



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 07:33 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](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

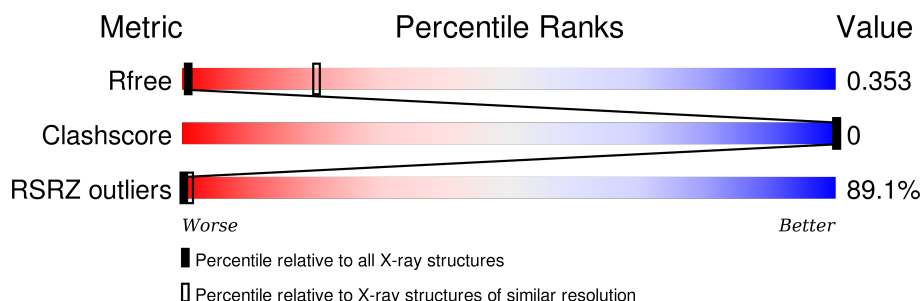
# 1 Overall quality at a glance

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))
$R_{free}$	91344	1162 (7.00-3.60)
Clashscore	102246	1007 (6.92-3.68)
RSRZ outliers	91569	1163 (7.00-3.60)

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	582	<div> <div>90%</div> <div>98%</div> </div>
1	B	582	<div> <div>89%</div> <div>98%</div> </div>
1	C	582	<div> <div>89%</div> <div>98%</div> </div>
1	D	582	<div> <div>90%</div> <div>98%</div> </div>
1	E	582	<div> <div>86%</div> <div>98%</div> </div>
1	F	582	<div> <div>86%</div> <div>98%</div> </div>
1	G	582	<div> <div>84%</div> <div>98%</div> </div>
1	H	582	<div> <div>86%</div> <div>98%</div> </div>

## 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.

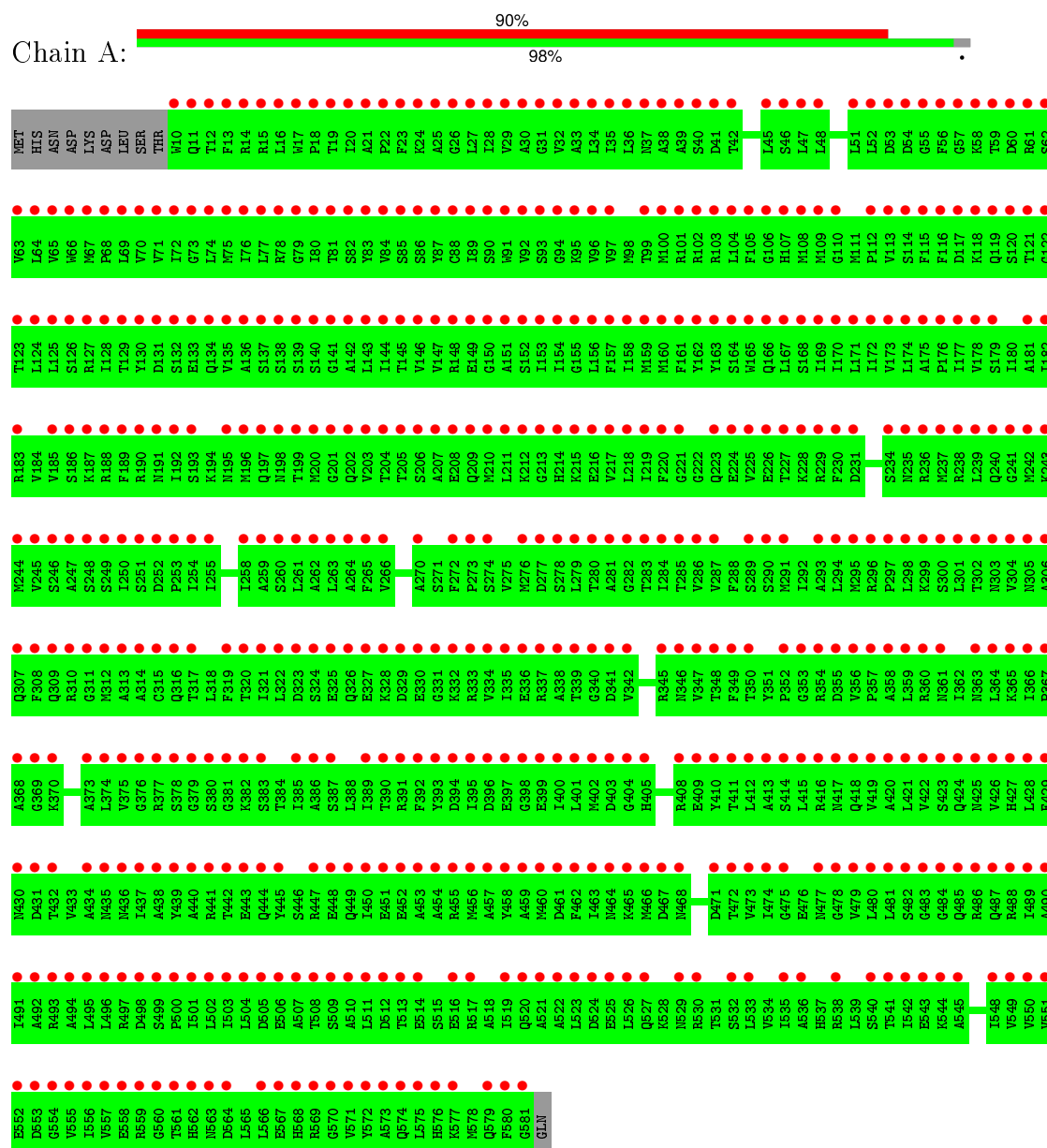
- Molecule 1 is a protein called Lipid A export ATP-binding/permease protein msbA.

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

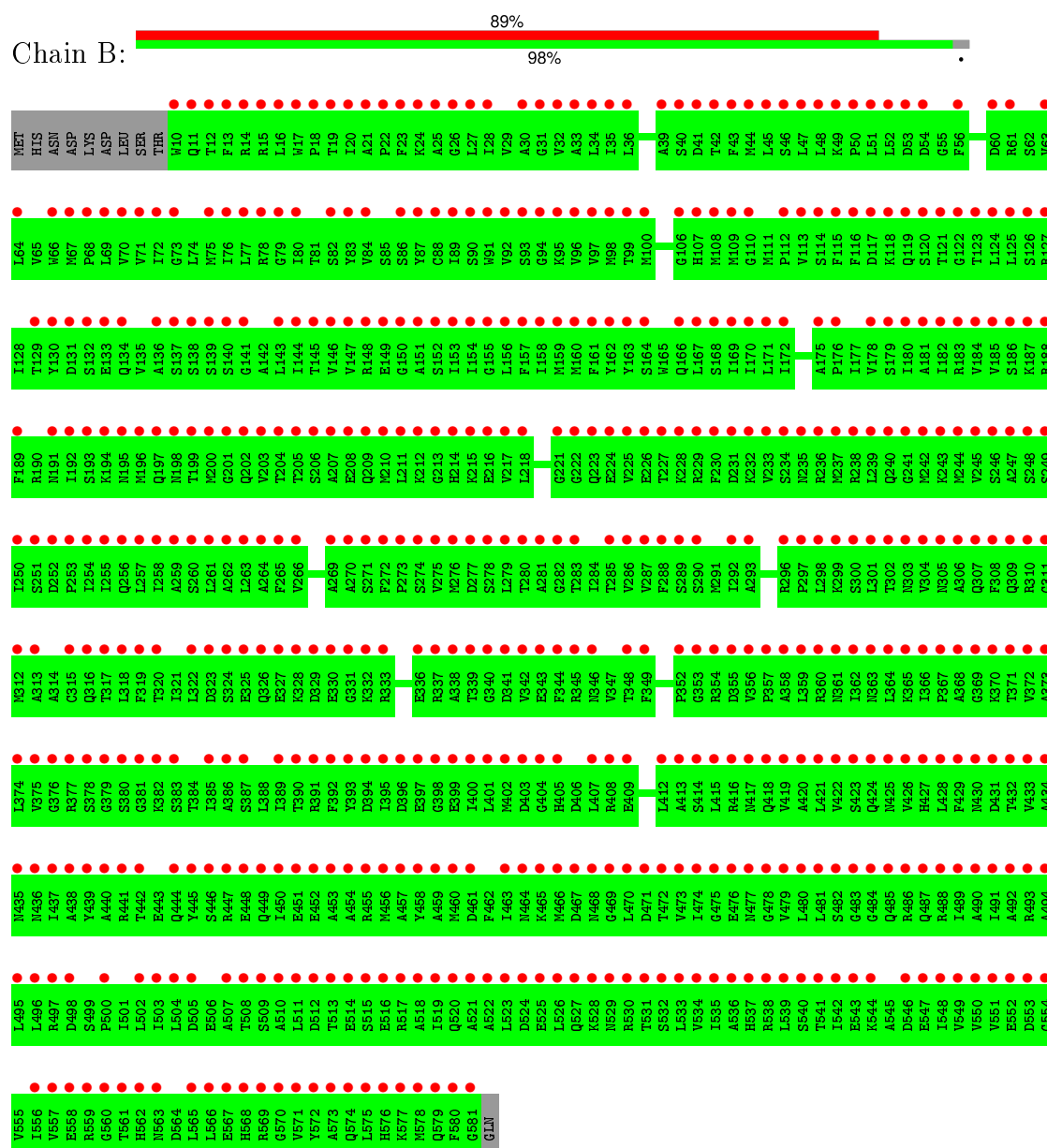
### 3 Residue-property plots

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 ( $RSRZ > 2$ ). 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.

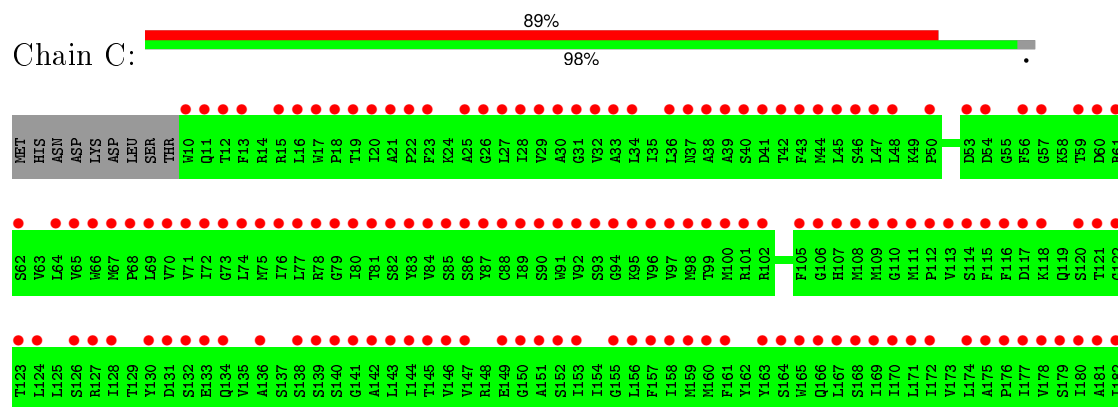
- Molecule 1: Lipid A export ATP-binding/permease protein msbA

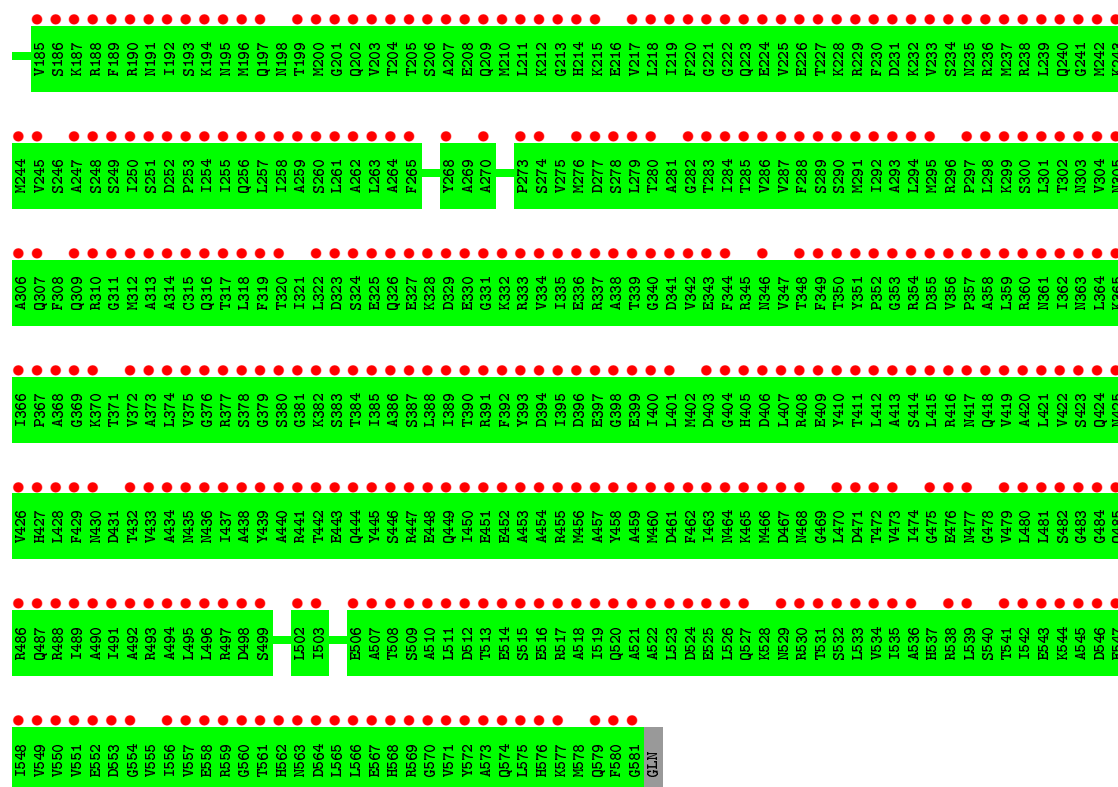


- Molecule 1: Lipid A export ATP-binding/permease protein msbA

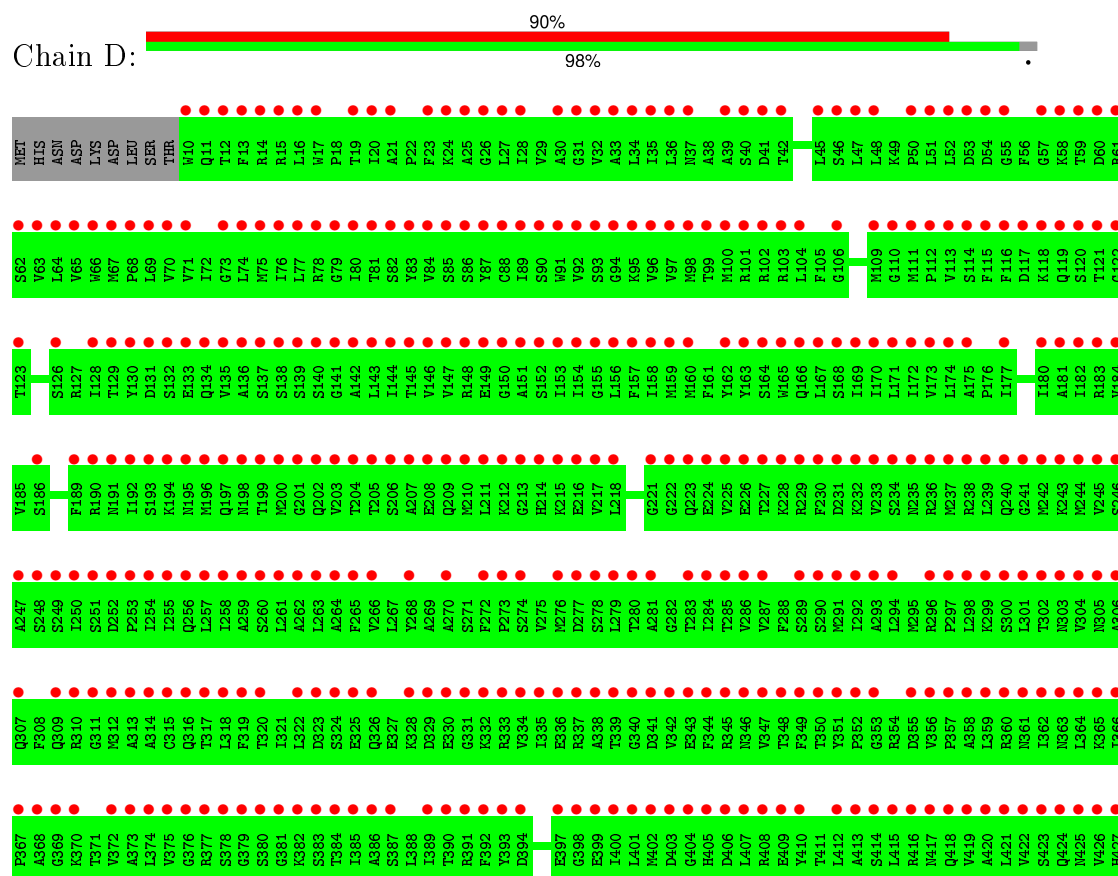


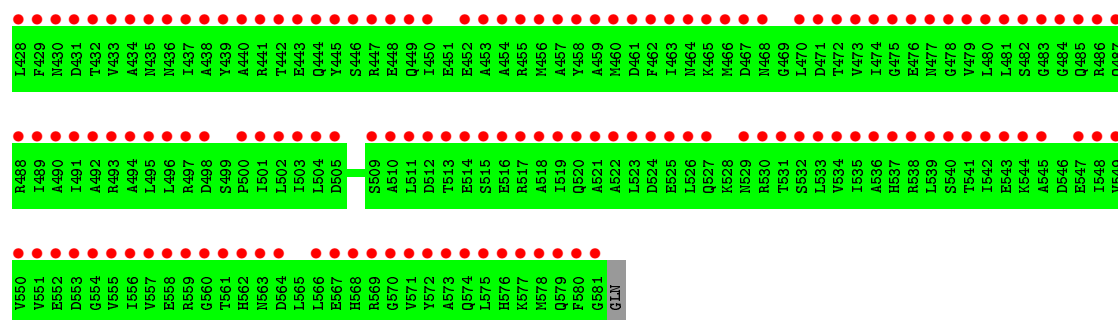
- Molecule 1: Lipid A export ATP-binding/permease protein msbA



