.0
1	A	562	HIS	5.0
1	D	229	ARG	5.0
1	F	71	VAL	5.0
1	C	386	ALA	5.0
1	D	476	GLU	5.0
1	H	405	HIS	5.0
1	F	162	TYR	5.0
1	F	66	TRP	5.0
1	D	115	PHE	5.0
1	D	386	ALA	5.0

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Mol	Chain	Res	Type	RSRZ
1	D	81	THR	5.0
1	F	513	THR	5.0
1	A	135	VAL	5.0
1	B	97	VAL	5.0
1	H	530	ARG	5.0
1	D	278	SER	5.0
1	F	210	MET	5.0
1	C	533	LEU	5.0
1	C	361	ASN	5.0
1	F	73	GLY	5.0
1	F	493	ARG	5.0
1	A	327	GLU	5.0
1	A	350	THR	5.0
1	B	202	GLN	5.0
1	G	139	SER	5.0
1	B	407	LEU	5.0
1	H	362	ILE	5.0
1	A	403	ASP	5.0
1	C	153	ILE	5.0
1	D	141	GLY	5.0
1	A	317	THR	5.0
1	C	238	ARG	5.0
1	A	107	HIS	4.9
1	C	440	ALA	4.9
1	F	85	SER	4.9
1	F	365	LYS	4.9
1	D	222	GLY	4.9
1	E	13	PHE	4.9
1	G	129	THR	4.9
1	B	184	VAL	4.9
1	C	475	GLY	4.9
1	A	540	SER	4.9
1	A	302	THR	4.9
1	C	290	SER	4.9
1	D	40	SER	4.9
1	F	36	LEU	4.9
1	E	205	THR	4.9
1	C	502	LEU	4.9
1	F	362	ILE	4.9
1	E	130	TYR	4.9
1	B	341	ASP	4.9
1	E	374	LEU	4.9

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Mol	Chain	Res	Type	RSRZ
1	A	387	SER	4.9
1	C	397	GLU	4.9
1	E	156	LEU	4.9
1	E	456	MET	4.9
1	G	160	MET	4.9
1	B	18	PRO	4.9
1	F	348	THR	4.9
1	B	487	GLN	4.9
1	C	306	ALA	4.9
1	E	566	LEU	4.9
1	G	21	ALA	4.9
1	A	545	ALA	4.9
1	G	353	GLY	4.9
1	A	81	THR	4.9
1	B	119	GLN	4.9
1	C	416	ARG	4.9
1	F	105	PHE	4.9
1	B	41	ASP	4.9
1	D	392	PHE	4.9
1	D	63	VAL	4.9
1	D	171	LEU	4.9
1	D	233	VAL	4.9
1	F	25	ALA	4.9
1	H	25	ALA	4.9
1	A	299	LYS	4.9
1	A	178	VAL	4.9
1	C	564	ASP	4.9
1	C	243	LYS	4.8
1	D	483	GLY	4.8
1	E	334	VAL	4.8
1	C	494	ALA	4.8
1	H	331	GLY	4.8
1	H	106	GLY	4.8
1	E	324	SER	4.8
1	A	386	ALA	4.8
1	D	406	ASP	4.8
1	B	470	LEU	4.8
1	A	85	SER	4.8
1	F	116	PHE	4.8
1	H	256	GLN	4.8
1	E	119	GLN	4.8
1	E	206	SER	4.8

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Mol	Chain	Res	Type	RSRZ
1	G	493	ARG	4.8
1	C	70	VAL	4.8
1	D	439	TYR	4.8
1	D	147	VAL	4.8
1	E	393	TYR	4.8
1	E	481	LEU	4.8
1	H	294	LEU	4.8
1	C	208	GLU	4.8
1	E	345	ARG	4.8
1	F	473	VAL	4.8
1	G	258	ILE	4.8
1	C	264	ALA	4.8
1	G	135	VAL	4.8
1	B	434	ALA	4.8
1	C	74	LEU	4.8
1	H	406	ASP	4.8
1	B	250	ILE	4.8
1	C	412	LEU	4.8
1	E	497	ARG	4.8
1	F	581	GLY	4.8
1	A	485	GLN	4.8
1	D	364	LEU	4.8
1	E	476	GLU	4.8
1	F	263	LEU	4.8
1	H	389	ILE	4.8
1	C	217	VAL	4.8
1	D	416	ARG	4.8
1	F	489	ILE	4.8
1	H	241	GLY	4.8
1	A	345	ARG	4.8
1	F	133	GLU	4.8
1	C	224	GLU	4.8
1	D	383	SER	4.8
1	B	376	GLY	4.8
1	B	200	MET	4.8
1	A	450	ILE	4.8
1	F	35	ILE	4.8
1	B	148	ARG	4.7
1	D	319	PHE	4.7
1	D	420	ALA	4.7
1	A	170	ILE	4.7
1	H	312	MET	4.7

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Mol	Chain	Res	Type	RSRZ
1	C	197	GLN	4.7
1	D	422	VAL	4.7
1	H	357	PRO	4.7
1	F	532	SER	4.7
1	D	375	VAL	4.7
1	G	552	GLU	4.7
1	H	201	GLY	4.7
1	B	32	VAL	4.7
1	C	573	ALA	4.7
1	C	152	SER	4.7
1	C	503	ILE	4.7
1	G	206	SER	4.7
1	B	445	TYR	4.7
1	E	254	ILE	4.7
1	H	282	GLY	4.7
1	A	51	LEU	4.7
1	A	52	LEU	4.7
1	D	47	LEU	4.7
1	A	132	SER	4.7
1	B	421	LEU	4.7
1	B	205	THR	4.7
1	B	270	ALA	4.7
1	F	490	ALA	4.7
1	H	105	PHE	4.7
1	F	313	ALA	4.7
1	F	157	PHE	4.7
1	C	16	LEU	4.7
1	G	494	ALA	4.7
1	E	335	ILE	4.7
1	A	543	GLU	4.7
1	F	224	GLU	4.7
1	D	268	TYR	4.7
1	F	124	LEU	4.7
1	F	533	LEU	4.7
1	A	278	SER	4.7
1	B	86	SER	4.7
1	G	433	VAL	4.7
1	E	424	GLN	4.7
1	B	305	ASN	4.7
1	C	210	MET	4.7
1	F	47	LEU	4.7
1	D	573	ALA	4.7

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Mol	Chain	Res	Type	RSRZ
1	A	521	ALA	4.7
1	H	440	ALA	4.7
1	G	144	ILE	4.7
1	E	272	PHE	4.6
1	C	388	LEU	4.6
1	H	40	SER	4.6
1	E	304	VAL	4.6
1	H	212	LYS	4.6
1	E	139	SER	4.6
1	F	152	SER	4.6
1	G	18	PRO	4.6
1	G	22	PRO	4.6
1	A	281	ALA	4.6
1	H	537	HIS	4.6
1	H	346	ASN	4.6
1	B	207	ALA	4.6
1	G	376	GLY	4.6
1	A	219	ILE	4.6
1	F	488	ARG	4.6
1	D	387	SER	4.6
1	E	37	ASN	4.6
1	A	440	ALA	4.6
1	G	105	PHE	4.6
1	A	221	GLY	4.6
1	B	157	PHE	4.6
1	F	361	ASN	4.6
1	F	334	VAL	4.6
1	E	118	LYS	4.6
1	F	127	ARG	4.6
1	A	92	VAL	4.6
1	D	512	ASP	4.6
1	A	541	THR	4.6
1	D	481	LEU	4.6
1	G	23	PHE	4.6
1	D	574	GLN	4.6
1	F	385	ILE	4.6
1	C	108	MET	4.6
1	E	532	SER	4.6
1	B	49	LYS	4.6
1	F	191	ASN	4.6
1	A	69	LEU	4.6
1	A	274	SER	4.6

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Mol	Chain	Res	Type	RSRZ
1	G	66	TRP	4.6
1	H	571	VAL	4.6
1	H	428	LEU	4.6
1	E	55	GLY	4.6
1	D	495	LEU	4.6
1	D	237	MET	4.6
1	D	293	ALA	4.6
1	D	345	ARG	4.6
1	E	504	LEU	4.6
1	F	395	ILE	4.5
1	C	105	PHE	4.5
1	A	423	SER	4.5
1	F	97	VAL	4.5
1	D	41	ASP	4.5
1	G	296	ARG	4.5
1	G	537	HIS	4.5
1	E	80	ILE	4.5
1	H	372	VAL	4.5
1	C	414	SER	4.5
1	A	210	MET	4.5
1	A	332	LYS	4.5
1	A	520	GLN	4.5
1	G	198	ASN	4.5
1	A	571	VAL	4.5
1	C	395	ILE	4.5
1	D	378	SER	4.5
1	H	151	ALA	4.5
1	H	458	TYR	4.5
1	B	238	ARG	4.5
1	C	350	THR	4.5
1	D	26	GLY	4.5
1	H	110	GLY	4.5
1	F	276	MET	4.5
1	A	202	GLN	4.5
1	B	160	MET	4.5
1	F	60	ASP	4.5
1	C	353	GLY	4.5
1	D	168	SER	4.5
1	E	569	ARG	4.5
1	C	527	GLN	4.5
1	E	182	ILE	4.5
1	C	541	THR	4.5

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Mol	Chain	Res	Type	RSRZ
1	G	561	THR	4.5
1	A	89	ILE	4.5
1	F	436	ASN	4.5
1	H	473	VAL	4.5
1	C	97	VAL	4.5
1	A	493	ARG	4.5
1	A	495	LEU	4.5
1	E	440	ALA	4.5
1	E	136	ALA	4.5
1	D	50	PRO	4.5
1	F	542	ILE	4.5
1	G	244	MET	4.5
1	H	490	ALA	4.5
1	H	505	ASP	4.5
1	A	525	GLU	4.5
1	H	17	TRP	4.5
1	D	522	ALA	4.5
1	D	568	HIS	4.5
1	E	577	LYS	4.5
1	F	367	PRO	4.5
1	D	536	ALA	4.5
1	B	535	ILE	4.5
1	E	400	ILE	4.5
1	E	437	ILE	4.5
1	F	297	PRO	4.5
1	C	539	LEU	4.5
1	E	218	LEU	4.5
1	E	257	LEU	4.5
1	F	260	SER	4.5
1	C	165	TRP	4.5
1	F	284	ILE	4.5
1	H	113	VAL	4.5
1	D	86	SER	4.5
1	B	428	LEU	4.4
1	D	118	LYS	4.4
1	D	218	LEU	4.4
1	B	493	ARG	4.4
1	E	358	ALA	4.4
1	H	231	ASP	4.4
1	C	56	PHE	4.4
1	F	414	SER	4.4
1	C	194	LYS	4.4

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Mol	Chain	Res	Type	RSRZ
1	G	225	VAL	4.4
1	F	182	ILE	4.4
1	G	124	LEU	4.4
1	G	356	VAL	4.4
1	B	204	THR	4.4
1	H	531	THR	4.4
1	E	281	ALA	4.4
1	C	22	PRO	4.4
1	B	44	MET	4.4
1	E	172	ILE	4.4
1	E	116	PHE	4.4
1	H	383	SER	4.4
1	C	377	ARG	4.4
1	E	112	PRO	4.4
1	B	556	ILE	4.4
1	A	363	ASN	4.4
1	G	256	GLN	4.4
1	H	229	ARG	4.4
1	B	500	PRO	4.4
1	D	561	THR	4.4
1	F	186	SER	4.4
1	H	320	THR	4.4
1	D	430	ASN	4.4
1	G	94	GLY	4.4
1	A	529	ASN	4.4
1	H	145	THR	4.4
1	H	521	ALA	4.4
1	F	382	LYS	4.3
1	H	192	ILE	4.3
1	F	460	MET	4.3
1	B	364	LEU	4.3
1	D	464	ASN	4.3
1	H	403	ASP	4.3
1	E	492	ALA	4.3
1	E	102	ARG	4.3
1	G	466	MET	4.3
1	B	409	GLU	4.3
1	C	340	GLY	4.3
1	F	77	LEU	4.3
1	F	455	ARG	4.3
1	C	143	LEU	4.3
1	E	12	THR	4.3