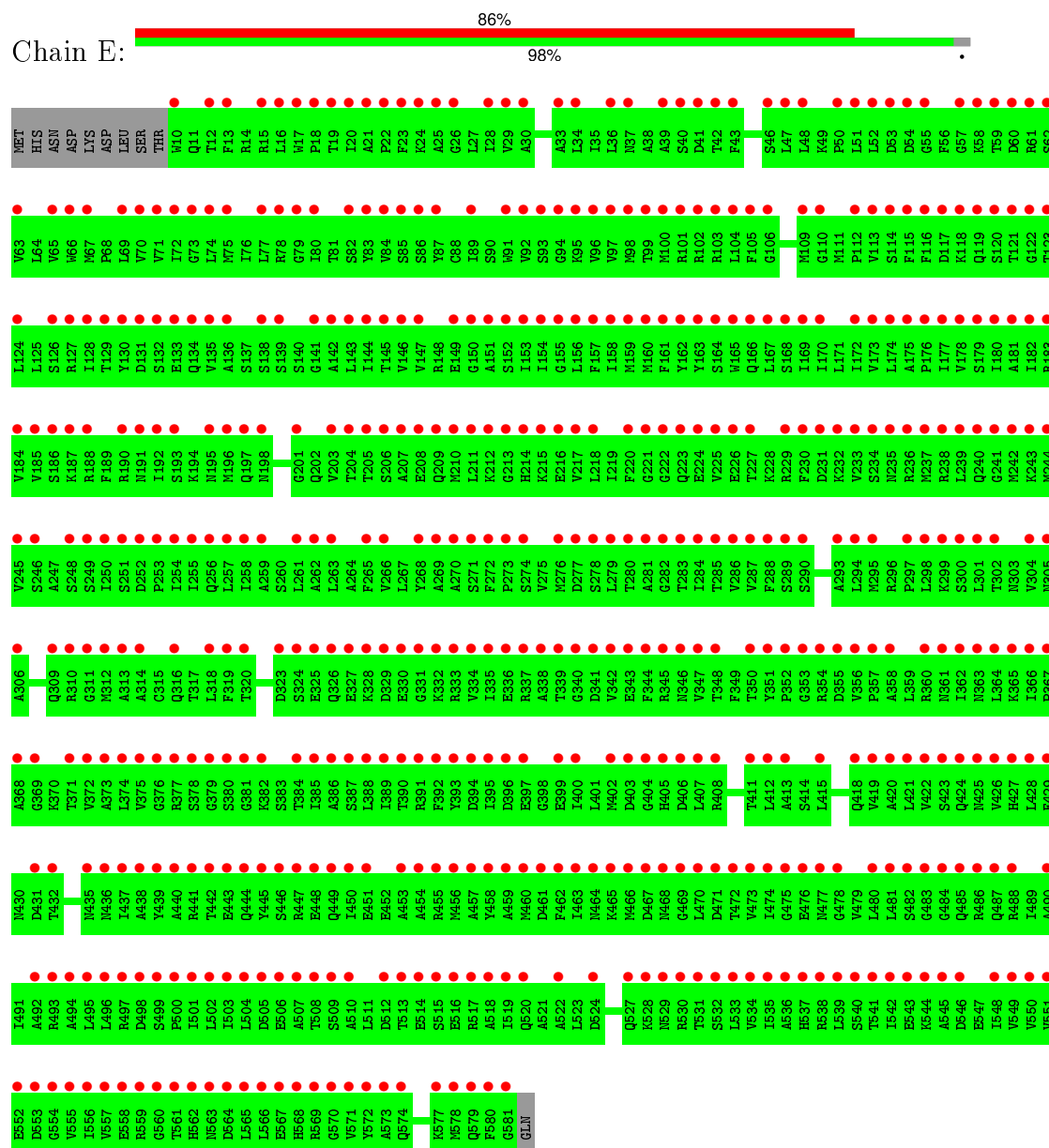


● Molecule 1: Lipid A export ATP-binding/permease protein msbA

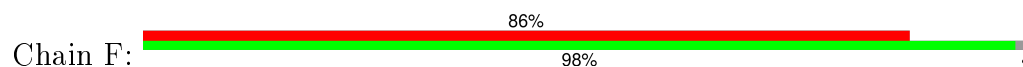




- Molecule 1: Lipid A export ATP-binding/permease protein msbA



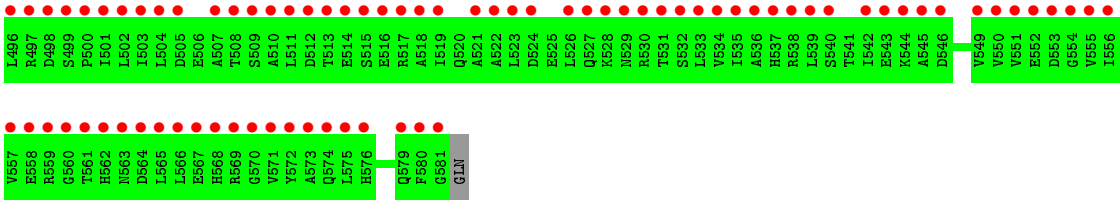
- Molecule 1: Lipid A export ATP-binding/permease protein msbA



MET	W10	Q11	Q12	Q13	Q14	Q15	Q16	Q17	Q18	Q19	Q20	Q21	Q22	Q23	Q24	Q25	Q26	Q27	Q28	Q29	Q30	Q31	Q32	Q33	Q34	Q35	Q36	Q37	Q38	Q39	Q40	Q41	Q42	Q43	Q44	Q45	Q46	Q47	Q48	Q49	Q50	Q51	Q52	Q53	Q54	Q55	Q56	Q57	Q58	Q59	Q60	Q61	Q62	Q63	Q64	Q65	Q66	Q67	Q68	Q69	Q70	Q71	Q72	Q73	Q74	Q75	Q76	Q77	Q78	Q79	Q80	Q81	Q82	Q83	Q84	Q85	Q86	Q87	Q88	Q89	Q90	Q91	Q92	Q93	Q94	Q95	Q96	Q97	Q98	Q99	Q100	Q101	Q102	Q103	Q104	Q105	Q106	Q107	Q108	Q109	Q110	Q111	Q112	Q113	Q114	Q115	Q116	Q117	Q118	Q119	Q120	Q121	Q122	Q123	Q124	Q125	Q126	Q127	Q128	Q129	Q130	Q131	Q132	Q133	Q134	Q135	Q136	Q137	Q138	Q139	Q140	Q141	Q142	Q143	Q144	Q145	Q146	Q147	Q148	Q149	Q150	Q151	Q152	Q153	Q154	Q155	Q156	Q157	Q158	Q159	Q160	Q161	Q162	Q163	Q164	Q165	Q166	Q167	Q168	Q169	Q170	Q171	Q172	Q173	Q174	Q175	Q176	Q177	Q178	Q179	Q180	Q181	Q182	Q183	Q184	Q185	Q186	Q187	Q188	Q189	Q190	Q191	Q192	Q193	Q194	Q195	Q196	Q197	Q198	Q199	Q200	Q201	Q202	Q203	Q204	Q205	Q206	Q207	Q208	Q209	Q210	Q211	Q212	Q213	Q214	Q215	Q216	Q217	Q218	Q219	Q220	Q221	Q222	Q223	Q224	Q225	Q226	Q227	Q228	Q229	Q230	Q231	Q232	Q233	Q234	Q235	Q236	Q237	Q238	Q239	Q240	Q241	Q242	Q243	Q244	Q245	Q246	Q247	Q248	Q249	Q250	Q251	Q252	Q253	Q254	Q255	Q256	Q257	Q258	Q259	Q260	Q261	Q262	Q263	Q264	Q265	Q266	Q267	Q268	Q269	Q270	Q271	Q272	Q273	Q274	Q275	Q276	Q277	Q278	Q279	Q280	Q281	Q282	Q283	Q284	Q285	Q286	Q287	Q288	Q289	Q290	Q291	Q292	Q293	Q294	Q295	Q296	Q297	Q298	Q299	Q300	Q301	Q302	Q303	Q304	Q305	Q306	Q307	Q308	Q309	Q310	Q311	Q312	Q313	Q314	Q315	Q316	Q317	Q318	Q319	Q320	Q321	Q322	Q323	Q324	Q325	Q326	Q327	Q328	Q329	Q330	Q331	Q332	Q333	Q334	Q335	Q336	Q337	Q338	Q339	Q340	Q341	Q342	Q343	Q344	Q345	Q346	Q347	Q348	Q349	Q350	Q351	Q352	Q353	Q354	Q355	Q356	Q357	Q358	Q359	Q360	Q361	Q362	Q363	Q364	Q365	Q366	Q367	Q368	Q369	Q370	Q371	Q372	Q373	Q374	Q375	Q376	Q377	Q378	Q379	Q380	Q381	Q382	Q383	Q384	Q385	Q386	Q387	Q388	Q389	Q390	Q391	Q392	Q393	Q394	Q395	Q396	Q397	Q398	Q399	Q400	Q401	Q402	Q403	Q404	Q405	Q406	Q407	Q408	Q409	Q410	Q411	Q412	Q413	Q414	Q415	Q416	Q417	Q418	Q419	Q420	Q421	Q422	Q423	Q424	Q425	Q426	Q427	Q428	Q429	Q430	Q431	Q432	Q433	Q434	Q435	Q436	Q437	Q438	Q439	Q440	Q441	Q442	Q443	Q444	Q445	Q446	Q447	Q448	Q449	Q450	Q451	Q452	Q453	Q454	Q455	Q456	Q457	Q458	Q459	Q460	Q461	Q462	Q463	Q464	Q465	Q466	Q467	Q468	Q469	Q470	Q471	Q472	Q473	Q474	Q475	Q476	Q477	Q478	Q479	Q480	Q481	Q482	Q483	Q484	Q485	Q486	Q487	Q488	Q489	Q490	Q491	Q492	Q493	Q494	Q495	Q496	Q497	Q498	Q499	Q500	Q501	Q502	Q503	Q504	Q505	Q506	Q507	Q508	Q509	Q510	Q511	Q512	Q513	Q514	Q515	Q516	Q517	Q518	Q519	Q520	Q521	Q522	Q523	Q524	Q525	Q526	Q527	Q528	Q529	Q530	Q531	Q532	Q533	Q534	Q535	Q536	Q537	Q538	Q539	Q540	Q541	Q542	Q543	Q544	Q545	Q546	Q547	Q548	Q549	Q550	Q551	Q552	Q553	Q554	Q555	Q556	Q557	Q558	Q559	Q560	Q561	Q562	Q563	Q564	Q565	Q566	Q567	Q568	Q569	Q570	Q571	Q572	Q573	Q574	Q575	Q576	Q577	Q578	Q579	Q580	Q581	Q582	Q583	Q584	Q585	Q586	Q587	Q588	Q589	Q590	Q591	Q592	Q593	Q594	Q595	Q596	Q597	Q598	Q599	Q600	Q601	Q602	Q603	Q604	Q605	Q606	Q607	Q608	Q609	Q610	Q611	Q612	Q613	Q614	Q615	Q616	Q617	Q618	Q619	Q620	Q621	Q622	Q623	Q624	Q625	Q626	Q627	Q628	Q629	Q630	Q631	Q632	Q633	Q634	Q635	Q636	Q637	Q638	Q639	Q640	Q641	Q642	Q643	Q644	Q645	Q646	Q647	Q648	Q649	Q650	Q651	Q652	Q653	Q654	Q655	Q656	Q657	Q658	Q659	Q660	Q661	Q662	Q663	Q664	Q665	Q666	Q667	Q668	Q669	Q670	Q671	Q672	Q673	Q674	Q675	Q676	Q677	Q678	Q679	Q680	Q681	Q682	Q683	Q684	Q685	Q686	Q687	Q688	Q689	Q690	Q691	Q692	Q693	Q694	Q695	Q696	Q697	Q698	Q699	Q700	Q701	Q702	Q703	Q704	Q705	Q706	Q707	Q708	Q709	Q710	Q711	Q712	Q713	Q714	Q715	Q716	Q717	Q718	Q719	Q720	Q721	Q722	Q723	Q724	Q725	Q726	Q727	Q728	Q729	Q730	Q731	Q732	Q733	Q734	Q735	Q736	Q737	Q738	Q739	Q740	Q741	Q742	Q743	Q744	Q745	Q746	Q747	Q748	Q749	Q750	Q751	Q752	Q753	Q754	Q755	Q756	Q757	Q758	Q759	Q760	Q761	Q762	Q763	Q764	Q765	Q766	Q767	Q768	Q769	Q770	Q771	Q772	Q773	Q774	Q775	Q776	Q777	Q778	Q779	Q780	Q781	Q782	Q783	Q784	Q785	Q786	Q787	Q788	Q789	Q790	Q791	Q792	Q793	Q794	Q795	Q796	Q797	Q798	Q799	Q800	Q801	Q802	Q803	Q804	Q805	Q806	Q807	Q808	Q809	Q810	Q811	Q812	Q813	Q814	Q815	Q816	Q817	Q818	Q819	Q820	Q821	Q822	Q823	Q824	Q825	Q826	Q827	Q828	Q829	Q830	Q831	Q832	Q833	Q834	Q835	Q836	Q837	Q838	Q839	Q840	Q841	Q842	Q843	Q844	Q845	Q846	Q847	Q848	Q849	Q850	Q851	Q852	Q853	Q854	Q855	Q856	Q857	Q858	Q859	Q860	Q861	Q862	Q863	Q864	Q865	Q866	Q867	Q868	Q869	Q870	Q871	Q872	Q873	Q874	Q875	Q876	Q877	Q878	Q879	Q880	Q881	Q882	Q883	Q884	Q885	Q886	Q887	Q888	Q889	Q890	Q891	Q892	Q893	Q894	Q895	Q896	Q897	Q898	Q899	Q900	Q901	Q902	Q903	Q904	Q905	Q906	Q907	Q908	Q909	Q910	Q911	Q912	Q913	Q914	Q915	Q916	Q917	Q918	Q919	Q920	Q921	Q922	Q923	Q924	Q925	Q926	Q927	Q928	Q929	Q930	Q931	Q932	Q933	Q934	Q935	Q936	Q937	Q938	Q939	Q940	Q941	Q942	Q943	Q944	Q945	Q946	Q947	Q948	Q949	Q950	Q951	Q952	Q953	Q954	Q955	Q956	Q957	Q958	Q959	Q960	Q961	Q962	Q963	Q964	Q965	Q966	Q967	Q968	Q969	Q970	Q971	Q972	Q973	Q974	Q975	Q976	Q977	Q978	Q979	Q980	Q981	Q982	Q983	Q984	Q985	Q986	Q987	Q988	Q989	Q990	Q991	Q992	Q993	Q994	Q995	Q996	Q997	Q998	Q999	Q1000	Q1001	Q1002	Q1003	Q1004	Q1005	Q1006	Q1007	Q1008	Q1009	Q1010	Q1011	Q1012	Q1013	Q1014	Q1015	Q1016	Q1017	Q1018	Q1019	Q1020	Q1021	Q102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## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	107.79 Å   126.07 Å   206.56 Å 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
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.08 (at 5.23 Å)	Xtriage
Refinement program	CNS 1.2	Depositor
R, $R_{free}$	0.276   ,   0.311 0.357   ,   0.353	Depositor DCC
$R_{free}$ test set	2490 reflections (6.90%)	DCC
Wilson B-factor (Å <sup>2</sup> )	260.4	Xtriage
Anisotropy	0.114	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.40 , 74.5	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.46$ , $\langle L^2 \rangle = 0.29$	Xtriage
Outliers	0 of 36078 reflections	Xtriage
$F_o, F_c$ correlation	0.85	EDS
Total number of atoms	4576	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	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.*

<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 ⓘ

### 5.1 Standard geometry ⓘ

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 5$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