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Mol	Chain	Res	Type	RSRZ
1	C	155	GLY	4.3
1	E	87	TYR	4.3
1	E	240	GLN	4.3
1	F	354	ARG	4.3
1	D	78	ARG	4.3
1	A	461	ASP	4.3
1	A	569	ARG	4.3
1	H	165	TRP	4.3
1	E	160	MET	4.3
1	G	321	ILE	4.3
1	C	387	SER	4.3
1	E	261	LEU	4.3
1	F	82	SER	4.3
1	B	327	GLU	4.3
1	C	543	GLU	4.3
1	E	239	LEU	4.3
1	G	15	ARG	4.3
1	H	104	LEU	4.3
1	C	339	THR	4.3
1	F	358	ALA	4.3
1	C	304	VAL	4.3
1	A	126	SER	4.3
1	A	358	ALA	4.3
1	E	507	ALA	4.3
1	H	381	GLY	4.3
1	C	415	LEU	4.3
1	G	88	CYS	4.3
1	B	492	ALA	4.3
1	C	311	GLY	4.3
1	B	538	ARG	4.3
1	B	574	GLN	4.3
1	B	141	GLY	4.3
1	F	566	LEU	4.3
1	H	503	ILE	4.3
1	C	546	ASP	4.3
1	C	574	GLN	4.3
1	G	240	GLN	4.3
1	H	285	THR	4.3
1	A	45	LEU	4.3
1	B	465	LYS	4.3
1	E	89	ILE	4.3
1	G	386	ALA	4.3

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Mol	Chain	Res	Type	RSRZ
1	F	486	ARG	4.2
1	E	581	GLY	4.2
1	G	175	ALA	4.2
1	H	174	LEU	4.2
1	F	163	TYR	4.2
1	F	183	ARG	4.2
1	B	288	PHE	4.2
1	C	214	HIS	4.2
1	F	515	SER	4.2
1	E	483	GLY	4.2
1	G	420	ALA	4.2
1	A	305	ASN	4.2
1	E	154	ILE	4.2
1	E	436	ASN	4.2
1	F	56	PHE	4.2
1	H	542	ILE	4.2
1	F	109	MET	4.2
1	B	162	TYR	4.2
1	G	300	SER	4.2
1	C	17	TRP	4.2
1	B	145	THR	4.2
1	C	524	ASP	4.2
1	A	39	ALA	4.2
1	F	366	ILE	4.2
1	G	31	GLY	4.2
1	B	110	GLY	4.2
1	E	318	LEU	4.2
1	H	281	ALA	4.2
1	C	436	ASN	4.2
1	A	60	ASP	4.2
1	D	374	LEU	4.2
1	C	428	LEU	4.2
1	A	160	MET	4.2
1	A	544	LYS	4.2
1	G	351	TYR	4.2
1	H	137	SER	4.2
1	C	92	VAL	4.2
1	G	287	VAL	4.2
1	B	429	PHE	4.2
1	E	128	ILE	4.2
1	E	531	THR	4.2
1	A	48	LEU	4.2

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Mol	Chain	Res	Type	RSRZ
1	H	187	LYS	4.2
1	G	569	ARG	4.2
1	F	389	ILE	4.2
1	F	521	ALA	4.2
1	G	482	SER	4.2
1	D	554	GLY	4.2
1	E	518	ALA	4.2
1	A	67	MET	4.1
1	H	33	ALA	4.1
1	A	279	LEU	4.1
1	B	236	ARG	4.1
1	G	402	MET	4.1
1	G	89	ILE	4.1
1	E	282	GLY	4.1
1	C	215	LYS	4.1
1	G	216	GLU	4.1
1	E	565	LEU	4.1
1	A	154	ILE	4.1
1	H	77	LEU	4.1
1	H	397	GLU	4.1
1	B	282	GLY	4.1
1	E	445	TYR	4.1
1	B	118	LYS	4.1
1	H	91	TRP	4.1
1	H	438	ALA	4.1
1	A	314	ALA	4.1
1	E	21	ALA	4.1
1	C	554	GLY	4.1
1	F	271	SER	4.1
1	D	385	ILE	4.1
1	D	475	GLY	4.1
1	A	538	ARG	4.1
1	F	14	ARG	4.1
1	F	238	ARG	4.1
1	H	564	ASP	4.1
1	C	146	VAL	4.1
1	F	38	ALA	4.1
1	H	524	ASP	4.1
1	D	88	CYS	4.1
1	F	501	ILE	4.1
1	H	207	ALA	4.1
1	D	12	THR	4.1

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Mol	Chain	Res	Type	RSRZ
1	H	136	ALA	4.1
1	A	250	ILE	4.1
1	F	15	ARG	4.1
1	F	286	VAL	4.1
1	F	226	GLU	4.1
1	B	263	LEU	4.1
1	H	345	ARG	4.1
1	H	206	SER	4.0
1	E	508	THR	4.0
1	D	279	LEU	4.0
1	F	564	ASP	4.0
1	F	580	PHE	4.0
1	F	242	MET	4.0
1	F	393	TYR	4.0
1	E	365	LYS	4.0
1	B	405	HIS	4.0
1	F	89	ILE	4.0
1	D	526	LEU	4.0
1	B	218	LEU	4.0
1	F	192	ILE	4.0
1	C	226	GLU	4.0
1	C	506	GLU	4.0
1	A	298	LEU	4.0
1	B	272	PHE	4.0
1	E	541	THR	4.0
1	C	309	GLN	4.0
1	E	474	ILE	4.0
1	G	83	TYR	4.0
1	G	465	LYS	4.0
1	G	440	ALA	4.0
1	H	513	THR	4.0
1	A	395	ILE	4.0
1	B	159	MET	4.0
1	C	364	LEU	4.0
1	C	534	VAL	4.0
1	D	486	ARG	4.0
1	D	294	LEU	4.0
1	E	60	ASP	4.0
1	F	394	ASP	4.0
1	D	492	ALA	4.0
1	H	143	LEU	4.0
1	D	344	PHE	4.0

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Mol	Chain	Res	Type	RSRZ
1	G	39	ALA	4.0
1	H	265	PHE	4.0
1	D	519	ILE	4.0
1	F	356	VAL	4.0
1	G	58	LYS	4.0
1	A	536	ALA	4.0
1	D	562	HIS	4.0
1	E	534	VAL	4.0
1	G	255	ILE	4.0
1	E	69	LEU	3.9
1	B	449	GLN	3.9
1	D	306	ALA	3.9
1	F	270	ALA	3.9
1	F	465	LYS	3.9
1	C	113	VAL	3.9
1	D	199	THR	3.9
1	H	107	HIS	3.9
1	H	519	ILE	3.9
1	E	233	VAL	3.9
1	F	546	ASP	3.9
1	F	255	ILE	3.9
1	E	62	SER	3.9
1	E	382	LYS	3.9
1	H	375	VAL	3.9
1	G	496	LEU	3.9
1	E	75	MET	3.9
1	C	188	ARG	3.9
1	C	422	VAL	3.9
1	B	292	ILE	3.9
1	D	159	MET	3.9
1	H	432	THR	3.9
1	E	16	LEU	3.9
1	G	422	VAL	3.9
1	E	58	LYS	3.9
1	F	381	GLY	3.9
1	F	450	ILE	3.9
1	C	379	GLY	3.9
1	F	427	HIS	3.9
1	B	146	VAL	3.9
1	E	320	THR	3.9
1	F	503	ILE	3.9
1	G	536	ALA	3.9

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Mol	Chain	Res	Type	RSRZ
1	H	49	LYS	3.9
1	E	524	ASP	3.9
1	D	116	PHE	3.9
1	H	526	LEU	3.9
1	G	429	PHE	3.9
1	B	522	ALA	3.9
1	D	169	ILE	3.9
1	E	428	LEU	3.9
1	H	558	GLU	3.9
1	H	101	ARG	3.9
1	C	139	SER	3.9
1	D	64	LEU	3.9
1	E	234	SER	3.9
1	F	199	THR	3.9
1	B	412	LEU	3.8
1	D	283	THR	3.8
1	D	335	ILE	3.8
1	G	190	ARG	3.8
1	G	545	ALA	3.8
1	B	422	VAL	3.8
1	A	157	PHE	3.8
1	B	281	ALA	3.8
1	H	158	ILE	3.8
1	F	114	SER	3.8
1	A	243	LYS	3.8
1	A	398	GLY	3.8
1	D	15	ARG	3.8
1	F	469	GLY	3.8
1	E	252	ASP	3.8
1	B	312	MET	3.8
1	G	532	SER	3.8
1	A	550	VAL	3.8
1	E	232	LYS	3.8
1	F	433	VAL	3.8
1	G	203	VAL	3.8
1	A	264	ALA	3.8
1	B	302	THR	3.8
1	E	196	MET	3.8
1	H	500	PRO	3.8
1	C	441	ARG	3.8
1	A	108	MET	3.8
1	H	305	ASN	3.8

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Mol	Chain	Res	Type	RSRZ
1	B	240	GLN	3.8
1	C	438	ALA	3.8
1	B	254	ILE	3.8
1	G	423	SER	3.8
1	C	213	GLY	3.8
1	G	118	LYS	3.8
1	G	346	ASN	3.8
1	G	435	ASN	3.8
1	B	194	LYS	3.8
1	A	86	SER	3.8
1	D	543	GLU	3.8
1	C	310	ARG	3.8
1	A	34	LEU	3.8
1	H	67	MET	3.8
1	H	528	LYS	3.8
1	A	134	GLN	3.8
1	F	418	GLN	3.8
1	B	149	GLU	3.8
1	D	460	MET	3.8
1	F	45	LEU	3.8
1	F	187	LYS	3.8
1	F	254	ILE	3.7
1	G	362	ILE	3.7
1	A	408	ARG	3.7
1	G	373	ALA	3.7
1	B	562	HIS	3.7
1	C	21	ALA	3.7
1	B	115	PHE	3.7
1	E	251	SER	3.7
1	H	533	LEU	3.7
1	F	55	GLY	3.7
1	G	279	LEU	3.7
1	B	82	SER	3.7
1	A	293	ALA	3.7
1	D	578	MET	3.7
1	B	322	LEU	3.7
1	A	73	GLY	3.7
1	G	260	SER	3.7
1	C	254	ILE	3.7
1	E	362	ILE	3.7
1	D	384	THR	3.7
1	H	508	THR	3.7

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Mol	Chain	Res	Type	RSRZ
1	E	373	ALA	3.7
1	D	432	THR	3.7
1	C	465	LYS	3.7
1	E	33	ALA	3.7
1	G	372	VAL	3.7
1	A	149	GLU	3.7
1	D	180	ILE	3.7
1	E	244	MET	3.7
1	D	146	VAL	3.7
1	D	404	GLY	3.7
1	G	59	THR	3.7
1	C	303	ASN	3.7
1	H	404	GLY	3.7
1	C	221	GLY	3.7
1	G	269	ALA	3.7
1	H	100	MET	3.7
1	C	365	LYS	3.7
1	H	369	GLY	3.7
1	G	481	LEU	3.7
1	H	495	LEU	3.7
1	G	68	PRO	3.7
1	C	83	TYR	3.7
1	A	102	ARG	3.7
1	E	415	LEU	3.7
1	D	437	ILE	3.7
1	A	295	MET	3.7
1	B	212	LYS	3.6
1	H	20	ILE	3.6
1	F	251	SER	3.6
1	H	148	ARG	3.6
1	F	435	ASN	3.6
1	C	437	ILE	3.6
1	D	130	TYR	3.6
1	E	227	THR	3.6
1	F	279	LEU	3.6
1	F	453	ALA	3.6
1	H	288	PHE	3.6
1	E	493	ARG	3.6
1	H	502	LEU	3.6
1	B	241	GLY	3.6
1	H	237	MET	3.6
1	F	360	ARG	3.6