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 ⓘ

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, 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	572/582 (98%)	7.64	524 (91%) 0 1	223, 300, 343, 343	0
1	B	572/582 (98%)	8.16	518 (90%) 0 1	218, 299, 340, 343	0
1	C	572/582 (98%)	7.55	520 (90%) 0 1	227, 310, 343, 343	0
1	D	572/582 (98%)	7.52	523 (91%) 0 1	238, 308, 343, 343	0
1	E	572/582 (98%)	6.62	499 (87%) 0 1	243, 317, 343, 343	0
1	F	572/582 (98%)	6.53	502 (87%) 0 1	229, 311, 343, 343	0
1	G	572/582 (98%)	6.58	488 (85%) 0 1	245, 320, 343, 343	0
1	H	572/582 (98%)	6.51	502 (87%) 0 1	236, 317, 343, 343	0
All	All	4576/4656 (98%)	7.14	4076 (89%) 0 1	218, 311, 343, 343	0

All (4076) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	377	ARG	36.1
1	D	243	LYS	35.1
1	B	324	SER	34.4
1	C	236	ARG	34.0
1	B	524	ASP	32.9
1	B	360	ARG	31.2
1	B	193	SER	30.0
1	D	299	LYS	29.6
1	G	131	ASP	29.3
1	D	253	PRO	29.1
1	H	483	GLY	28.8
1	B	186	SER	28.4
1	B	370	LYS	28.4
1	H	300	SER	28.2
1	C	473	VAL	27.0
1	C	193	SER	26.6

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Mol	Chain	Res	Type	RSRZ
1	H	377	ARG	26.2
1	C	448	GLU	26.2
1	D	380	SER	26.0
1	H	482	SER	25.9
1	C	175	ALA	25.9
1	A	247	ALA	25.4
1	C	519	ILE	25.3
1	B	70	VAL	25.0
1	B	170	ILE	24.8
1	A	323	ASP	24.6
1	D	32	VAL	24.6
1	C	359	LEU	24.2
1	A	248	SER	24.0
1	C	561	THR	24.0
1	H	34	LEU	24.0
1	G	295	MET	23.8
1	F	170	ILE	23.8
1	C	520	GLN	23.7
1	H	573	ALA	23.7
1	E	546	ASP	23.7
1	H	182	ILE	23.5
1	G	154	ILE	23.3
1	B	323	ASP	23.2
1	A	340	GLY	23.2
1	C	147	VAL	23.2
1	F	44	MET	23.1
1	G	141	GLY	23.1
1	B	31	GLY	23.1
1	G	115	PHE	23.1
1	B	192	ILE	23.0
1	F	317	THR	23.0
1	A	468	ASN	22.9
1	E	209	GLN	22.8
1	A	80	ILE	22.8
1	A	563	ASN	22.8
1	C	191	ASN	22.7
1	B	67	MET	22.6
1	C	32	VAL	22.6
1	G	46	SER	22.6
1	E	396	ASP	22.5
1	C	320	THR	22.4
1	D	425	ASN	22.4

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Mol	Chain	Res	Type	RSRZ
1	B	25	ALA	22.3
1	G	556	ILE	22.3
1	G	277	ASP	22.2
1	B	171	LEU	22.1
1	A	252	ASP	22.1
1	H	425	ASN	22.0
1	H	78	ARG	21.8
1	H	450	ILE	21.7
1	D	20	ILE	21.5
1	B	548	ILE	21.5
1	A	503	ILE	21.4
1	B	16	LEU	21.3
1	A	166	GLN	21.2
1	C	563	ASN	21.1
1	C	460	MET	21.0
1	D	90	SER	20.9
1	G	563	ASN	20.8
1	B	15	ARG	20.7
1	A	383	SER	20.7
1	G	425	ASN	20.7
1	B	76	ILE	20.7
1	A	79	GLY	20.7
1	C	579	GLN	20.6
1	C	233	VAL	20.5
1	D	301	LEU	20.4
1	H	235	ASN	20.4
1	C	247	ALA	20.3
1	G	44	MET	20.3
1	G	158	ILE	20.2
1	G	50	PRO	20.2
1	B	558	GLU	20.1
1	A	150	GLY	20.1
1	H	467	ASP	20.1
1	E	100	MET	20.0
1	H	368	ALA	19.9
1	D	515	SER	19.9
1	C	28	ILE	19.9
1	H	164	SER	19.8
1	H	181	ALA	19.8
1	H	226	GLU	19.8
1	C	417	ASN	19.8
1	D	223	GLN	19.7

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	F	343	GLU	19.7
1	B	94	GLY	19.6
1	A	273	PRO	19.5
1	F	404	GLY	19.5
1	F	519	ILE	19.5
1	G	164	SER	19.5
1	F	445	TYR	19.4
1	B	425	ASN	19.4
1	B	525	GLU	19.4
1	B	228	LYS	19.4
1	G	285	THR	19.4
1	A	46	SER	19.4
1	C	471	ASP	19.4
1	G	249	SER	19.4
1	C	262	ALA	19.3
1	B	559	ARG	19.3
1	D	559	ARG	19.2
1	F	544	LYS	19.2
1	B	378	SER	19.1
1	D	93	SER	19.1
1	E	285	THR	19.1
1	D	576	HIS	19.0
1	C	445	TYR	19.0
1	C	79	GLY	19.0
1	H	42	THR	19.0
1	D	326	GLN	18.9
1	A	341	ASP	18.9
1	D	181	ALA	18.8
1	F	500	PRO	18.8
1	D	31	GLY	18.8
1	F	158	ILE	18.7
1	H	146	VAL	18.6
1	D	566	LEU	18.6
1	C	170	ILE	18.6
1	A	259	ALA	18.6
1	A	125	LEU	18.6
1	G	291	MET	18.5
1	G	45	LEU	18.5
1	H	21	ALA	18.5
1	A	163	TYR	18.4
1	B	277	ASP	18.3
1	A	47	LEU	18.3

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Mol	Chain	Res	Type	RSRZ
1	B	22	PRO	18.3
1	B	319	PHE	18.3
1	G	25	ALA	18.3
1	D	304	VAL	18.2
1	E	164	SER	18.2
1	B	508	THR	18.2
1	G	34	LEU	18.2
1	B	359	LEU	18.2
1	F	327	GLU	18.2
1	G	165	TRP	18.1
1	B	122	GLY	18.1
1	B	182	ILE	18.1
1	A	400	ILE	18.1
1	H	355	ASP	18.1
1	B	249	SER	18.0
1	C	18	PRO	18.0
1	A	576	HIS	18.0
1	B	34	LEU	18.0
1	C	117	ASP	17.9
1	E	23	PHE	17.9
1	D	252	ASP	17.9
1	G	196	MET	17.9
1	B	95	LYS	17.8
1	D	166	GLN	17.8
1	F	131	ASP	17.8
1	D	471	ASP	17.8
1	C	362	ILE	17.7
1	A	249	SER	17.7
1	E	146	VAL	17.7
1	D	577	LYS	17.7
1	A	147	VAL	17.7
1	D	46	SER	17.7
1	A	510	ALA	17.6
1	F	439	TYR	17.6
1	C	324	SER	17.6
1	C	252	ASP	17.6
1	D	158	ILE	17.5
1	E	159	MET	17.5
1	D	62	SER	17.5
1	C	287	VAL	17.4
1	A	242	MET	17.4
1	C	134	GLN	17.4

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Mol	Chain	Res	Type	RSRZ
1	A	175	ALA	17.4
1	A	297	PRO	17.3
1	C	259	ALA	17.3
1	G	176	PRO	17.3
1	H	169	ILE	17.3
1	C	166	GLN	17.3
1	C	325	GLU	17.2
1	D	313	ALA	17.2
1	B	520	GLN	17.2
1	E	183	ARG	17.2
1	A	16	LEU	17.2
1	H	80	ILE	17.1
1	B	36	LEU	17.1
1	F	399	GLU	17.1
1	C	352	PRO	17.1
1	B	475	GLY	17.1
1	B	13	PHE	17.0
1	A	349	PHE	17.0
1	D	191	ASN	17.0
1	E	15	ARG	17.0
1	B	35	ILE	17.0
1	B	261	LEU	17.0
1	H	332	LYS	16.9
1	A	167	LEU	16.9
1	H	64	LEU	16.9
1	A	172	ILE	16.9
1	B	577	LYS	16.9
1	D	312	MET	16.9
1	G	334	VAL	16.8
1	A	448	GLU	16.8
1	A	182	ILE	16.7
1	G	323	ASP	16.7
1	H	81	THR	16.7
1	E	500	PRO	16.6
1	G	522	ALA	16.6
1	D	324	SER	16.6
1	E	238	ARG	16.6
1	B	191	ASN	16.5
1	A	309	GLN	16.5
1	B	46	SER	16.5
1	C	283	THR	16.5
1	D	262	ALA	16.5

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Mol	Chain	Res	Type	RSRZ
1	H	448	GLU	16.5
1	B	320	THR	16.5
1	A	524	ASP	16.5
1	D	557	VAL	16.5
1	H	327	GLU	16.5
1	E	141	GLY	16.5
1	A	360	ARG	16.5
1	B	252	ASP	16.4
1	A	127	ARG	16.4
1	C	457	ALA	16.4
1	E	512	ASP	16.4
1	H	277	ASP	16.3
1	G	272	PHE	16.3
1	F	378	SER	16.3
1	C	31	GLY	16.3
1	C	121	THR	16.3
1	B	380	SER	16.2
1	C	378	SER	16.2
1	B	258	ILE	16.2
1	F	543	GLU	16.2
1	C	454	ALA	16.2
1	A	103	ARG	16.2
1	A	136	ALA	16.2
1	F	68	PRO	16.2
1	F	248	SER	16.2
1	B	502	LEU	16.2
1	C	37	ASN	16.2
1	D	361	ASN	16.1
1	E	573	ALA	16.1
1	G	467	ASP	16.1
1	A	467	ASP	16.1
1	D	224	GLU	16.1
1	G	510	ALA	16.1
1	H	156	LEU	16.0
1	G	148	ARG	16.0
1	C	461	ASP	16.0
1	H	186	SER	16.0
1	H	86	SER	16.0
1	F	144	ILE	16.0
1	E	371	THR	16.0
1	E	475	GLY	16.0
1	F	134	GLN	16.0

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	A	337	ARG	16.0
1	C	326	GLN	15.9
1	E	82	SER	15.9
1	C	94	GLY	15.9
1	F	80	ILE	15.9
1	A	206	SER	15.9
1	A	261	LEU	15.9
1	C	285	THR	15.9
1	A	368	ALA	15.9
1	H	336	GLU	15.9
1	H	196	MET	15.9
1	D	468	ASN	15.9
1	B	68	PRO	15.8
1	E	372	VAL	15.8
1	H	580	PHE	15.8
1	F	349	PHE	15.8
1	F	379	GLY	15.8
1	H	468	ASN	15.8
1	A	62	SER	15.8
1	A	128	ILE	15.8
1	F	396	ASP	15.8
1	D	333	ARG	15.8
1	H	330	GLU	15.8
1	D	467	ASP	15.8
1	B	187	LYS	15.8
1	A	90	SER	15.8
1	E	93	SER	15.8
1	D	570	GLY	15.8
1	E	361	ASN	15.7
1	E	178	VAL	15.7
1	C	538	ARG	15.7
1	C	156	LEU	15.7
1	D	182	ILE	15.7
1	B	299	LYS	15.7
1	B	325	GLU	15.7
1	G	183	ARG	15.6
1	E	343	GLU	15.6
1	G	519	ILE	15.6
1	C	549	VAL	15.6
1	G	562	HIS	15.6
1	B	511	LEU	15.6
1	B	20	ILE	15.5

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Mol	Chain	Res	Type	RSRZ
1	C	521	ALA	15.5
1	H	456	MET	15.5
1	F	459	ALA	15.5
1	C	223	GLN	15.5
1	G	243	LYS	15.5
1	A	367	PRO	15.5
1	B	43	PHE	15.5
1	B	563	ASN	15.4
1	E	369	GLY	15.4
1	D	556	ILE	15.4
1	F	302	THR	15.4
1	G	169	ILE	15.3
1	A	262	ALA	15.3
1	C	323	ASP	15.3
1	A	513	THR	15.3
1	B	246	SER	15.3
1	B	399	GLU	15.3
1	B	551	VAL	15.3
1	G	381	GLY	15.3
1	A	25	ALA	15.2
1	A	23	PHE	15.2
1	B	529	ASN	15.2
1	B	482	SER	15.2
1	C	116	PHE	15.2
1	F	305	ASN	15.2
1	G	12	THR	15.2
1	G	539	LEU	15.2
1	B	480	LEU	15.1
1	D	58	LYS	15.1
1	E	204	THR	15.1
1	E	468	ASN	15.1
1	D	316	GLN	15.1
1	C	240	GLN	15.1
1	F	498	ASP	15.1
1	H	543	GLU	15.1
1	A	193	SER	15.1
1	D	369	GLY	15.1
1	A	186	SER	15.1
1	B	243	LYS	15.1
1	C	423	SER	15.1
1	B	514	GLU	15.1
1	F	185	VAL	15.1

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Mol	Chain	Res	Type	RSRZ
1	B	79	GLY	15.1
1	F	142	ALA	15.0
1	E	249	SER	15.0
1	E	439	TYR	15.0
1	D	254	ILE	15.0
1	E	98	MET	14.9
1	A	21	ALA	14.9
1	G	37	ASN	14.9
1	B	457	ALA	14.9
1	B	423	SER	14.9
1	E	92	VAL	14.9
1	D	143	LEU	14.8
1	E	425	ASN	14.8
1	B	349	PHE	14.8
1	G	304	VAL	14.7
1	D	113	VAL	14.7
1	A	169	ILE	14.7
1	B	93	SER	14.6
1	H	522	ALA	14.6
1	C	131	ASP	14.6
1	E	133	GLU	14.6
1	H	387	SER	14.6
1	C	560	GLY	14.5
1	D	134	GLN	14.5
1	C	398	GLY	14.5
1	A	192	ILE	14.5
1	F	79	GLY	14.5
1	H	489	ILE	14.5
1	D	366	ILE	14.5
1	E	40	SER	14.5
1	F	444	GLN	14.4
1	A	253	PRO	14.4
1	H	252	ASP	14.4
1	D	214	HIS	14.4
1	H	447	ARG	14.4
1	A	339	THR	14.4
1	C	91	TRP	14.4
1	E	283	THR	14.4
1	G	333	ARG	14.4
1	B	576	HIS	14.4
1	D	101	ARG	14.4
1	A	479	VAL	14.3

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Mol	Chain	Res	Type	RSRZ
1	A	530	ARG	14.3
1	F	559	ARG	14.3
1	H	453	ALA	14.3
1	F	175	ALA	14.3
1	C	150	GLY	14.3
1	G	546	ASP	14.3
1	C	566	LEU	14.3
1	C	158	ILE	14.3
1	G	140	SER	14.2
1	G	35	ILE	14.2
1	E	235	ASN	14.2
1	C	145	THR	14.2
1	F	350	THR	14.2
1	H	191	ASN	14.2
1	A	254	ILE	14.1
1	H	488	ARG	14.1
1	F	41	ASP	14.1
1	A	246	SER	14.1
1	A	506	GLU	14.1
1	A	22	PRO	14.1
1	B	526	LEU	14.1
1	F	510	ALA	14.1
1	E	117	ASP	14.0
1	G	43	PHE	14.0
1	H	129	THR	14.0
1	E	83	TYR	14.0
1	H	134	GLN	14.0
1	C	467	ASP	14.0
1	D	131	ASP	14.0
1	D	196	MET	14.0
1	D	424	GLN	14.0
1	A	463	ILE	14.0
1	C	425	ASN	14.0
1	A	31	GLY	13.9
1	D	23	PHE	13.9
1	F	204	THR	13.9
1	C	349	PHE	13.9
1	G	430	ASN	13.9
1	B	188	ARG	13.9
1	A	54	ASP	13.9
1	B	132	SER	13.9
1	D	136	ALA	13.9

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Mol	Chain	Res	Type	RSRZ
1	A	116	PHE	13.9
1	D	352	PRO	13.9
1	B	71	VAL	13.9
1	A	204	THR	13.9
1	H	566	LEU	13.9
1	D	563	ASN	13.8
1	C	393	TYR	13.8
1	F	115	PHE	13.8
1	G	64	LEU	13.8
1	B	230	PHE	13.8
1	B	175	ALA	13.8
1	D	192	ILE	13.8
1	F	529	ASN	13.8
1	H	43	PHE	13.8
1	H	413	ALA	13.8
1	G	317	THR	13.8
1	E	191	ASN	13.7
1	B	546	ASP	13.7
1	D	95	LYS	13.7
1	E	458	TYR	13.7
1	B	296	ARG	13.7
1	A	168	SER	13.7
1	E	226	GLU	13.7
1	D	242	MET	13.6
1	B	227	THR	13.6
1	H	310	ARG	13.6
1	B	235	ASN	13.6
1	C	466	MET	13.6
1	B	126	SER	13.6
1	B	244	MET	13.6
1	F	30	ALA	13.6
1	D	195	ASN	13.6
1	A	573	ALA	13.6
1	B	253	PRO	13.6
1	F	265	PHE	13.6
1	D	466	MET	13.5
1	E	132	SER	13.5
1	B	195	ASN	13.5
1	D	142	ALA	13.5
1	A	235	ASN	13.5
1	C	256	GLN	13.5
1	E	287	VAL	13.5