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Mol	Chain	Res	Type	RSRZ
1	F	88	CYS	3.6
1	F	562	HIS	3.6
1	A	364	LEU	3.6
1	E	347	VAL	3.6
1	F	121	THR	3.6
1	G	521	ALA	3.6
1	D	302	THR	3.6
1	G	352	PRO	3.6
1	H	246	SER	3.6
1	E	331	GLY	3.6
1	G	370	LYS	3.6
1	H	549	VAL	3.6
1	C	206	SER	3.6
1	G	84	VAL	3.6
1	E	195	ASN	3.6
1	B	234	SER	3.6
1	H	384	THR	3.6
1	F	408	ARG	3.6
1	A	437	ILE	3.6
1	F	412	LEU	3.6
1	B	143	LEU	3.6
1	C	159	MET	3.6
1	F	299	LYS	3.6
1	H	286	VAL	3.6
1	D	491	ILE	3.6
1	C	577	LYS	3.6
1	D	309	GLN	3.6
1	D	194	LYS	3.6
1	D	434	ALA	3.6
1	E	149	GLU	3.6
1	A	346	ASN	3.6
1	A	270	ALA	3.6
1	A	548	ILE	3.6
1	C	177	ILE	3.6
1	D	458	TYR	3.6
1	H	439	TYR	3.6
1	H	569	ARG	3.5
1	F	207	ALA	3.5
1	H	382	LYS	3.5
1	H	82	SER	3.5
1	D	564	ASP	3.5
1	G	10	TRP	3.5

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Mol	Chain	Res	Type	RSRZ
1	C	550	VAL	3.5
1	D	310	ARG	3.5
1	F	241	GLY	3.5
1	A	324	SER	3.5
1	C	204	THR	3.5
1	G	19	THR	3.5
1	B	161	PHE	3.5
1	A	238	ARG	3.5
1	C	334	VAL	3.5
1	E	293	ALA	3.5
1	G	199	THR	3.5
1	C	174	LEU	3.5
1	E	24	LYS	3.5
1	A	284	ILE	3.5
1	H	32	VAL	3.5
1	H	141	GLY	3.5
1	A	486	ARG	3.5
1	G	492	ALA	3.5
1	B	210	MET	3.5
1	A	308	PHE	3.5
1	F	151	ALA	3.5
1	F	525	GLU	3.5
1	B	437	ILE	3.5
1	D	280	THR	3.5
1	G	109	MET	3.5
1	D	433	VAL	3.5
1	C	491	ILE	3.5
1	E	231	ASP	3.5
1	B	368	ALA	3.5
1	H	376	GLY	3.5
1	G	349	PHE	3.5
1	A	354	ARG	3.5
1	G	138	SER	3.5
1	E	485	GLN	3.5
1	F	29	VAL	3.5
1	H	374	LEU	3.5
1	E	151	ALA	3.5
1	C	313	ALA	3.5
1	B	158	ILE	3.5
1	C	98	MET	3.5
1	C	250	ILE	3.5
1	C	433	VAL	3.5

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Mol	Chain	Res	Type	RSRZ
1	D	89	ILE	3.5
1	E	375	VAL	3.5
1	F	258	ILE	3.5
1	B	56	PHE	3.4
1	H	57	GLY	3.4
1	C	509	SER	3.4
1	E	104	LEU	3.4
1	G	104	LEU	3.4
1	C	403	ASP	3.4
1	D	213	GLY	3.4
1	G	184	VAL	3.4
1	G	335	ILE	3.4
1	H	119	GLN	3.4
1	F	506	GLU	3.4
1	F	484	GLY	3.4
1	A	195	ASN	3.4
1	A	517	ARG	3.4
1	G	265	PHE	3.4
1	H	449	GLN	3.4
1	A	459	ALA	3.4
1	E	135	VAL	3.4
1	E	384	THR	3.4
1	E	26	GLY	3.4
1	F	132	SER	3.4
1	B	521	ALA	3.4
1	D	54	ASP	3.4
1	D	436	ASN	3.4
1	C	277	ASP	3.4
1	B	266	VAL	3.4
1	H	175	ALA	3.4
1	F	520	GLN	3.4
1	H	16	LEU	3.4
1	A	33	ALA	3.4
1	A	141	GLY	3.4
1	H	24	LYS	3.4
1	H	540	SER	3.4
1	H	316	GLN	3.4
1	F	168	SER	3.4
1	G	247	ALA	3.4
1	A	183	ARG	3.3
1	D	228	LYS	3.3
1	G	382	LYS	3.3

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Mol	Chain	Res	Type	RSRZ
1	E	143	LEU	3.3
1	H	302	THR	3.3
1	C	245	VAL	3.3
1	A	239	LEU	3.3
1	F	264	ALA	3.3
1	B	26	GLY	3.3
1	E	319	PHE	3.3
1	F	530	ARG	3.3
1	H	416	ARG	3.3
1	A	280	THR	3.3
1	C	220	PHE	3.3
1	E	126	SER	3.3
1	G	524	ASP	3.3
1	G	319	PHE	3.3
1	C	523	LEU	3.3
1	E	444	GLN	3.3
1	F	531	THR	3.3
1	G	65	VAL	3.3
1	A	429	PHE	3.3
1	E	545	ALA	3.3
1	C	127	ARG	3.3
1	E	297	PRO	3.3
1	C	493	ARG	3.3
1	A	316	GLN	3.3
1	A	522	ALA	3.3
1	A	260	SER	3.3
1	G	477	ASN	3.3
1	A	38	ALA	3.3
1	D	71	VAL	3.3
1	G	486	ARG	3.3
1	G	462	PHE	3.3
1	B	510	ALA	3.3
1	C	343	GLU	3.3
1	C	545	ALA	3.3
1	D	547	GLU	3.3
1	G	506	GLU	3.3
1	G	400	ILE	3.2
1	D	322	LEU	3.2
1	E	211	LEU	3.2
1	F	480	LEU	3.2
1	D	534	VAL	3.2
1	C	112	PRO	3.2

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Mol	Chain	Res	Type	RSRZ
1	H	232	LYS	3.2
1	H	287	VAL	3.2
1	G	90	SER	3.2
1	D	292	ILE	3.2
1	F	198	ASN	3.2
1	G	69	LEU	3.2
1	B	40	SER	3.2
1	F	523	LEU	3.2
1	F	90	SER	3.2
1	H	319	PHE	3.2
1	A	266	VAL	3.2
1	G	344	PHE	3.2
1	A	365	LYS	3.2
1	D	575	LEU	3.2
1	G	578	MET	3.2
1	B	415	LEU	3.2
1	H	307	GLN	3.2
1	A	272	PHE	3.2
1	A	402	MET	3.2
1	D	381	GLY	3.2
1	F	466	MET	3.2
1	B	290	SER	3.2
1	F	193	SER	3.2
1	E	109	MET	3.2
1	F	178	VAL	3.2
1	E	506	GLU	3.2
1	B	450	ILE	3.2
1	F	553	ASP	3.2
1	G	95	LYS	3.2
1	G	241	GLY	3.2
1	A	306	ALA	3.2
1	C	140	SER	3.2
1	E	39	ALA	3.2
1	C	64	LEU	3.1
1	H	271	SER	3.1
1	C	130	TYR	3.1
1	F	409	GLU	3.1
1	E	150	GLY	3.1
1	H	478	GLY	3.1
1	H	545	ALA	3.1
1	D	520	GLN	3.1
1	F	43	PHE	3.1

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Mol	Chain	Res	Type	RSRZ
1	C	530	ARG	3.1
1	E	499	SER	3.1
1	G	232	LYS	3.1
1	H	463	ILE	3.1
1	A	120	SER	3.1
1	A	409	GLU	3.1
1	H	299	LYS	3.1
1	F	429	PHE	3.1
1	F	475	GLY	3.1
1	G	173	VAL	3.1
1	F	108	MET	3.1
1	C	195	ASN	3.1
1	E	469	GLY	3.1
1	H	250	ILE	3.1
1	F	371	THR	3.1
1	C	192	ILE	3.1
1	E	86	SER	3.1
1	E	220	PHE	3.1
1	H	511	LEU	3.1
1	H	140	SER	3.1
1	E	298	LEU	3.1
1	C	203	VAL	3.1
1	A	379	GLY	3.1
1	B	298	LEU	3.1
1	B	50	PRO	3.1
1	C	84	VAL	3.1
1	D	270	ALA	3.1
1	G	428	LEU	3.1
1	A	475	GLY	3.1
1	H	560	GLY	3.1
1	H	236	ARG	3.1
1	F	561	THR	3.1
1	D	438	ALA	3.1
1	E	446	SER	3.1
1	G	14	ARG	3.1
1	H	267	LEU	3.0
1	D	527	GLN	3.0
1	G	442	THR	3.0
1	A	404	GLY	3.0
1	B	387	SER	3.0
1	D	287	VAL	3.0
1	E	352	PRO	3.0

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Mol	Chain	Res	Type	RSRZ
1	G	526	LEU	3.0
1	D	183	ARG	3.0
1	H	54	ASP	3.0
1	F	468	ASN	3.0
1	H	202	GLN	3.0
1	B	543	GLU	3.0
1	B	237	MET	3.0
1	C	54	ASP	3.0
1	F	40	SER	3.0
1	D	409	GLU	3.0
1	D	339	THR	3.0
1	G	55	GLY	3.0
1	H	262	ALA	3.0
1	C	239	LEU	3.0
1	E	48	LEU	3.0
1	G	292	ILE	3.0
1	G	106	GLY	3.0
1	B	491	ILE	3.0
1	F	110	GLY	3.0
1	G	502	LEU	3.0
1	F	293	ALA	3.0
1	E	214	HIS	3.0
1	A	82	SER	3.0
1	H	441	ARG	3.0
1	D	119	GLN	3.0
1	F	554	GLY	3.0
1	C	212	LYS	3.0
1	D	68	PRO	3.0
1	G	100	MET	3.0
1	F	451	GLU	3.0
1	H	365	LYS	3.0
1	G	472	THR	3.0
1	D	382	LYS	3.0
1	G	374	LEU	3.0
1	H	26	GLY	3.0
1	G	505	ASP	3.0
1	G	417	ASN	3.0
1	B	579	GLN	3.0
1	H	373	ALA	3.0
1	F	545	ALA	3.0
1	F	423	SER	3.0
1	D	555	VAL	2.9

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Mol	Chain	Res	Type	RSRZ
1	F	75	MET	2.9
1	F	309	GLN	2.9
1	G	17	TRP	2.9
1	F	495	LEU	2.9
1	A	443	GLU	2.9
1	A	491	ILE	2.9
1	B	372	VAL	2.9
1	A	101	ARG	2.9
1	E	453	ALA	2.9
1	B	283	THR	2.9
1	G	449	GLN	2.9
1	E	161	PHE	2.9
1	E	438	ALA	2.9
1	H	553	ASP	2.9
1	C	315	CYS	2.9
1	B	507	ALA	2.9
1	E	258	ILE	2.9
1	D	85	SER	2.9
1	F	161	PHE	2.9
1	E	549	VAL	2.9
1	F	87	TYR	2.9
1	C	307	GLN	2.9
1	B	504	LEU	2.9
1	E	192	ILE	2.9
1	G	108	MET	2.9
1	C	384	THR	2.9
1	H	290	SER	2.9
1	E	405	HIS	2.9
1	G	371	THR	2.9
1	A	97	VAL	2.9
1	C	372	VAL	2.9
1	F	18	PRO	2.9
1	A	118	LYS	2.9
1	A	159	MET	2.9
1	H	284	ILE	2.9
1	A	579	GLN	2.9
1	D	225	VAL	2.9
1	G	342	VAL	2.9
1	E	548	ILE	2.9
1	G	82	SER	2.9
1	B	152	SER	2.9
1	D	372	VAL	2.9

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Mol	Chain	Res	Type	RSRZ
1	E	188	ARG	2.9
1	G	63	VAL	2.8
1	C	429	PHE	2.8
1	G	28	ILE	2.8
1	H	157	PHE	2.8
1	C	331	GLY	2.8
1	D	346	ASN	2.8
1	A	28	ILE	2.8
1	E	316	GLN	2.8
1	D	440	ALA	2.8
1	H	539	LEU	2.8
1	C	354	ARG	2.8
1	H	392	PHE	2.8
1	A	283	THR	2.8
1	F	369	GLY	2.8
1	H	504	LEU	2.8
1	F	244	MET	2.8
1	B	573	ALA	2.8
1	C	102	ARG	2.8
1	H	318	LEU	2.8
1	C	222	GLY	2.8
1	C	409	GLU	2.8
1	D	160	MET	2.8
1	H	527	GLN	2.8
1	G	167	LEU	2.8
1	D	11	GLN	2.8
1	H	13	PHE	2.8
1	H	358	ALA	2.8
1	G	487	GLN	2.8
1	A	442	THR	2.8
1	E	516	GLU	2.8
1	C	507	ALA	2.8
1	F	139	SER	2.8
1	F	472	THR	2.8
1	B	108	MET	2.8
1	A	285	THR	2.8
1	B	310	ARG	2.8
1	H	61	ARG	2.8
1	C	120	SER	2.8
1	F	160	MET	2.8
1	H	340	GLY	2.8
1	B	123	THR	2.8