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Mol	Chain	Res	Type	RSRZ
1	A	574	GLN	13.5
1	C	255	ILE	13.5
1	E	363	ASN	13.5
1	B	466	MET	13.5
1	G	156	LEU	13.5
1	C	66	TRP	13.4
1	B	166	GLN	13.4
1	A	581	GLY	13.4
1	G	379	GLY	13.4
1	D	117	ASP	13.4
1	G	513	THR	13.4
1	E	421	LEU	13.4
1	F	143	LEU	13.4
1	H	378	SER	13.4
1	C	480	LEU	13.4
1	F	336	GLU	13.3
1	D	353	GLY	13.3
1	E	157	PHE	13.3
1	C	257	LEU	13.3
1	A	356	VAL	13.3
1	F	560	GLY	13.3
1	A	378	SER	13.3
1	F	447	ARG	13.3
1	E	144	ILE	13.3
1	D	121	THR	13.3
1	E	447	ARG	13.3
1	H	454	ALA	13.3
1	B	566	LEU	13.3
1	F	289	SER	13.3
1	D	505	ASP	13.3
1	H	28	ILE	13.3
1	A	366	ILE	13.3
1	A	419	VAL	13.3
1	D	57	GLY	13.2
1	A	24	LYS	13.2
1	B	279	LEU	13.2
1	G	103	ARG	13.2
1	B	245	VAL	13.2
1	F	301	LEU	13.2
1	F	330	GLU	13.2
1	F	52	LEU	13.2
1	D	323	ASP	13.2

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Mol	Chain	Res	Type	RSRZ
1	A	145	THR	13.2
1	C	242	MET	13.2
1	D	24	LYS	13.2
1	F	130	TYR	13.2
1	B	424	GLN	13.1
1	A	265	PHE	13.1
1	A	301	LEU	13.1
1	A	122	GLY	13.1
1	F	119	GLN	13.1
1	A	484	GLY	13.1
1	G	311	GLY	13.1
1	G	411	THR	13.1
1	B	248	SER	13.0
1	G	36	LEU	13.0
1	A	480	LEU	13.0
1	D	457	ALA	13.0
1	H	176	PRO	13.0
1	C	297	PRO	13.0
1	A	231	ASP	13.0
1	C	249	SER	13.0
1	G	498	ASP	13.0
1	A	348	THR	13.0
1	B	541	THR	13.0
1	D	16	LEU	13.0
1	B	435	ASN	13.0
1	C	73	GLY	13.0
1	C	151	ALA	13.0
1	H	94	GLY	13.0
1	A	199	THR	13.0
1	A	19	THR	13.0
1	C	391	ARG	13.0
1	G	359	LEU	13.0
1	B	474	ILE	13.0
1	G	29	VAL	12.9
1	D	144	ILE	12.9
1	E	379	GLY	12.9
1	G	116	PHE	12.9
1	B	301	LEU	12.9
1	E	225	VAL	12.9
1	D	156	LEU	12.9
1	F	230	PHE	12.9
1	D	479	VAL	12.9

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Mol	Chain	Res	Type	RSRZ
1	G	338	ALA	12.9
1	C	575	LEU	12.9
1	D	444	GLN	12.9
1	H	144	ILE	12.9
1	A	320	THR	12.8
1	B	361	ASN	12.8
1	G	282	GLY	12.8
1	E	514	GLU	12.8
1	A	325	GLU	12.8
1	C	332	LYS	12.8
1	G	544	LYS	12.8
1	C	513	THR	12.8
1	F	377	ARG	12.8
1	C	218	LEU	12.8
1	E	482	SER	12.7
1	F	332	LYS	12.7
1	G	325	GLU	12.7
1	A	95	LYS	12.7
1	B	455	ARG	12.7
1	A	567	GLU	12.7
1	E	190	ARG	12.7
1	E	354	ARG	12.7
1	C	456	MET	12.7
1	G	120	SER	12.7
1	C	251	SER	12.7
1	E	463	ILE	12.6
1	F	368	ALA	12.6
1	C	44	MET	12.6
1	H	431	ASP	12.6
1	A	181	ALA	12.6
1	A	32	VAL	12.6
1	F	458	TYR	12.6
1	D	358	ALA	12.6
1	C	444	GLN	12.6
1	A	171	LEU	12.6
1	A	447	ARG	12.6
1	A	144	ILE	12.6
1	E	187	LYS	12.6
1	B	549	VAL	12.6
1	E	263	LEU	12.6
1	B	401	LEU	12.5
1	C	482	SER	12.6

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Mol	Chain	Res	Type	RSRZ
1	G	579	GLN	12.5
1	G	197	GLN	12.5
1	G	363	ASN	12.5
1	A	146	VAL	12.5
1	B	532	SER	12.5
1	D	145	THR	12.5
1	F	277	ASP	12.5
1	H	171	LEU	12.5
1	F	548	ILE	12.5
1	F	283	THR	12.5
1	D	367	PRO	12.5
1	A	357	PRO	12.5
1	D	300	SER	12.5
1	B	358	ALA	12.5
1	G	159	MET	12.5
1	G	567	GLU	12.5
1	D	514	GLU	12.5
1	A	390	THR	12.5
1	B	215	LYS	12.5
1	E	170	ILE	12.5
1	A	115	PHE	12.4
1	D	60	ASP	12.4
1	E	28	ILE	12.4
1	C	12	THR	12.4
1	F	311	GLY	12.4
1	E	66	TRP	12.4
1	F	123	THR	12.4
1	C	401	LEU	12.4
1	G	194	LYS	12.4
1	F	335	ILE	12.4
1	D	245	VAL	12.4
1	A	483	GLY	12.4
1	A	559	ARG	12.3
1	H	386	ALA	12.3
1	D	170	ILE	12.3
1	D	530	ARG	12.3
1	C	182	ILE	12.3
1	A	223	GLN	12.3
1	D	474	ILE	12.3
1	B	531	THR	12.3
1	H	170	ILE	12.3
1	C	328	LYS	12.3

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Mol	Chain	Res	Type	RSRZ
1	C	46	SER	12.3
1	F	173	VAL	12.3
1	A	300	SER	12.2
1	F	363	ASN	12.2
1	F	497	ARG	12.2
1	C	48	LEU	12.2
1	C	301	LEU	12.2
1	E	265	PHE	12.2
1	B	242	MET	12.2
1	C	47	LEU	12.2
1	G	76	ILE	12.2
1	A	96	VAL	12.2
1	B	144	ILE	12.2
1	E	284	ILE	12.2
1	G	542	ILE	12.1
1	A	313	ALA	12.1
1	E	163	TYR	12.1
1	D	139	SER	12.1
1	B	273	PRO	12.1
1	D	76	ILE	12.1
1	G	463	ILE	12.1
1	B	231	ASP	12.1
1	A	205	THR	12.1
1	D	273	PRO	12.1
1	D	579	GLN	12.1
1	E	413	ALA	12.1
1	B	473	VAL	12.0
1	D	265	PHE	12.0
1	D	175	ALA	12.0
1	F	426	VAL	12.0
1	F	155	GLY	12.0
1	B	21	ALA	12.0
1	B	259	ALA	12.0
1	E	487	GLN	12.0
1	B	453	ALA	12.0
1	D	303	ASN	12.0
1	E	50	PRO	12.0
1	C	99	THR	12.0
1	B	181	ALA	12.0
1	B	355	ASP	12.0
1	C	348	THR	12.0
1	F	235	ASN	11.9

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Mol	Chain	Res	Type	RSRZ
1	E	572	TYR	11.9
1	C	57	GLY	11.9
1	C	443	GLU	11.9
1	C	118	LYS	11.9
1	F	201	GLY	11.9
1	B	328	LYS	11.9
1	A	322	LEU	11.9
1	E	407	LEU	11.9
1	B	121	THR	11.9
1	H	498	ASP	11.9
1	B	329	ASP	11.9
1	C	369	GLY	11.9
1	B	330	GLU	11.9
1	F	10	TRP	11.9
1	G	177	ILE	11.9
1	E	562	HIS	11.8
1	E	467	ASP	11.8
1	F	228	LYS	11.8
1	D	87	TYR	11.8
1	D	357	PRO	11.8
1	B	47	LEU	11.8
1	C	76	ILE	11.8
1	B	197	GLN	11.8
1	D	197	GLN	11.8
1	G	559	ARG	11.8
1	B	223	GLN	11.8
1	C	424	GLN	11.8
1	A	66	TRP	11.8
1	A	94	GLY	11.7
1	B	367	PRO	11.7
1	B	17	TRP	11.7
1	B	66	TRP	11.7
1	B	567	GLU	11.7
1	B	113	VAL	11.7
1	B	131	ASP	11.7
1	D	28	ILE	11.7
1	E	329	ASP	11.7
1	B	280	THR	11.7
1	C	19	THR	11.7
1	H	476	GLU	11.7
1	E	165	TRP	11.7
1	F	67	MET	11.7

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Mol	Chain	Res	Type	RSRZ
1	G	456	MET	11.7
1	E	278	SER	11.7
1	H	499	SER	11.7
1	B	226	GLU	11.7
1	B	155	GLY	11.7
1	A	65	VAL	11.6
1	D	496	LEU	11.6
1	H	424	GLN	11.6
1	D	338	ALA	11.6
1	A	355	ASP	11.6
1	C	360	ARG	11.6
1	F	42	THR	11.6
1	H	39	ALA	11.6
1	F	135	VAL	11.6
1	D	153	ILE	11.6
1	C	93	SER	11.6
1	H	371	THR	11.6
1	F	318	LEU	11.6
1	G	457	ALA	11.6
1	B	515	SER	11.6
1	B	189	PHE	11.6
1	G	354	ARG	11.5
1	F	167	LEU	11.5
1	A	397	GLU	11.5
1	D	455	ARG	11.5
1	F	34	LEU	11.5
1	B	467	ASP	11.5
1	A	557	VAL	11.5
1	D	92	VAL	11.5
1	E	426	VAL	11.5
1	D	33	ALA	11.5
1	D	202	GLN	11.5
1	A	143	LEU	11.5
1	D	355	ASP	11.5
1	C	389	ILE	11.4
1	D	517	ARG	11.4
1	G	426	VAL	11.4
1	A	560	GLY	11.4
1	G	572	TYR	11.4
1	C	514	GLU	11.4
1	D	513	THR	11.4
1	E	471	ASP	11.4

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Mol	Chain	Res	Type	RSRZ
1	E	537	HIS	11.4
1	F	281	ALA	11.4
1	E	286	VAL	11.4
1	A	380	SER	11.4
1	F	261	LEU	11.4
1	E	184	VAL	11.4
1	A	418	GLN	11.4
1	G	443	GLU	11.4
1	C	568	HIS	11.4
1	B	348	THR	11.3
1	H	512	ASP	11.3
1	B	477	ASN	11.3
1	C	200	MET	11.3
1	D	516	GLU	11.3
1	F	180	ILE	11.3
1	H	518	ALA	11.3
1	D	417	ASN	11.3
1	H	209	GLN	11.3
1	G	310	ARG	11.3
1	G	413	ALA	11.3
1	D	452	GLU	11.3
1	B	356	VAL	11.3
1	G	337	ARG	11.3
1	H	255	ILE	11.3
1	E	47	LEU	11.3
1	B	571	VAL	11.3
1	A	91	TRP	11.3
1	E	301	LEU	11.3
1	B	408	ARG	11.3
1	C	163	TYR	11.2
1	H	117	ASP	11.2
1	C	115	PHE	11.2
1	H	72	ILE	11.2
1	G	117	ASP	11.2
1	D	157	PHE	11.2
1	F	188	ARG	11.2
1	H	248	SER	11.2
1	B	459	ALA	11.2
1	B	30	ALA	11.2
1	C	284	ILE	11.2
1	B	293	ALA	11.2
1	E	353	GLY	11.2

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Mol	Chain	Res	Type	RSRZ
1	D	297	PRO	11.1
1	F	351	TYR	11.1
1	G	38	ALA	11.1
1	G	142	ALA	11.1
1	C	356	VAL	11.1
1	D	155	GLY	11.1
1	H	289	SER	11.1
1	E	253	PRO	11.1
1	C	293	ALA	11.1
1	C	106	GLY	11.1
1	B	167	LEU	11.1
1	D	571	VAL	11.1
1	F	11	GLN	11.1
1	B	333	ARG	11.1
1	H	230	PHE	11.1
1	H	66	TRP	11.1
1	H	565	LEU	11.1
1	C	45	LEU	11.1
1	D	331	GLY	11.1
1	B	14	ARG	11.1
1	F	326	GLN	11.1
1	F	425	ASN	11.0
1	H	343	GLU	11.0
1	C	479	VAL	11.0
1	F	76	ILE	11.0
1	E	207	ALA	11.0
1	F	461	ASP	11.0
1	H	486	ARG	11.0
1	H	579	GLN	11.0
1	C	329	ASP	11.0
1	H	419	VAL	11.0
1	C	260	SER	11.0
1	H	35	ILE	11.0
1	E	110	GLY	11.0
1	G	42	THR	11.0
1	C	95	LYS	11.0
1	H	337	ARG	11.0
1	G	271	SER	11.0
1	B	547	GLU	11.0
1	D	454	ALA	11.0
1	F	416	ARG	11.0
1	B	362	ILE	11.0

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Mol	Chain	Res	Type	RSRZ
1	A	42	THR	11.0
1	C	338	ALA	11.0
1	H	41	ASP	10.9
1	B	185	VAL	10.9
1	B	112	PRO	10.9
1	B	136	ALA	10.9
1	B	134	GLN	10.9
1	F	194	LYS	10.9
1	B	400	ILE	10.9
1	D	394	ASP	10.9
1	E	248	SER	10.9
1	C	572	TYR	10.9
1	A	497	ARG	10.9
1	G	409	GLU	10.9
1	D	150	GLY	10.9
1	E	403	ASP	10.9
1	G	60	ASP	10.9
1	C	511	LEU	10.9
1	G	182	ILE	10.9
1	A	329	ASP	10.8
1	H	276	MET	10.8
1	B	276	MET	10.8
1	B	383	SER	10.8
1	C	459	ALA	10.8
1	D	413	ALA	10.8
1	F	118	LYS	10.8
1	G	168	SER	10.8
1	D	548	ILE	10.8
1	F	352	PRO	10.8
1	D	122	GLY	10.8
1	C	258	ILE	10.8
1	D	359	LEU	10.8
1	G	147	VAL	10.8
1	D	449	GLN	10.8
1	E	70	VAL	10.8
1	H	204	THR	10.8
1	C	316	GLN	10.8
1	D	164	SER	10.8
1	H	304	VAL	10.8
1	A	304	VAL	10.8
1	B	64	LEU	10.8
1	D	120	SER	10.8

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Mol	Chain	Res	Type	RSRZ
1	E	337	ARG	10.8
1	D	91	TRP	10.8
1	B	196	MET	10.7
1	A	512	ASP	10.7
1	D	217	VAL	10.7
1	E	338	ALA	10.7
1	D	74	LEU	10.7
1	G	580	PHE	10.7
1	H	363	ASN	10.7
1	H	445	TYR	10.7
1	G	239	LEU	10.7
1	E	36	LEU	10.7
1	F	23	PHE	10.7
1	D	503	ILE	10.6
1	C	261	LEU	10.6
1	F	212	LYS	10.6
1	A	426	VAL	10.6
1	F	245	VAL	10.6
1	A	35	ILE	10.6
1	C	394	ASP	10.6
1	D	52	LEU	10.6
1	H	460	MET	10.6
1	E	480	LEU	10.6
1	E	568	HIS	10.6
1	G	152	SER	10.6
1	B	99	THR	10.6
1	D	340	GLY	10.6
1	B	418	GLN	10.6
1	A	333	ARG	10.6
1	B	96	VAL	10.6
1	E	368	ALA	10.6
1	E	386	ALA	10.6
1	F	383	SER	10.6
1	F	153	ILE	10.6
1	B	251	SER	10.6
1	C	580	PHE	10.6
1	A	258	ILE	10.6
1	H	338	ALA	10.6
1	E	186	SER	10.6
1	E	302	THR	10.6
1	D	305	ASN	10.5
1	A	177	ILE	10.5

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Mol	Chain	Res	Type	RSRZ
1	A	556	ILE	10.5
1	D	111	MET	10.5
1	C	15	ARG	10.5
1	E	560	GLY	10.5
1	A	377	ARG	10.5
1	F	231	ASP	10.5
1	E	255	ILE	10.5
1	D	511	LEU	10.5
1	F	218	LEU	10.5
1	D	447	ARG	10.5
1	H	225	VAL	10.5
1	G	368	ALA	10.5
1	E	59	THR	10.5
1	D	461	ASP	10.5
1	G	378	SER	10.5
1	A	226	GLU	10.5
1	H	313	ALA	10.5
1	B	229	ARG	10.5
1	C	87	TYR	10.5
1	D	351	TYR	10.5
1	D	482	SER	10.5
1	B	569	ARG	10.5
1	A	55	GLY	10.5
1	F	312	MET	10.5
1	G	361	ASN	10.5
1	D	137	SER	10.5
1	E	22	PRO	10.5
1	B	503	ILE	10.5
1	F	146	VAL	10.5
1	C	485	GLN	10.5
1	H	102	ARG	10.5
1	E	355	ASP	10.5
1	B	316	GLN	10.5
1	E	356	VAL	10.4
1	C	570	GLY	10.4
1	C	180	ILE	10.4
1	E	510	ALA	10.4
1	A	78	ARG	10.4
1	B	247	ALA	10.4
1	G	254	ILE	10.4
1	F	214	HIS	10.4
1	B	138	SER	10.4