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Mol	Chain	Res	Type	RSRZ
1	H	451	GLU	2.8
1	G	507	ALA	2.8
1	C	496	LEU	2.8
1	H	254	ILE	2.8
1	F	373	ALA	2.8
1	D	504	LEU	2.8
1	F	257	LEU	2.8
1	G	407	LEU	2.8
1	D	343	GLU	2.8
1	B	416	ARG	2.8
1	F	101	ARG	2.8
1	C	341	ASP	2.7
1	F	202	GLN	2.7
1	G	464	ASN	2.7
1	E	330	GLU	2.7
1	E	505	ASP	2.7
1	D	311	GLY	2.7
1	F	315	CYS	2.7
1	G	453	ALA	2.7
1	B	381	GLY	2.7
1	F	303	ASN	2.7
1	C	495	LEU	2.7
1	H	494	ALA	2.7
1	F	304	VAL	2.7
1	F	411	THR	2.7
1	A	347	VAL	2.7
1	F	278	SER	2.7
1	B	61	ARG	2.7
1	H	159	MET	2.7
1	A	492	ALA	2.7
1	D	435	ASN	2.7
1	A	458	TYR	2.7
1	E	314	ALA	2.7
1	G	56	PHE	2.7
1	G	143	LEU	2.7
1	G	387	SER	2.7
1	H	92	VAL	2.7
1	D	429	PHE	2.7
1	A	508	THR	2.7
1	E	380	SER	2.7
1	A	14	ARG	2.7
1	G	178	VAL	2.7

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Mol	Chain	Res	Type	RSRZ
1	C	470	LEU	2.7
1	B	313	ALA	2.7
1	C	29	VAL	2.7
1	C	547	GLU	2.7
1	H	122	GLY	2.7
1	C	111	MET	2.7
1	C	508	THR	2.7
1	H	523	LEU	2.7
1	F	196	MET	2.7
1	G	11	GLN	2.7
1	B	439	TYR	2.7
1	G	53	ASP	2.7
1	B	222	GLY	2.7
1	H	124	LEU	2.7
1	A	405	HIS	2.7
1	C	450	ILE	2.7
1	E	478	GLY	2.7
1	F	507	ALA	2.7
1	G	49	LYS	2.7
1	E	175	ALA	2.6
1	G	191	ASN	2.6
1	D	291	MET	2.6
1	A	138	SER	2.6
1	B	137	SER	2.6
1	D	423	SER	2.6
1	E	406	ASP	2.6
1	C	75	MET	2.6
1	D	523	LEU	2.6
1	H	507	ALA	2.6
1	H	477	ASN	2.6
1	B	395	ILE	2.6
1	B	318	LEU	2.6
1	C	280	THR	2.6
1	F	59	THR	2.6
1	C	33	ALA	2.6
1	H	475	GLY	2.6
1	B	53	ASP	2.6
1	C	292	ILE	2.6
1	C	556	ILE	2.6
1	F	219	ILE	2.6
1	H	76	ILE	2.6
1	B	414	SER	2.6

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Mol	Chain	Res	Type	RSRZ
1	B	458	TYR	2.6
1	C	268	TYR	2.6
1	G	365	LYS	2.6
1	D	550	VAL	2.6
1	E	173	VAL	2.6
1	G	531	THR	2.6
1	A	220	PHE	2.6
1	D	27	LEU	2.6
1	E	442	THR	2.6
1	F	138	SER	2.6
1	G	136	ALA	2.6
1	H	309	GLN	2.6
1	H	208	GLU	2.6
1	A	359	LEU	2.6
1	H	83	TYR	2.6
1	C	40	SER	2.6
1	H	234	SER	2.6
1	D	184	VAL	2.6
1	G	385	ILE	2.6
1	B	578	MET	2.6
1	F	374	LEU	2.6
1	H	195	ASN	2.6
1	F	437	ILE	2.6
1	D	462	PHE	2.6
1	B	433	VAL	2.6
1	E	461	ASP	2.6
1	F	478	GLY	2.6
1	H	177	ILE	2.6
1	A	478	GLY	2.6
1	A	551	VAL	2.6
1	E	201	GLY	2.5
1	B	513	THR	2.5
1	B	88	CYS	2.5
1	F	31	GLY	2.5
1	E	348	THR	2.5
1	F	81	THR	2.5
1	G	307	GLN	2.5
1	A	436	ASN	2.5
1	C	85	SER	2.5
1	E	402	MET	2.5
1	C	282	GLY	2.5
1	C	373	ALA	2.5

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Mol	Chain	Res	Type	RSRZ
1	G	192	ILE	2.5
1	G	162	TYR	2.5
1	H	575	LEU	2.5
1	D	232	LYS	2.5
1	C	265	PHE	2.5
1	H	258	ILE	2.5
1	E	25	ALA	2.5
1	E	455	ARG	2.5
1	H	12	THR	2.5
1	D	227	THR	2.5
1	H	233	VAL	2.5
1	C	344	PHE	2.5
1	F	54	ASP	2.5
1	D	135	VAL	2.5
1	E	43	PHE	2.5
1	G	437	ILE	2.5
1	F	49	LYS	2.5
1	E	459	ALA	2.5
1	H	342	VAL	2.5
1	G	221	GLY	2.5
1	B	45	LEU	2.5
1	F	420	ALA	2.5
1	A	535	ILE	2.5
1	G	293	ALA	2.5
1	F	474	ILE	2.5
1	G	489	ILE	2.5
1	F	236	ARG	2.5
1	G	473	VAL	2.5
1	F	370	LYS	2.5
1	F	156	LEU	2.5
1	G	348	THR	2.5
1	E	129	THR	2.5
1	D	415	LEU	2.5
1	C	522	ALA	2.4
1	F	269	ALA	2.4
1	E	142	ALA	2.4
1	H	321	ILE	2.4
1	E	299	LYS	2.4
1	B	544	LYS	2.4
1	F	197	GLN	2.4
1	H	268	TYR	2.4
1	D	281	ALA	2.4