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Mol	Chain	Res	Type	RSRZ
1	E	564	ASP	10.4
1	D	569	ARG	10.4
1	F	274	SER	10.4
1	F	154	ILE	10.4
1	D	10	TRP	10.4
1	A	188	ARG	10.4
1	G	534	VAL	10.4
1	C	228	LYS	10.4
1	C	122	GLY	10.4
1	D	558	GLU	10.4
1	A	516	GLU	10.4
1	F	184	VAL	10.3
1	G	574	GLN	10.3
1	D	53	ASP	10.3
1	D	61	ARG	10.3
1	H	199	THR	10.3
1	B	570	GLY	10.3
1	C	484	GLY	10.3
1	B	426	VAL	10.3
1	B	287	VAL	10.3
1	G	483	GLY	10.3
1	A	137	SER	10.3
1	F	150	GLY	10.3
1	B	336	GLU	10.3
1	F	63	VAL	10.3
1	E	325	GLU	10.3
1	D	329	ASP	10.3
1	A	255	ILE	10.3
1	A	558	GLU	10.3
1	D	200	MET	10.3
1	H	147	VAL	10.3
1	B	23	PHE	10.3
1	E	570	GLY	10.3
1	B	338	ALA	10.3
1	B	581	GLY	10.2
1	C	186	SER	10.2
1	H	323	ASP	10.2
1	B	150	GLY	10.2
1	B	446	SER	10.2
1	C	96	VAL	10.2
1	G	298	LEU	10.2
1	A	303	ASN	10.2

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Mol	Chain	Res	Type	RSRZ
1	C	498	ASP	10.2
1	E	127	ARG	10.2
1	A	482	SER	10.2
1	E	420	ALA	10.2
1	E	449	GLN	10.2
1	G	179	SER	10.2
1	A	185	VAL	10.2
1	G	446	SER	10.2
1	H	423	SER	10.2
1	B	75	MET	10.2
1	B	262	ALA	10.2
1	C	34	LEU	10.2
1	B	39	ALA	10.1
1	D	348	THR	10.1
1	B	11	GLN	10.1
1	H	485	GLN	10.1
1	E	152	SER	10.1
1	F	174	LEU	10.1
1	G	70	VAL	10.1
1	D	443	GLU	10.1
1	B	90	SER	10.1
1	D	138	SER	10.1
1	B	483	GLY	10.1
1	D	198	ASN	10.1
1	G	391	ARG	10.1
1	B	24	LYS	10.1
1	G	153	ILE	10.1
1	G	231	ASP	10.1
1	B	28	ILE	10.1
1	B	214	HIS	10.1
1	B	199	THR	10.1
1	F	340	GLY	10.1
1	H	22	PRO	10.1
1	E	212	LYS	10.1
1	F	476	GLU	10.1
1	F	117	ASP	10.1
1	D	260	SER	10.1
1	G	235	ASN	10.1
1	C	383	SER	10.1
1	H	544	LYS	10.1
1	A	161	PHE	10.1
1	F	122	GLY	10.1

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Mol	Chain	Res	Type	RSRZ
1	H	418	GLN	10.1
1	A	236	ARG	10.1
1	A	481	LEU	10.0
1	C	181	ALA	10.0
1	A	113	VAL	10.0
1	D	581	GLY	10.0
1	G	554	GLY	10.0
1	A	438	ALA	10.0
1	G	322	LEU	10.0
1	A	68	PRO	10.0
1	E	280	THR	10.0
1	E	229	ARG	10.0
1	A	439	TYR	10.0
1	D	337	ARG	10.0
1	E	509	SER	10.0
1	D	350	THR	10.0
1	H	227	THR	10.0
1	A	72	ILE	10.0
1	C	559	ARG	10.0
1	C	447	ARG	10.0
1	F	522	ALA	10.0
1	G	286	VAL	10.0
1	H	60	ASP	10.0
1	C	408	ARG	10.0
1	D	226	GLU	10.0
1	G	452	GLU	10.0
1	H	59	THR	10.0
1	C	355	ASP	10.0
1	A	454	ALA	10.0
1	F	346	ASN	9.9
1	D	373	ALA	9.9
1	D	401	LEU	9.9
1	A	289	SER	9.9
1	B	278	SER	9.9
1	F	540	SER	9.9
1	A	287	VAL	9.9
1	E	333	ARG	9.9
1	A	153	ILE	9.9
1	E	180	ILE	9.9
1	D	453	ALA	9.9
1	E	540	SER	9.9
1	H	559	ARG	9.9

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Mol	Chain	Res	Type	RSRZ
1	F	556	ILE	9.9
1	A	392	PHE	9.9
1	D	456	MET	9.9
1	F	72	ILE	9.9
1	A	215	LYS	9.9
1	C	472	THR	9.9
1	G	294	LEU	9.9
1	D	239	LEU	9.9
1	D	99	THR	9.9
1	A	218	LEU	9.9
1	E	503	ILE	9.9
1	D	541	THR	9.9
1	G	497	ARG	9.9
1	D	259	ALA	9.9
1	G	358	ALA	9.9
1	E	412	LEU	9.9
1	B	326	GLN	9.9
1	G	30	ALA	9.8
1	H	166	GLN	9.8
1	D	286	VAL	9.8
1	H	214	HIS	9.8
1	C	358	ALA	9.8
1	C	80	ILE	9.8
1	E	266	VAL	9.8
1	A	445	TYR	9.8
1	B	114	SER	9.8
1	C	164	SER	9.8
1	E	277	ASP	9.8
1	E	519	ILE	9.8
1	A	580	PHE	9.8
1	C	27	LEU	9.8
1	F	27	LEU	9.8
1	E	408	ARG	9.8
1	B	19	THR	9.8
1	D	94	GLY	9.7
1	E	158	ILE	9.7
1	H	121	THR	9.7
1	C	335	ILE	9.7
1	H	444	GLN	9.7
1	F	295	MET	9.7
1	D	463	ILE	9.7
1	A	119	GLN	9.7

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Mol	Chain	Res	Type	RSRZ
1	D	538	ARG	9.7
1	B	54	ASP	9.7
1	D	405	HIS	9.7
1	B	300	SER	9.7
1	G	517	ARG	9.7
1	B	497	ARG	9.7
1	H	79	GLY	9.6
1	B	396	ASP	9.6
1	D	400	ILE	9.6
1	G	527	GLN	9.6
1	F	33	ALA	9.6
1	C	432	THR	9.6
1	A	331	GLY	9.6
1	C	62	SER	9.6
1	C	464	ASN	9.6
1	D	473	VAL	9.6
1	H	135	VAL	9.6
1	F	12	THR	9.6
1	D	59	THR	9.6
1	D	83	TYR	9.6
1	G	350	THR	9.6
1	F	282	GLY	9.6
1	A	425	ASN	9.6
1	B	163	TYR	9.6
1	G	266	VAL	9.6
1	G	248	SER	9.6
1	C	209	GLN	9.6
1	E	495	LEU	9.6
1	D	535	ILE	9.6
1	C	176	PRO	9.6
1	D	152	SER	9.6
1	D	459	ALA	9.6
1	E	404	GLY	9.6
1	H	568	HIS	9.6
1	D	393	TYR	9.5
1	E	97	VAL	9.5
1	G	186	SER	9.5
1	E	435	ASN	9.5
1	G	444	GLN	9.5
1	C	581	GLY	9.5
1	F	574	GLN	9.5
1	D	480	LEU	9.5

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Mol	Chain	Res	Type	RSRZ
1	B	417	ASN	9.5
1	A	83	TYR	9.5
1	C	418	GLN	9.5
1	E	222	GLY	9.5
1	F	406	ASP	9.5
1	A	424	GLN	9.5
1	A	164	SER	9.5
1	C	10	TRP	9.5
1	F	570	GLY	9.5
1	D	572	TYR	9.5
1	A	176	PRO	9.5
1	D	248	SER	9.5
1	F	535	ILE	9.5
1	A	328	LYS	9.5
1	D	328	LYS	9.5
1	C	160	MET	9.5
1	A	416	ARG	9.4
1	A	76	ILE	9.4
1	F	159	MET	9.4
1	C	196	MET	9.4
1	A	12	THR	9.4
1	D	518	ALA	9.4
1	D	341	ASP	9.4
1	F	337	ARG	9.4
1	F	552	GLU	9.4
1	G	134	GLN	9.4
1	A	420	ALA	9.4
1	B	481	LEU	9.4
1	G	305	ASN	9.4
1	D	539	LEU	9.4
1	E	84	VAL	9.4
1	C	30	ALA	9.4
1	F	181	ALA	9.4
1	B	580	PHE	9.4
1	A	151	ALA	9.4
1	C	199	THR	9.4
1	D	489	ILE	9.4
1	F	534	VAL	9.3
1	F	48	LEU	9.3
1	F	569	ARG	9.3
1	A	123	THR	9.3
1	H	379	GLY	9.3

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Mol	Chain	Res	Type	RSRZ
1	B	60	ASP	9.3
1	H	399	GLU	9.3
1	D	285	THR	9.3
1	D	123	THR	9.3
1	F	551	VAL	9.3
1	H	430	ASN	9.3
1	E	42	THR	9.3
1	E	176	PRO	9.3
1	G	209	GLN	9.3
1	F	329	ASP	9.3
1	E	166	GLN	9.3
1	H	333	ARG	9.3
1	A	389	ILE	9.3
1	B	106	GLY	9.3
1	H	238	ARG	9.3
1	G	242	MET	9.3
1	G	303	ASN	9.3
1	G	448	GLU	9.3
1	B	427	HIS	9.3
1	C	330	GLU	9.2
1	C	390	THR	9.2
1	H	427	HIS	9.2
1	F	215	LYS	9.2
1	H	295	MET	9.2
1	B	441	ARG	9.2
1	G	474	ILE	9.2
1	G	573	ALA	9.2
1	B	393	TYR	9.2
1	D	51	LEU	9.2
1	A	196	MET	9.2
1	A	58	LYS	9.2
1	B	87	TYR	9.2
1	B	225	VAL	9.2
1	H	118	LYS	9.2
1	C	576	HIS	9.2
1	E	169	ILE	9.2
1	C	244	MET	9.2
1	C	529	ASN	9.2
1	B	130	TYR	9.2
1	C	463	ILE	9.2
1	B	460	MET	9.2
1	B	432	THR	9.2

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Mol	Chain	Res	Type	RSRZ
1	A	444	GLN	9.2
1	B	332	LYS	9.2
1	H	497	ARG	9.2
1	H	297	PRO	9.2
1	A	207	ALA	9.2
1	D	540	SER	9.2
1	H	127	ARG	9.1
1	E	10	TRP	9.1
1	D	376	GLY	9.1
1	C	571	VAL	9.1
1	E	328	LYS	9.1
1	F	456	MET	9.1
1	G	227	THR	9.1
1	E	259	ALA	9.1
1	D	112	PRO	9.1
1	B	461	ASP	9.1
1	B	484	GLY	9.1
1	A	336	GLU	9.1
1	E	245	VAL	9.1
1	B	100	MET	9.1
1	C	202	GLN	9.1
1	H	150	GLY	9.1
1	C	399	GLU	9.1
1	E	555	VAL	9.1
1	E	529	ASN	9.1
1	E	341	ASP	9.1
1	B	391	ARG	9.1
1	D	167	LEU	9.1
1	E	488	ARG	9.1
1	B	178	VAL	9.1
1	D	210	MET	9.1
1	E	528	LYS	9.0
1	B	430	ASN	9.0
1	H	244	MET	9.0
1	E	103	ARG	9.0
1	G	215	LYS	9.0
1	B	27	LEU	9.0
1	F	467	ASP	9.0
1	E	46	SER	9.0
1	D	315	CYS	9.0
1	A	393	TYR	9.0
1	D	103	ARG	9.0

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Mol	Chain	Res	Type	RSRZ
1	H	210	MET	9.0
1	D	560	GLY	9.0
1	C	248	SER	9.0
1	C	427	HIS	9.0
1	H	155	GLY	9.0
1	C	26	GLY	9.0
1	G	128	ILE	9.0
1	G	302	THR	9.0
1	E	397	GLU	9.0
1	H	421	LEU	9.0
1	C	299	LYS	9.0
1	A	511	LEU	9.0
1	C	253	PRO	9.0
1	H	435	ASN	9.0
1	H	15	ARG	9.0
1	C	169	ILE	9.0
1	E	390	THR	9.0
1	A	53	ASP	9.0
1	A	334	VAL	9.0
1	E	91	TRP	9.0
1	C	439	TYR	9.0
1	B	436	ASN	9.0
1	G	459	ALA	9.0
1	H	335	ILE	9.0
1	D	549	VAL	9.0
1	B	285	THR	9.0
1	A	464	ASN	9.0
1	G	250	ILE	9.0
1	F	74	LEU	8.9
1	A	441	ARG	8.9
1	D	485	GLN	8.9
1	H	249	SER	8.9
1	G	80	ILE	8.9
1	D	165	TRP	8.9
1	G	202	GLN	8.9
1	C	59	THR	8.9
1	F	223	GLN	8.9
1	G	73	GLY	8.9
1	D	567	GLU	8.9
1	D	332	LYS	8.9
1	D	402	MET	8.9
1	H	412	LEU	8.9

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Mol	Chain	Res	Type	RSRZ
1	F	95	LYS	8.9
1	F	528	LYS	8.9
1	C	230	PHE	8.9
1	F	470	LEU	8.9
1	H	314	ALA	8.9
1	B	289	SER	8.9
1	B	308	PHE	8.9
1	E	501	ILE	8.9
1	A	63	VAL	8.9
1	B	232	LYS	8.9
1	E	290	SER	8.9
1	E	279	LEU	8.8
1	E	538	ARG	8.8
1	E	389	ILE	8.8
1	A	381	GLY	8.8
1	B	505	ASP	8.8
1	B	539	LEU	8.8
1	F	290	SER	8.8
1	A	26	GLY	8.8
1	C	405	HIS	8.8
1	E	61	ARG	8.8
1	G	207	ALA	8.8
1	A	532	SER	8.8
1	G	540	SER	8.8
1	A	61	ARG	8.8
1	A	277	ASP	8.8
1	E	450	ILE	8.8
1	D	193	SER	8.8
1	D	261	LEU	8.8
1	F	99	THR	8.8
1	G	471	ASP	8.8
1	G	431	ASP	8.8
1	E	113	VAL	8.8
1	F	165	TRP	8.8
1	G	503	ILE	8.8
1	H	546	ASP	8.8
1	G	230	PHE	8.8
1	H	329	ASP	8.8
1	G	280	THR	8.8
1	H	328	LYS	8.8
1	B	307	GLN	8.8
1	C	558	GLU	8.8

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Mol	Chain	Res	Type	RSRZ
1	B	151	ALA	8.8
1	F	229	ARG	8.8
1	G	357	PRO	8.8
1	F	571	VAL	8.8
1	G	447	ARG	8.8
1	A	191	ASN	8.8
1	B	154	ILE	8.8
1	F	567	GLU	8.7
1	C	368	ALA	8.7
1	E	340	GLY	8.7
1	H	536	ALA	8.7
1	H	481	LEU	8.7
1	D	446	SER	8.7
1	F	294	LEU	8.7
1	H	515	SER	8.7
1	D	362	ILE	8.7
1	F	86	SER	8.7
1	C	376	GLY	8.7
1	E	536	ALA	8.7
1	A	310	ARG	8.7
1	C	380	SER	8.7
1	F	319	PHE	8.7
1	C	453	ALA	8.7
1	C	552	GLU	8.7
1	D	30	ALA	8.7
1	G	399	GLU	8.7
1	E	313	ALA	8.7
1	C	72	ILE	8.7
1	A	209	GLN	8.7
1	D	370	LYS	8.7
1	D	66	TRP	8.7
1	B	69	LEU	8.6
1	D	442	THR	8.6
1	F	578	MET	8.6
1	D	419	VAL	8.6
1	A	229	ARG	8.6
1	H	487	GLN	8.6
1	C	167	LEU	8.6
1	D	365	LYS	8.6
1	F	403	ASP	8.6
1	G	571	VAL	8.6
1	F	511	LEU	8.6

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Mol	Chain	Res	Type	RSRZ
1	C	235	ASN	8.6
1	E	230	PHE	8.6
1	F	325	GLU	8.6
1	B	397	GLU	8.6
1	A	577	LYS	8.6
1	G	509	SER	8.6
1	G	514	GLU	8.6
1	D	231	ASP	8.6
1	F	333	ARG	8.6
1	D	230	PHE	8.6
1	H	85	SER	8.6
1	C	133	GLU	8.6
1	G	397	GLU	8.6
1	C	535	ILE	8.5
1	E	332	LYS	8.5
1	D	410	TYR	8.5
1	A	200	MET	8.5
1	H	446	SER	8.5
1	D	349	PHE	8.5
1	G	424	GLN	8.5
1	A	129	THR	8.5
1	H	90	SER	8.5
1	A	561	THR	8.5
1	A	502	LEU	8.5
1	E	237	MET	8.5
1	C	382	LYS	8.5
1	B	540	SER	8.5
1	B	572	TYR	8.5
1	F	568	HIS	8.5
1	F	400	ILE	8.5
1	C	319	PHE	8.5
1	F	316	GLN	8.5
1	D	249	SER	8.5
1	A	455	ARG	8.4
1	F	106	GLY	8.4
1	C	569	ARG	8.4
1	B	440	ALA	8.4
1	G	396	ASP	8.4
1	G	427	HIS	8.4
1	B	448	GLU	8.4
1	E	289	SER	8.4
1	C	39	ALA	8.4

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Mol	Chain	Res	Type	RSRZ
1	B	517	ARG	8.4
1	D	55	GLY	8.4
1	G	328	LYS	8.4
1	A	399	GLU	8.4
1	H	501	ILE	8.4
1	E	262	ALA	8.4
1	A	427	HIS	8.4
1	A	462	PHE	8.4
1	H	194	LYS	8.4
1	F	417	ASN	8.4
1	F	494	ALA	8.4
1	G	112	PRO	8.4
1	G	568	HIS	8.4
1	G	485	GLN	8.4
1	B	303	ASN	8.4
1	C	211	LEU	8.4
1	G	133	GLU	8.4
1	E	423	SER	8.4
1	F	51	LEU	8.3
1	D	545	ALA	8.3
1	D	163	TYR	8.3
1	C	477	ASN	8.3
1	E	122	GLY	8.3
1	G	529	ASN	8.3
1	A	155	GLY	8.3
1	A	282	GLY	8.3
1	B	92	VAL	8.3
1	F	308	PHE	8.3
1	B	342	VAL	8.3
1	C	136	ALA	8.3
1	G	219	ILE	8.3
1	E	357	PRO	8.3
1	D	552	GLU	8.3
1	A	460	MET	8.3
1	D	35	ILE	8.3
1	H	14	ARG	8.3
1	F	471	ASP	8.3
1	F	499	SER	8.3
1	G	501	ILE	8.3
1	B	264	ALA	8.3
1	F	222	GLY	8.3
1	B	478	GLY	8.3

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Mol	Chain	Res	Type	RSRZ
1	F	359	LEU	8.3
1	G	454	ALA	8.3
1	D	391	ARG	8.3
1	E	72	ILE	8.3
1	G	558	GLU	8.3
1	H	278	SER	8.3
1	E	181	ALA	8.3
1	E	432	THR	8.3
1	B	48	LEU	8.3
1	B	575	LEU	8.3
1	E	306	ALA	8.3
1	A	330	GLU	8.3
1	B	91	TRP	8.3
1	G	41	ASP	8.3
1	A	472	THR	8.3
1	B	156	LEU	8.3
1	D	431	ASP	8.3
1	F	537	HIS	8.3
1	F	112	PRO	8.2
1	H	443	GLU	8.2
1	E	210	MET	8.2
1	H	222	GLY	8.2
1	B	451	GLU	8.2
1	G	343	GLU	8.2
1	A	566	LEU	8.2
1	E	399	GLU	8.2
1	H	303	ASN	8.2
1	E	385	ILE	8.2
1	B	404	GLY	8.2
1	F	209	GLN	8.2
1	D	330	GLU	8.2
1	G	405	HIS	8.2
1	F	26	GLY	8.2
1	F	273	PRO	8.2
1	C	426	VAL	8.2
1	E	131	ASP	8.2
1	E	431	ASP	8.2
1	B	77	LEU	8.2
1	B	125	LEU	8.2
1	A	148	ARG	8.2
1	C	333	ARG	8.2
1	F	28	ILE	8.2

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Mol	Chain	Res	Type	RSRZ
1	G	570	GLY	8.2
1	D	36	LEU	8.2
1	H	395	ILE	8.2
1	D	298	LEU	8.2
1	H	93	SER	8.2
1	A	430	ASN	8.2
1	E	311	GLY	8.2
1	F	32	VAL	8.2
1	A	93	SER	8.2
1	C	38	ALA	8.2
1	H	572	TYR	8.1
1	A	523	LEU	8.1
1	H	509	SER	8.1
1	G	520	GLN	8.1
1	C	548	ILE	8.1
1	G	229	ARG	8.1
1	E	558	GLU	8.1
1	C	69	LEU	8.1
1	C	109	MET	8.1
1	H	556	ILE	8.1
1	B	516	GLU	8.1
1	E	419	VAL	8.1
1	A	30	ALA	8.1
1	F	424	GLN	8.1
1	C	468	ASN	8.1
1	A	121	THR	8.1
1	G	491	ILE	8.1
1	G	47	LEU	8.1
1	C	225	VAL	8.1
1	F	94	GLY	8.1
1	G	113	VAL	8.1
1	C	100	MET	8.1
1	A	501	ILE	8.1
1	D	70	VAL	8.1
1	E	326	GLN	8.1
1	H	131	ASP	8.1
1	C	138	SER	8.1
1	G	461	ASP	8.1
1	E	443	GLU	8.1
1	F	454	ALA	8.1
1	G	267	LEU	8.1
1	H	535	ILE	8.1

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Mol	Chain	Res	Type	RSRZ
1	C	185	VAL	8.1
1	E	300	SER	8.0
1	H	37	ASN	8.0
1	D	207	ALA	8.0
1	E	580	PHE	8.0
1	F	563	ASN	8.0
1	B	471	ASP	8.0
1	E	571	VAL	8.0
1	G	13	PHE	8.0
1	G	163	TYR	8.0
1	A	17	TRP	8.0
1	F	140	SER	8.0
1	E	185	VAL	8.0
1	H	245	VAL	8.0
1	D	258	ILE	8.0
1	D	307	GLN	8.0
1	E	336	GLU	8.0
1	F	78	ARG	8.0
1	E	18	PRO	8.0
1	A	211	LEU	8.0
1	G	214	HIS	8.0
1	A	190	ARG	8.0
1	B	354	ARG	8.0
1	C	327	GLU	8.0
1	F	190	ARG	8.0
1	E	376	GLY	8.0
1	G	329	ASP	8.0
1	G	564	ASP	8.0
1	H	48	LEU	8.0
1	G	146	VAL	8.0
1	D	255	ILE	7.9
1	A	212	LYS	7.9
1	H	496	LEU	7.9
1	A	201	GLY	7.9
1	A	401	LEU	7.9
1	E	106	GLY	7.9
1	H	190	ARG	7.9
1	B	369	GLY	7.9
1	H	411	THR	7.9
1	D	580	PHE	7.9
1	G	170	ILE	7.9
1	D	390	THR	7.9

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Mol	Chain	Res	Type	RSRZ
1	G	450	ILE	7.9
1	D	73	GLY	7.9
1	G	451	GLU	7.9
1	F	287	VAL	7.9
1	G	228	LYS	7.9
1	D	427	HIS	7.9
1	A	417	ASN	7.9
1	E	527	GLN	7.9
1	D	39	ALA	7.9
1	H	55	GLY	7.9
1	F	240	GLN	7.9
1	B	139	SER	7.9
1	H	394	ASP	7.9
1	H	408	ARG	7.9
1	E	138	SER	7.9
1	A	452	GLU	7.9
1	E	147	VAL	7.9
1	C	516	GLU	7.9
1	H	115	PHE	7.9
1	B	392	PHE	7.8
1	C	273	PRO	7.8
1	F	347	VAL	7.8
1	H	108	MET	7.8
1	C	404	GLY	7.8
1	F	440	ALA	7.8
1	D	212	LYS	7.8
1	C	65	VAL	7.8
1	E	542	ILE	7.8
1	A	20	ILE	7.8
1	E	208	GLU	7.8
1	E	496	LEU	7.8
1	B	454	ALA	7.8
1	A	213	GLY	7.8
1	E	517	ARG	7.8
1	H	436	ASN	7.8
1	F	307	GLN	7.8
1	A	572	TYR	7.8
1	G	458	TYR	7.8
1	F	483	GLY	7.8
1	B	179	SER	7.8
1	A	106	GLY	7.8
1	C	161	PHE	7.8

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Mol	Chain	Res	Type	RSRZ
1	F	386	ALA	7.8
1	B	216	GLU	7.8
1	H	163	TYR	7.8
1	H	283	THR	7.8
1	E	174	LEU	7.8
1	H	461	ASP	7.8
1	F	376	GLY	7.8
1	E	124	LEU	7.8
1	D	553	ASP	7.7
1	E	224	GLU	7.7
1	E	559	ARG	7.7
1	C	442	THR	7.7
1	E	490	ALA	7.7
1	B	530	ARG	7.7
1	C	157	PHE	7.7
1	E	344	PHE	7.7
1	A	131	ASP	7.7
1	F	448	GLU	7.7
1	D	356	VAL	7.7
1	H	139	SER	7.7
1	B	452	GLU	7.7
1	A	294	LEU	7.7
1	F	344	PHE	7.7
1	G	208	GLU	7.7
1	G	284	ILE	7.7
1	E	394	ASP	7.7
1	G	289	SER	7.7
1	G	439	TYR	7.7
1	E	378	SER	7.7
1	A	41	ASP	7.7
1	B	553	ASP	7.7
1	E	520	GLN	7.7
1	B	133	GLU	7.7
1	D	19	THR	7.7
1	D	428	LEU	7.7
1	G	336	GLU	7.7
1	D	151	ALA	7.7
1	A	110	GLY	7.7
1	E	462	PHE	7.7
1	C	144	ILE	7.7
1	D	69	LEU	7.7
1	F	547	GLU	7.7

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Mol	Chain	Res	Type	RSRZ
1	F	58	LYS	7.6
1	C	363	ASN	7.6
1	A	290	SER	7.6
1	F	21	ALA	7.6
1	H	87	TYR	7.6
1	D	488	ARG	7.6
1	G	543	GLU	7.6
1	B	183	ARG	7.6
1	A	84	VAL	7.6
1	E	448	GLU	7.6
1	G	547	GLU	7.6
1	B	486	ARG	7.6
1	D	490	ALA	7.6
1	A	326	GLN	7.6
1	D	82	SER	7.6
1	E	274	SER	7.6
1	H	315	CYS	7.6
1	B	72	ILE	7.6
1	G	204	THR	7.6
1	D	102	ARG	7.6
1	A	489	ILE	7.6
1	H	538	ARG	7.6
1	C	420	ALA	7.6
1	A	276	MET	7.6
1	D	45	LEU	7.6
1	F	100	MET	7.6
1	B	211	LEU	7.6
1	F	538	ARG	7.6
1	C	396	ASP	7.6
1	G	283	THR	7.6
1	C	413	ALA	7.6
1	E	51	LEU	7.5
1	G	130	TYR	7.5
1	A	197	GLN	7.5
1	A	553	ASP	7.5
1	F	390	THR	7.5
1	H	280	THR	7.5
1	H	291	MET	7.5
1	A	507	ALA	7.5
1	C	488	ARG	7.5
1	G	114	SER	7.5
1	C	305	ASN	7.5

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Mol	Chain	Res	Type	RSRZ
1	C	567	GLU	7.5
1	C	400	ILE	7.5
1	D	189	PHE	7.5
1	A	370	LYS	7.5
1	A	319	PHE	7.5
1	F	328	LYS	7.5
1	B	390	THR	7.5
1	B	80	ILE	7.5
1	F	555	VAL	7.5
1	B	444	GLN	7.5
1	G	262	ALA	7.5
1	B	117	ASP	7.5
1	E	193	SER	7.5
1	G	123	THR	7.5
1	F	322	LEU	7.5
1	G	541	THR	7.5
1	G	145	THR	7.5
1	E	323	ASP	7.5
1	B	260	SER	7.5
1	A	224	GLU	7.5
1	F	323	ASP	7.5
1	G	495	LEU	7.5
1	E	20	ILE	7.4
1	F	331	GLY	7.4
1	D	336	GLU	7.4
1	G	226	GLU	7.4
1	G	394	ASP	7.4
1	H	75	MET	7.4
1	A	473	VAL	7.4
1	B	496	LEU	7.4
1	A	505	ASP	7.4
1	H	380	SER	7.4
1	B	398	GLY	7.4
1	B	217	VAL	7.4
1	C	317	THR	7.4
1	F	61	ARG	7.4
1	H	38	ALA	7.4
1	D	203	VAL	7.4
1	H	10	TRP	7.4
1	E	574	GLN	7.4
1	B	420	ALA	7.4
1	E	213	GLY	7.4

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Mol	Chain	Res	Type	RSRZ
1	C	78	ARG	7.4
1	C	274	SER	7.4
1	B	317	THR	7.4
1	B	339	THR	7.4
1	H	311	GLY	7.4
1	A	105	PHE	7.3
1	D	42	THR	7.3
1	C	20	ILE	7.3
1	C	407	LEU	7.3
1	B	120	SER	7.3
1	D	17	TRP	7.3
1	H	68	PRO	7.3
1	B	374	LEU	7.3
1	G	74	LEU	7.3
1	A	75	MET	7.3
1	C	446	SER	7.3
1	D	407	LEU	7.3
1	E	115	PHE	7.3
1	E	168	SER	7.3
1	F	53	ASP	7.3
1	A	11	GLN	7.3
1	D	421	LEU	7.3
1	F	401	LEU	7.3
1	A	338	ALA	7.3
1	F	463	ILE	7.3
1	H	459	ALA	7.3
1	H	574	GLN	7.3
1	B	337	ARG	7.3
1	C	553	ASP	7.3
1	A	203	VAL	7.3
1	B	561	THR	7.3
1	G	538	ARG	7.3
1	E	543	GLU	7.3
1	E	472	THR	7.3
1	C	237	MET	7.3
1	A	519	ILE	7.3
1	G	480	LEU	7.3
1	A	173	VAL	7.3
1	B	63	VAL	7.3
1	G	488	ARG	7.3
1	A	514	GLU	7.3
1	E	74	LEU	7.3

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Mol	Chain	Res	Type	RSRZ
1	D	100	MET	7.3
1	C	510	ALA	7.3
1	F	413	ALA	7.3
1	A	435	ASN	7.3
1	E	270	ALA	7.3
1	A	391	ARG	7.3
1	B	10	TRP	7.3
1	E	153	ILE	7.2
1	G	555	VAL	7.2
1	H	361	ASN	7.2
1	F	64	LEU	7.2
1	D	244	MET	7.2
1	G	418	GLN	7.2
1	E	53	ASP	7.2
1	H	172	ILE	7.2
1	H	534	VAL	7.2
1	F	83	TYR	7.2
1	E	19	THR	7.2
1	C	515	SER	7.2
1	B	172	ILE	7.2
1	C	336	GLU	7.2
1	B	534	VAL	7.2
1	F	211	LEU	7.2
1	A	70	VAL	7.2
1	B	256	GLN	7.2
1	H	95	LYS	7.2
1	B	373	ALA	7.2
1	F	549	VAL	7.2
1	H	491	ILE	7.2
1	H	562	HIS	7.2
1	C	434	ALA	7.2
1	E	246	SER	7.2
1	F	164	SER	7.2
1	B	109	MET	7.2
1	D	96	VAL	7.2
1	C	455	ARG	7.2
1	D	106	GLY	7.1
1	F	539	LEU	7.1
1	C	124	LEU	7.1
1	A	165	TRP	7.1
1	C	270	ALA	7.1
1	A	112	PRO	7.1

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Mol	Chain	Res	Type	RSRZ
1	A	465	LYS	7.1
1	B	78	ARG	7.1
1	C	542	ILE	7.1
1	F	422	VAL	7.1
1	E	544	LYS	7.1
1	F	39	ALA	7.1
1	B	201	GLY	7.1
1	A	394	ASP	7.1
1	A	488	ARG	7.1
1	B	509	SER	7.1
1	D	363	ASN	7.1
1	G	393	TYR	7.1
1	C	430	ASN	7.1
1	A	36	LEU	7.1
1	E	350	THR	7.1
1	E	486	ARG	7.1
1	F	421	LEU	7.1
1	A	477	ASN	7.1
1	H	306	ALA	7.1
1	H	492	ALA	7.1
1	E	217	VAL	7.1
1	G	318	LEU	7.1
1	H	563	ASN	7.1
1	E	67	MET	7.1
1	H	128	ILE	7.1
1	G	78	ARG	7.1
1	B	402	MET	7.1
1	H	551	VAL	7.1
1	D	186	SER	7.1
1	A	421	LEU	7.1
1	C	392	PHE	7.1
1	E	552	GLU	7.0
1	B	447	ARG	7.0
1	A	139	SER	7.0
1	D	132	SER	7.0
1	F	355	ASP	7.0
1	F	147	VAL	7.0
1	E	387	SER	7.0
1	H	434	ALA	7.0
1	B	352	PRO	7.0
1	D	465	LYS	7.0
1	G	101	ARG	7.0