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Mol	Chain	Res	Type	RSRZ
1	D	296	ARG	2.4
1	B	275	VAL	2.4
1	B	129	THR	2.4
1	G	201	GLY	2.4
1	C	229	ARG	2.4
1	G	20	ILE	2.4
1	H	493	ARG	2.4
1	B	239	LEU	2.4
1	A	342	VAL	2.4
1	F	189	PHE	2.4
1	F	452	GLU	2.4
1	A	74	LEU	2.4
1	D	317	THR	2.4
1	F	517	ARG	2.4
1	A	570	GLY	2.4
1	D	377	ARG	2.4
1	E	162	TYR	2.4
1	E	366	ILE	2.4
1	G	270	ALA	2.4
1	A	130	TYR	2.4
1	C	322	LEU	2.4
1	D	493	ARG	2.4
1	C	81	THR	2.4
1	H	130	TYR	2.4
1	C	60	ASP	2.4
1	E	464	ASN	2.4
1	H	19	THR	2.4
1	E	94	GLY	2.4
1	H	251	SER	2.4
1	C	295	MET	2.4
1	G	122	GLY	2.4
1	D	251	SER	2.3
1	H	532	SER	2.3
1	C	53	ASP	2.3
1	C	411	THR	2.3
1	D	172	ILE	2.3
1	H	516	GLU	2.3
1	G	301	LEU	2.3
1	D	34	LEU	2.3
1	F	375	VAL	2.3
1	E	388	LEU	2.3
1	E	477	ASN	2.3

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Mol	Chain	Res	Type	RSRZ
1	G	290	SER	2.3
1	E	351	TYR	2.3
1	A	474	ILE	2.3
1	G	253	PRO	2.3
1	G	500	PRO	2.3
1	B	527	GLN	2.3
1	C	107	HIS	2.3
1	G	476	GLU	2.3
1	H	348	THR	2.3
1	A	410	TYR	2.3
1	G	410	TYR	2.3
1	A	228	LYS	2.3
1	A	385	ILE	2.3
1	H	240	GLN	2.3
1	G	549	VAL	2.3
1	H	71	VAL	2.3
1	C	231	ASP	2.3
1	H	407	LEU	2.3
1	F	502	LEU	2.3
1	G	263	LEU	2.3
1	B	568	HIS	2.3
1	H	154	ILE	2.3
1	H	410	TYR	2.3
1	E	310	ARG	2.3
1	D	240	GLN	2.3
1	H	266	VAL	2.3
1	E	563	ASN	2.3
1	E	484	GLY	2.3
1	F	481	LEU	2.3
1	B	371	THR	2.3
1	G	383	SER	2.2
1	H	125	LEU	2.2
1	D	129	THR	2.2
1	H	247	ALA	2.2
1	F	227	THR	2.2
1	F	508	THR	2.2
1	H	189	PHE	2.2
1	G	445	TYR	2.2
1	E	77	LEU	2.2
1	G	119	GLN	2.2
1	G	223	GLN	2.2
1	C	374	LEU	2.2

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Mol	Chain	Res	Type	RSRZ
1	D	109	MET	2.2
1	D	140	SER	2.2
1	F	250	ILE	2.2
1	H	200	MET	2.2
1	H	417	ASN	2.2
1	A	552	GLU	2.2
1	A	237	MET	2.2
1	B	469	GLY	2.2
1	H	353	GLY	2.2
1	C	342	VAL	2.2
1	D	501	ILE	2.2
1	G	320	THR	2.2
1	F	509	SER	2.2
1	H	301	LEU	2.2
1	F	247	ALA	2.2
1	A	198	ASN	2.2
1	A	432	THR	2.2
1	D	221	GLY	2.2
1	B	512	ASP	2.2
1	G	218	LEU	2.2
1	H	264	ALA	2.2
1	H	253	PRO	2.2
1	H	576	HIS	2.2
1	C	178	VAL	2.2
1	F	442	THR	2.2
1	H	274	SER	2.2
1	E	411	THR	2.1
1	E	221	GLY	2.1
1	G	57	GLY	2.1
1	H	385	ILE	2.1
1	B	565	LEU	2.1
1	C	544	LYS	2.1
1	E	454	ALA	2.1
1	F	438	ALA	2.1
1	G	52	LEU	2.1
1	A	18	PRO	2.1
1	D	250	ILE	2.1
1	D	98	MET	2.1
1	A	208	GLU	2.1
1	A	500	PRO	2.1
1	C	458	TYR	2.1
1	C	23	PHE	2.1

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Mol	Chain	Res	Type	RSRZ
1	B	84	VAL	2.1
1	G	434	ALA	2.1
1	F	536	ALA	2.1
1	E	522	ALA	2.1
1	B	208	GLU	2.1
1	E	465	LYS	2.1
1	E	561	THR	2.1
1	D	525	GLU	2.1
1	D	403	ASP	2.1
1	G	251	SER	2.1
1	B	98	MET	2.1
1	A	142	ALA	2.1
1	A	526	LEU	2.1
1	D	241	GLY	2.1
1	D	276	MET	2.1
1	D	533	LEU	2.1
1	G	97	VAL	2.1
1	B	271	SER	2.1
1	E	579	GLN	2.1
1	F	172	ILE	2.1
1	D	65	VAL	2.1
1	D	97	VAL	2.1
1	H	398	GLY	2.1
1	A	575	LEU	2.1
1	G	211	LEU	2.1
1	D	399	GLU	2.1
1	A	64	LEU	2.1
1	F	320	THR	2.1
1	A	124	LEU	2.1
1	H	298	LEU	2.0
1	A	77	LEU	2.0
1	H	552	GLU	2.0
1	B	346	ASN	2.0
1	F	477	ASN	2.0
1	C	13	PHE	2.0
1	A	244	MET	2.0
1	C	536	ALA	2.0
1	F	246	SER	2.0
1	G	16	LEU	2.0
1	H	354	ARG	2.0
1	A	422	VAL	2.0
1	G	217	VAL	2.0

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Mol	Chain	Res	Type	RSRZ
1	F	13	PHE	2.0
1	E	360	ARG	2.0
1	H	462	PHE	2.0
1	A	490	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.