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Mol	Chain	Res	Type	RSRZ
1	G	185	VAL	7.0
1	F	259	ALA	7.0
1	H	469	GLY	7.0
1	E	120	SER	7.0
1	F	526	LEU	7.0
1	H	31	GLY	7.0
1	C	370	LYS	7.0
1	E	539	LEU	7.0
1	G	33	ALA	7.0
1	G	26	GLY	7.0
1	D	289	SER	7.0
1	E	567	GLU	7.0
1	E	418	GLN	7.0
1	B	357	PRO	7.0
1	G	278	SER	7.0
1	B	363	ASN	7.0
1	A	174	LEU	7.0
1	B	554	GLY	7.0
1	F	136	ALA	7.0
1	C	41	ASP	7.0
1	C	532	SER	7.0
1	G	193	SER	7.0
1	E	34	LEU	7.0
1	H	484	GLY	7.0
1	B	140	SER	7.0
1	B	309	GLN	7.0
1	C	263	LEU	7.0
1	D	484	GLY	7.0
1	C	481	LEU	7.0
1	A	241	GLY	6.9
1	C	110	GLY	6.9
1	C	562	HIS	6.9
1	E	177	ILE	6.9
1	C	410	TYR	6.9
1	B	127	ARG	6.9
1	D	14	ARG	6.9
1	C	351	TYR	6.9
1	H	420	ALA	6.9
1	H	529	ASN	6.9
1	C	300	SER	6.9
1	A	431	ASP	6.9
1	B	431	ASP	6.9

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Mol	Chain	Res	Type	RSRZ
1	A	499	SER	6.9
1	H	123	THR	6.9
1	G	200	MET	6.9
1	G	332	LYS	6.9
1	H	426	VAL	6.9
1	E	71	VAL	6.9
1	A	156	LEU	6.9
1	H	103	ARG	6.9
1	F	446	SER	6.9
1	B	542	ILE	6.9
1	H	23	PHE	6.9
1	H	116	PHE	6.9
1	H	293	ALA	6.9
1	H	308	PHE	6.9
1	B	169	ILE	6.9
1	F	65	VAL	6.9
1	E	223	GLN	6.9
1	E	41	ASP	6.9
1	A	104	LEU	6.9
1	E	78	ARG	6.9
1	H	160	MET	6.9
1	B	286	VAL	6.8
1	H	466	MET	6.8
1	E	167	LEU	6.8
1	D	509	SER	6.8
1	F	216	GLU	6.8
1	B	537	HIS	6.8
1	B	468	ASN	6.8
1	H	193	SER	6.8
1	H	56	PHE	6.8
1	F	113	VAL	6.8
1	C	492	ALA	6.8
1	H	352	PRO	6.8
1	B	255	ILE	6.8
1	F	176	PRO	6.8
1	H	414	SER	6.8
1	B	394	ASP	6.8
1	B	490	ALA	6.8
1	E	250	ILE	6.8
1	E	466	MET	6.8
1	F	405	HIS	6.8
1	B	488	ARG	6.8

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Mol	Chain	Res	Type	RSRZ
1	B	331	GLY	6.8
1	D	408	ARG	6.8
1	G	93	SER	6.8
1	H	393	TYR	6.8
1	H	555	VAL	6.8
1	H	223	GLN	6.8
1	B	343	GLU	6.7
1	A	227	THR	6.7
1	A	466	MET	6.7
1	G	155	GLY	6.7
1	H	317	THR	6.7
1	D	414	SER	6.7
1	E	381	GLY	6.7
1	G	419	VAL	6.7
1	F	527	GLN	6.7
1	G	475	GLY	6.7
1	B	494	ALA	6.7
1	B	124	LEU	6.7
1	G	61	ARG	6.7
1	G	490	ALA	6.7
1	F	93	SER	6.7
1	D	37	ASN	6.7
1	F	256	GLN	6.7
1	E	515	SER	6.7
1	C	551	VAL	6.7
1	E	551	VAL	6.7
1	H	517	ARG	6.7
1	D	162	TYR	6.7
1	D	531	THR	6.7
1	F	496	LEU	6.7
1	G	408	ARG	6.7
1	G	553	ASP	6.7
1	G	436	ASN	6.7
1	D	114	SER	6.7
1	D	256	GLN	6.7
1	F	430	ASN	6.7
1	D	284	ILE	6.7
1	H	183	ARG	6.7
1	D	426	VAL	6.7
1	D	487	GLN	6.6
1	B	164	SER	6.6
1	D	334	VAL	6.6

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Mol	Chain	Res	Type	RSRZ
1	E	395	ILE	6.6
1	G	316	GLN	6.6
1	A	109	MET	6.6
1	C	86	SER	6.6
1	B	311	GLY	6.6
1	H	437	ILE	6.6
1	B	419	VAL	6.6
1	E	294	LEU	6.6
1	E	96	VAL	6.6
1	H	324	SER	6.6
1	B	377	ARG	6.6
1	B	495	LEU	6.6
1	A	71	VAL	6.6
1	G	174	LEU	6.6
1	H	510	ALA	6.6
1	C	201	GLY	6.6
1	F	129	THR	6.6
1	B	519	ILE	6.6
1	H	270	ALA	6.6
1	B	198	ASN	6.6
1	B	345	ARG	6.6
1	H	99	THR	6.6
1	F	91	TRP	6.6
1	G	40	SER	6.6
1	C	385	ILE	6.6
1	B	297	PRO	6.6
1	F	514	GLU	6.6
1	F	516	GLU	6.6
1	B	552	GLU	6.6
1	D	75	MET	6.6
1	A	312	MET	6.6
1	E	73	GLY	6.6
1	G	550	VAL	6.6
1	F	310	ARG	6.6
1	D	204	THR	6.6
1	G	195	ASN	6.6
1	B	209	GLN	6.6
1	D	290	SER	6.6
1	D	325	GLU	6.6
1	C	88	CYS	6.6
1	F	249	SER	6.6
1	B	42	THR	6.6

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Mol	Chain	Res	Type	RSRZ
1	G	171	LEU	6.6
1	B	153	ILE	6.5
1	D	173	VAL	6.5
1	D	238	ARG	6.5
1	B	168	SER	6.5
1	A	291	MET	6.5
1	C	487	GLN	6.5
1	E	243	LYS	6.5
1	G	86	SER	6.5
1	C	36	LEU	6.5
1	G	535	ILE	6.5
1	C	419	VAL	6.5
1	D	177	ILE	6.5
1	A	533	LEU	6.5
1	A	361	ASN	6.5
1	C	77	LEU	6.5
1	A	37	ASN	6.5
1	B	304	VAL	6.5
1	D	263	LEU	6.5
1	F	380	SER	6.5
1	D	215	LYS	6.5
1	G	581	GLY	6.5
1	E	57	GLY	6.5
1	C	489	ILE	6.5
1	D	236	ARG	6.5
1	H	396	ASP	6.5
1	F	357	PRO	6.5
1	F	20	ILE	6.5
1	A	214	HIS	6.5
1	B	180	ILE	6.5
1	C	337	ARG	6.5
1	E	550	VAL	6.5
1	B	456	MET	6.5
1	C	114	SER	6.4
1	E	556	ILE	6.4
1	E	99	THR	6.4
1	F	504	LEU	6.4
1	F	243	LYS	6.4
1	G	132	SER	6.4
1	B	340	GLY	6.4
1	A	374	LEU	6.4
1	D	397	GLU	6.4

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Mol	Chain	Res	Type	RSRZ
1	H	205	THR	6.4
1	G	62	SER	6.4
1	A	158	ILE	6.4
1	E	241	GLY	6.4
1	F	518	ALA	6.4
1	F	487	GLN	6.4
1	F	267	LEU	6.4
1	D	524	ASP	6.4
1	B	375	VAL	6.4
1	A	415	LEU	6.4
1	A	414	SER	6.4
1	E	305	ASN	6.4
1	B	83	TYR	6.4
1	B	403	ASP	6.4
1	G	528	LYS	6.4
1	C	132	SER	6.4
1	H	581	GLY	6.4
1	D	551	VAL	6.4
1	F	19	THR	6.4
1	C	241	GLY	6.4
1	E	198	ASN	6.4
1	E	533	LEU	6.4
1	F	443	GLU	6.4
1	G	533	LEU	6.4
1	B	442	THR	6.3
1	H	215	LYS	6.4
1	C	291	MET	6.3
1	H	570	GLY	6.3
1	E	121	THR	6.3
1	A	449	GLN	6.3
1	G	79	GLY	6.3
1	C	71	VAL	6.3
1	G	518	ALA	6.3
1	B	257	LEU	6.3
1	G	51	LEU	6.3
1	F	300	SER	6.3
1	H	224	GLU	6.3
1	E	79	GLY	6.3
1	A	321	ILE	6.3
1	G	412	LEU	6.3
1	E	256	GLN	6.3
1	G	121	THR	6.3

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Mol	Chain	Res	Type	RSRZ
1	H	138	SER	6.3
1	C	172	ILE	6.3
1	F	419	VAL	6.3
1	E	271	SER	6.3
1	E	273	PRO	6.3
1	B	438	ALA	6.3
1	C	483	GLY	6.3
1	C	123	THR	6.3
1	C	126	SER	6.3
1	D	418	GLN	6.3
1	A	15	ARG	6.3
1	D	126	SER	6.3
1	F	268	TYR	6.3
1	G	340	GLY	6.3
1	E	535	ILE	6.3
1	B	274	SER	6.3
1	D	201	GLY	6.3
1	E	498	ASP	6.2
1	F	104	LEU	6.2
1	A	494	ALA	6.2
1	C	517	ARG	6.2
1	C	406	ASP	6.2
1	G	281	ALA	6.2
1	C	512	ASP	6.2
1	C	298	LEU	6.2
1	D	154	ILE	6.2
1	A	117	ASP	6.2
1	G	523	LEU	6.2
1	H	349	PHE	6.2
1	A	527	GLN	6.2
1	F	288	PHE	6.2
1	C	82	SER	6.2
1	H	514	GLU	6.2
1	A	230	PHE	6.2
1	A	554	GLY	6.2
1	G	236	ARG	6.2
1	H	391	ARG	6.2
1	A	542	ILE	6.2
1	D	360	ARG	6.2
1	G	403	ASP	6.2
1	B	379	GLY	6.2
1	F	280	THR	6.2

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Mol	Chain	Res	Type	RSRZ
1	C	232	LYS	6.2
1	E	346	ASN	6.2
1	H	360	ARG	6.2
1	C	90	SER	6.2
1	A	369	GLY	6.2
1	E	295	MET	6.2
1	G	24	LYS	6.2
1	F	428	LEU	6.2
1	A	353	GLY	6.2
1	D	320	THR	6.2
1	B	269	ALA	6.2
1	H	51	LEU	6.2
1	H	185	VAL	6.2
1	F	541	THR	6.2
1	E	392	PHE	6.2
1	H	30	ALA	6.2
1	A	487	GLN	6.2
1	F	434	ALA	6.2
1	F	573	ALA	6.2
1	D	128	ILE	6.2
1	G	312	MET	6.2
1	H	242	MET	6.2
1	B	413	ALA	6.2
1	H	221	GLY	6.1
1	A	434	ALA	6.1
1	E	179	SER	6.1
1	C	279	LEU	6.1
1	C	357	PRO	6.1
1	F	252	ASP	6.1
1	H	465	LYS	6.1
1	D	13	PHE	6.1
1	G	276	MET	6.1
1	G	314	ALA	6.1
1	G	326	GLN	6.1
1	A	10	TRP	6.1
1	D	494	ALA	6.1
1	A	504	LEU	6.1
1	B	176	PRO	6.1
1	H	273	PRO	6.1
1	A	382	LYS	6.1
1	H	11	GLN	6.1
1	D	79	GLY	6.1

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Mol	Chain	Res	Type	RSRZ
1	H	44	MET	6.1
1	G	324	SER	6.1
1	A	335	ILE	6.1
1	D	104	LEU	6.1
1	B	206	SER	6.1
1	C	346	ASN	6.1
1	G	205	THR	6.1
1	H	132	SER	6.1
1	A	509	SER	6.1
1	B	476	GLU	6.1
1	F	103	ARG	6.1
1	A	549	VAL	6.1
1	E	85	SER	6.1
1	E	268	TYR	6.1
1	A	88	CYS	6.1
1	D	174	LEU	6.1
1	A	234	SER	6.1
1	G	345	ARG	6.1
1	A	376	GLY	6.1
1	E	29	VAL	6.1
1	H	228	LYS	6.1
1	D	532	SER	6.1
1	G	369	GLY	6.1
1	G	395	ILE	6.1
1	C	526	LEU	6.1
1	E	216	GLU	6.1
1	D	448	GLU	6.0
1	A	498	ASP	6.0
1	C	219	ILE	6.0
1	C	476	GLU	6.0
1	G	99	THR	6.0
1	B	464	ASN	6.0
1	F	572	TYR	6.0
1	F	206	SER	6.0
1	A	457	ALA	6.0
1	D	235	ASN	6.0
1	B	560	GLY	6.0
1	H	359	LEU	6.0
1	H	239	LEU	6.0
1	H	554	GLY	6.0
1	A	162	TYR	6.0
1	C	557	VAL	6.0

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Mol	Chain	Res	Type	RSRZ
1	B	33	ALA	6.0
1	F	232	LYS	6.0
1	C	490	ALA	6.0
1	F	512	ASP	6.0
1	F	491	ILE	6.0
1	H	347	VAL	6.0
1	H	390	THR	6.0
1	E	269	ALA	6.0
1	F	179	SER	6.0
1	G	327	GLU	6.0
1	D	542	ILE	6.0
1	B	472	THR	6.0
1	C	314	ALA	6.0
1	A	179	SER	6.0
1	A	451	GLU	6.0
1	D	510	ALA	6.0
1	H	197	GLN	6.0
1	C	499	SER	6.0
1	A	187	LYS	6.0
1	A	453	ALA	6.0
1	D	148	ARG	5.9
1	C	207	ALA	5.9
1	C	375	VAL	5.9
1	F	37	ASN	5.9
1	B	498	ASP	5.9
1	G	72	ILE	5.9
1	D	246	SER	5.9
1	A	413	ALA	5.9
1	A	564	ASP	5.9
1	D	149	GLU	5.9
1	G	212	LYS	5.9
1	E	494	ALA	5.9
1	C	486	ARG	5.9
1	E	52	LEU	5.9
1	C	286	VAL	5.9
1	C	421	LEU	5.9
1	C	449	GLN	5.9
1	B	550	VAL	5.9
1	G	421	LEU	5.9
1	A	87	TYR	5.9
1	E	513	THR	5.9
1	A	412	LEU	5.9

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Mol	Chain	Res	Type	RSRZ
1	H	219	ILE	5.9
1	A	140	SER	5.9
1	C	227	THR	5.9
1	D	314	ALA	5.9
1	B	213	GLY	5.9
1	B	366	ILE	5.9
1	E	276	MET	5.9
1	D	247	ALA	5.9
1	E	203	VAL	5.9
1	G	551	VAL	5.9
1	E	95	LYS	5.9
1	C	128	ILE	5.9
1	E	197	GLN	5.9
1	D	398	GLY	5.9
1	G	172	ILE	5.9
1	G	375	VAL	5.9
1	G	499	SER	5.9
1	G	515	SER	5.9
1	G	390	THR	5.9
1	B	518	ALA	5.9
1	E	155	GLY	5.9
1	D	441	ARG	5.9
1	F	577	LYS	5.8
1	A	245	VAL	5.8
1	D	67	MET	5.8
1	E	457	ALA	5.8
1	H	464	ASN	5.8
1	H	198	ASN	5.8
1	A	496	LEU	5.8
1	C	42	THR	5.8
1	F	70	VAL	5.8
1	E	309	GLN	5.8
1	G	85	SER	5.8
1	H	442	THR	5.8
1	E	554	GLY	5.8
1	F	217	VAL	5.8
1	G	389	ILE	5.8
1	F	141	GLY	5.8
1	H	452	GLU	5.8
1	G	484	GLY	5.8
1	A	251	SER	5.8
1	G	557	VAL	5.8

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Mol	Chain	Res	Type	RSRZ
1	A	352	PRO	5.8
1	C	179	SER	5.8
1	H	325	GLU	5.8
1	D	472	THR	5.8
1	G	96	VAL	5.8
1	A	133	GLU	5.8
1	D	25	ALA	5.8
1	H	422	VAL	5.8
1	C	25	ALA	5.8
1	A	217	VAL	5.8
1	E	553	ASP	5.8
1	H	339	THR	5.8
1	H	388	LEU	5.8
1	F	345	ARG	5.8
1	G	149	GLU	5.8
1	G	355	ASP	5.8
1	A	373	ALA	5.8
1	B	557	VAL	5.8
1	D	77	LEU	5.8
1	D	502	LEU	5.8
1	E	54	ASP	5.8
1	E	502	LEU	5.8
1	H	480	LEU	5.8
1	F	128	ILE	5.8
1	C	276	MET	5.7
1	F	579	GLN	5.7
1	A	100	MET	5.7
1	D	216	GLU	5.7
1	E	327	GLU	5.7
1	D	209	GLN	5.7
1	D	347	VAL	5.7
1	H	350	THR	5.7
1	E	63	VAL	5.7
1	F	22	PRO	5.7
1	F	166	GLN	5.7
1	D	84	VAL	5.7
1	D	498	ASP	5.7
1	D	529	ASN	5.7
1	E	134	GLN	5.7
1	E	339	THR	5.7
1	D	368	ALA	5.7
1	H	457	ALA	5.7

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Mol	Chain	Res	Type	RSRZ
1	F	431	ASP	5.7
1	D	190	ARG	5.7
1	B	353	GLY	5.7
1	D	48	LEU	5.7
1	F	195	ASN	5.7
1	D	234	SER	5.7
1	H	326	GLN	5.7
1	H	184	VAL	5.7
1	E	427	HIS	5.7
1	G	508	THR	5.7
1	A	456	MET	5.7
1	B	485	GLN	5.7
1	C	189	PHE	5.7
1	B	147	VAL	5.7
1	F	96	VAL	5.7
1	F	145	THR	5.7
1	G	166	GLN	5.7
1	G	377	ARG	5.7
1	E	242	MET	5.7
1	H	409	GLU	5.7
1	A	152	SER	5.7
1	G	299	LYS	5.7
1	C	142	ALA	5.7
1	C	294	LEU	5.6
1	H	366	ILE	5.6
1	E	578	MET	5.6
1	F	524	ASP	5.6
1	H	557	VAL	5.6
1	F	262	ALA	5.6
1	D	342	VAL	5.6
1	H	109	MET	5.6
1	D	208	GLU	5.6
1	E	342	VAL	5.6
1	H	126	SER	5.6
1	C	11	GLN	5.6
1	A	27	LEU	5.6
1	A	315	CYS	5.6
1	B	12	THR	5.6
1	B	385	ILE	5.6
1	G	259	ALA	5.6
1	C	141	GLY	5.6
1	C	289	SER	5.6

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Mol	Chain	Res	Type	RSRZ
1	C	318	LEU	5.6
1	D	80	ILE	5.6
1	E	123	THR	5.6
1	F	338	ALA	5.6
1	C	50	PRO	5.6
1	D	266	VAL	5.6
1	D	412	LEU	5.6
1	A	568	HIS	5.6
1	C	101	ARG	5.6
1	C	518	ALA	5.6
1	C	68	PRO	5.6
1	C	278	SER	5.6
1	A	13	PHE	5.6
1	C	190	ARG	5.6
1	E	441	ARG	5.6
1	C	171	LEU	5.6
1	B	386	ALA	5.6
1	D	521	ALA	5.6
1	B	389	ILE	5.6
1	E	114	SER	5.6
1	B	51	LEU	5.6
1	B	489	ILE	5.6
1	B	463	ILE	5.6
1	C	302	THR	5.6
1	G	530	ARG	5.6
1	D	133	GLU	5.6
1	A	396	ASP	5.6
1	E	30	ALA	5.5
1	A	216	GLU	5.5
1	E	65	VAL	5.5
1	C	89	ILE	5.5
1	D	318	LEU	5.5
1	B	479	VAL	5.5
1	D	110	GLY	5.5
1	D	537	HIS	5.5
1	H	550	VAL	5.5
1	C	205	THR	5.5
1	B	533	LEU	5.5
1	D	544	LYS	5.5
1	A	225	VAL	5.5
1	C	61	ARG	5.5
1	F	550	VAL	5.5

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Mol	Chain	Res	Type	RSRZ
1	A	57	GLY	5.5
1	A	296	ARG	5.5
1	E	105	PHE	5.5
1	H	47	LEU	5.5
1	H	279	LEU	5.5
1	B	73	GLY	5.5
1	G	432	THR	5.5
1	C	497	ARG	5.5
1	F	298	LEU	5.5
1	C	435	ASN	5.5
1	G	384	THR	5.5
1	H	213	GLY	5.5
1	H	334	VAL	5.5
1	C	386	ALA	5.5
1	D	497	ARG	5.5
1	F	162	TYR	5.5
1	B	344	PHE	5.5
1	F	266	VAL	5.5
1	B	89	ILE	5.5
1	C	531	THR	5.5
1	D	211	LEU	5.5
1	D	386	ALA	5.5
1	H	73	GLY	5.5
1	G	360	ARG	5.5
1	E	17	TRP	5.4
1	D	272	PHE	5.4
1	F	364	LEU	5.4
1	C	452	GLU	5.4
1	D	389	ILE	5.4
1	B	203	VAL	5.4
1	E	391	ARG	5.4
1	G	468	ASN	5.4
1	C	440	ALA	5.4
1	F	66	TRP	5.4
1	H	168	SER	5.4
1	A	555	VAL	5.4
1	A	263	LEU	5.4
1	B	233	VAL	5.4
1	A	428	LEU	5.4
1	C	234	SER	5.4
1	H	58	LYS	5.4
1	A	375	VAL	5.4

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Mol	Chain	Res	Type	RSRZ
1	B	365	LYS	5.4
1	A	286	VAL	5.4
1	E	130	TYR	5.4
1	C	149	GLU	5.4
1	C	462	PHE	5.4
1	D	477	ASN	5.4
1	A	189	PHE	5.4
1	D	379	GLY	5.4
1	C	306	ALA	5.4
1	F	237	MET	5.4
1	G	21	ALA	5.4
1	A	545	ALA	5.4
1	H	65	VAL	5.4
1	A	99	THR	5.4
1	F	576	HIS	5.4
1	A	471	ASP	5.4
1	E	367	PRO	5.4
1	B	265	PHE	5.3
1	E	429	PHE	5.3
1	A	40	SER	5.3
1	B	382	LYS	5.3
1	C	533	LEU	5.3
1	H	25	ALA	5.3
1	B	407	LEU	5.3
1	A	114	SER	5.3
1	F	25	ALA	5.3
1	H	362	ILE	5.3
1	D	81	THR	5.3
1	F	513	THR	5.3
1	C	494	ALA	5.3
1	H	18	PRO	5.3
1	B	224	GLU	5.3
1	A	29	VAL	5.3
1	E	473	VAL	5.3
1	C	153	ILE	5.3
1	A	562	HIS	5.3
1	F	71	VAL	5.3
1	H	567	GLU	5.3
1	G	315	CYS	5.3
1	A	386	ALA	5.3
1	D	115	PHE	5.3
1	A	350	THR	5.3

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Mol	Chain	Res	Type	RSRZ
1	G	273	PRO	5.3
1	D	277	ASP	5.3
1	F	36	LEU	5.3
1	H	405	HIS	5.3
1	C	502	LEU	5.3
1	E	374	LEU	5.3
1	H	367	PRO	5.3
1	F	362	ILE	5.3
1	A	317	THR	5.3
1	C	525	GLU	5.3
1	E	156	LEU	5.3
1	A	135	VAL	5.3
1	B	97	VAL	5.3
1	D	206	SER	5.3
1	D	439	TYR	5.3
1	E	393	TYR	5.3
1	E	566	LEU	5.3
1	C	367	PRO	5.3
1	A	302	THR	5.3
1	F	324	SER	5.3
1	G	129	THR	5.3
1	C	264	ALA	5.3
1	F	210	MET	5.3
1	B	434	ALA	5.3
1	F	73	GLY	5.2
1	E	205	THR	5.2
1	E	13	PHE	5.2
1	D	141	GLY	5.2
1	D	476	GLU	5.2
1	D	274	SER	5.2
1	A	107	HIS	5.2
1	D	500	PRO	5.2
1	F	348	THR	5.2
1	D	171	LEU	5.2
1	B	184	VAL	5.2
1	C	475	GLY	5.2
1	A	81	THR	5.2
1	D	222	GLY	5.2
1	D	420	ALA	5.2
1	E	215	LYS	5.2
1	G	127	ARG	5.2
1	A	403	ASP	5.2

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Mol	Chain	Res	Type	RSRZ
1	D	229	ARG	5.2
1	A	327	GLU	5.2
1	H	50	PRO	5.2
1	B	470	LEU	5.2
1	C	573	ALA	5.2
1	B	202	GLN	5.2
1	B	445	TYR	5.2
1	D	278	SER	5.2
1	E	456	MET	5.2
1	G	139	SER	5.2
1	G	160	MET	5.2
1	F	105	PHE	5.2
1	B	315	CYS	5.2
1	F	490	ALA	5.2
1	D	392	PHE	5.2
1	E	481	LEU	5.2
1	H	294	LEU	5.2
1	B	270	ALA	5.2
1	G	353	GLY	5.2
1	D	63	VAL	5.2
1	F	313	ALA	5.2
1	B	341	ASP	5.2
1	D	233	VAL	5.2
1	G	494	ALA	5.2
1	D	268	TYR	5.1
1	H	530	ARG	5.1
1	F	85	SER	5.1
1	G	258	ILE	5.1
1	F	493	ARG	5.1
1	C	74	LEU	5.1
1	C	397	GLU	5.1
1	A	178	VAL	5.1
1	A	540	SER	5.1
1	B	250	ILE	5.1
1	D	40	SER	5.1
1	E	334	VAL	5.1
1	C	412	LEU	5.1
1	D	364	LEU	5.1
1	F	263	LEU	5.1
1	H	389	ILE	5.1
1	C	238	ARG	5.1
1	F	116	PHE	5.1

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Mol	Chain	Res	Type	RSRZ
1	A	387	SER	5.1
1	C	290	SER	5.1
1	F	489	ILE	5.1
1	D	483	GLY	5.1
1	C	361	ASN	5.1
1	D	573	ALA	5.1
1	H	106	GLY	5.1
1	H	331	GLY	5.1
1	A	521	ALA	5.1
1	B	41	ASP	5.1
1	H	440	ALA	5.1
1	B	487	GLN	5.1
1	A	450	ILE	5.1
1	C	70	VAL	5.1
1	F	35	ILE	5.1
1	B	119	GLN	5.1
1	D	147	VAL	5.1
1	A	170	ILE	5.1
1	C	564	ASP	5.1
1	C	503	ILE	5.1
1	D	47	LEU	5.1
1	D	406	ASP	5.1
1	A	281	ALA	5.1
1	F	473	VAL	5.1
1	G	135	VAL	5.1
1	A	51	LEU	5.1
1	A	52	LEU	5.1
1	E	254	ILE	5.1
1	B	207	ALA	5.1
1	B	421	LEU	5.1
1	F	581	GLY	5.1
1	C	217	VAL	5.1
1	A	440	ALA	5.1
1	C	416	ARG	5.1
1	C	16	LEU	5.0
1	H	241	GLY	5.0
1	D	319	PHE	5.0
1	F	533	LEU	5.0
1	E	324	SER	5.0
1	E	335	ILE	5.0
1	F	47	LEU	5.0
1	F	124	LEU	5.0

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Mol	Chain	Res	Type	RSRZ
1	A	85	SER	5.0
1	F	365	LYS	5.0
1	H	256	GLN	5.0
1	B	18	PRO	5.0
1	B	200	MET	5.0
1	B	205	THR	5.0
1	B	376	GLY	5.0
1	C	208	GLU	5.0
1	E	206	SER	5.0
1	H	406	ASP	5.0
1	D	422	VAL	5.0
1	E	119	GLN	5.0
1	D	375	VAL	5.0
1	B	32	VAL	5.0
1	H	201	GLY	5.0
1	H	312	MET	5.0
1	G	144	ILE	5.0
1	C	388	LEU	5.0
1	D	293	ALA	5.0
1	E	476	GLU	5.0
1	G	493	ARG	5.0
1	F	157	PHE	5.0
1	H	105	PHE	5.0
1	H	282	GLY	5.0
1	C	224	GLU	5.0
1	A	485	GLN	5.0
1	F	133	GLU	5.0
1	H	458	TYR	5.0
1	E	345	ARG	5.0
1	H	151	ALA	5.0
1	D	383	SER	5.0
1	G	66	TRP	5.0
1	G	433	VAL	5.0
1	E	497	ARG	4.9
1	G	552	GLU	4.9
1	A	219	ILE	4.9
1	A	299	LYS	4.9
1	C	243	LYS	4.9
1	D	416	ARG	4.9
1	C	210	MET	4.9
1	F	532	SER	4.9
1	C	197	GLN	4.9

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Mol	Chain	Res	Type	RSRZ
1	D	481	LEU	4.9
1	E	272	PHE	4.9
1	G	206	SER	4.9
1	A	345	ARG	4.9
1	F	385	ILE	4.9
1	E	440	ALA	4.9
1	B	148	ARG	4.9
1	C	152	SER	4.9
1	A	69	LEU	4.9
1	A	132	SER	4.9
1	E	304	VAL	4.9
1	A	543	GLU	4.9
1	E	136	ALA	4.9
1	F	224	GLU	4.9
1	H	428	LEU	4.9
1	H	490	ALA	4.9
1	D	495	LEU	4.9
1	A	541	THR	4.9
1	D	522	ALA	4.9
1	E	504	LEU	4.9
1	B	157	PHE	4.9
1	D	536	ALA	4.9
1	G	105	PHE	4.9
1	H	537	HIS	4.9
1	G	376	GLY	4.9
1	F	395	ILE	4.9
1	A	278	SER	4.9
1	B	86	SER	4.9
1	E	80	ILE	4.9
1	E	358	ALA	4.9
1	E	424	GLN	4.9
1	A	221	GLY	4.9
1	C	395	ILE	4.9
1	F	334	VAL	4.9
1	A	92	VAL	4.9
1	G	23	PHE	4.9
1	H	357	PRO	4.9
1	H	17	TRP	4.9
1	E	281	ALA	4.8
1	C	165	TRP	4.8
1	C	108	MET	4.8
1	C	105	PHE	4.8

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	C	350	THR	4.8
1	H	571	VAL	4.8
1	E	139	SER	4.8
1	F	152	SER	4.8
1	H	40	SER	4.8
1	E	182	ILE	4.8
1	E	55	GLY	4.8
1	A	89	ILE	4.8
1	A	495	LEU	4.8
1	D	512	ASP	4.8
1	B	305	ASN	4.8
1	F	97	VAL	4.8
1	A	571	VAL	4.8
1	D	237	MET	4.8
1	D	387	SER	4.8
1	H	372	VAL	4.8
1	F	542	ILE	4.8
1	G	537	HIS	4.8
1	C	541	THR	4.8
1	A	210	MET	4.8
1	B	535	ILE	4.8
1	C	539	LEU	4.8
1	E	257	LEU	4.8
1	G	561	THR	4.8
1	E	400	ILE	4.8
1	E	437	ILE	4.8
1	D	218	LEU	4.8
1	E	218	LEU	4.8
1	F	284	ILE	4.8
1	H	110	GLY	4.8
1	B	428	LEU	4.8
1	D	574	GLN	4.8
1	D	26	GLY	4.8
1	F	488	ARG	4.8
1	H	521	ALA	4.8
1	E	532	SER	4.8
1	B	160	MET	4.8
1	F	276	MET	4.8
1	A	274	SER	4.8
1	C	353	GLY	4.8
1	D	41	ASP	4.8
1	F	127	ARG	4.8

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Mol	Chain	Res	Type	RSRZ
1	G	124	LEU	4.8
1	E	492	ALA	4.8
1	H	346	ASN	4.8
1	F	182	ILE	4.8
1	G	18	PRO	4.8
1	G	22	PRO	4.8
1	C	97	VAL	4.8
1	E	87	TYR	4.8
1	H	473	VAL	4.7
1	E	37	ASN	4.7
1	F	361	ASN	4.7
1	A	423	SER	4.7
1	E	172	ILE	4.7
1	F	60	ASP	4.7
1	A	520	GLN	4.7
1	C	414	SER	4.7
1	H	212	LYS	4.7
1	B	204	THR	4.7
1	D	568	HIS	4.7
1	B	556	ILE	4.7
1	G	244	MET	4.7
1	H	113	VAL	4.7
1	D	345	ARG	4.7
1	D	378	SER	4.7
1	F	191	ASN	4.7
1	C	56	PHE	4.7
1	H	531	THR	4.7
1	A	202	GLN	4.7
1	A	358	ALA	4.7
1	F	358	ALA	4.7
1	G	296	ARG	4.7
1	G	225	VAL	4.7
1	E	507	ALA	4.7
1	B	492	ALA	4.7
1	G	356	VAL	4.7
1	H	505	ASP	4.7
1	C	527	GLN	4.7
1	D	168	SER	4.7
1	B	238	ARG	4.7
1	E	116	PHE	4.7
1	E	118	LYS	4.7
1	H	165	TRP	4.7

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Mol	Chain	Res	Type	RSRZ
1	A	525	GLU	4.7
1	B	364	LEU	4.7
1	G	198	ASN	4.7
1	H	192	ILE	4.7
1	H	320	THR	4.7
1	G	175	ALA	4.7
1	G	386	ALA	4.7
1	D	561	THR	4.7
1	B	49	LYS	4.7
1	H	231	ASP	4.7
1	E	569	ARG	4.7
1	F	163	TYR	4.7
1	G	420	ALA	4.7
1	B	44	MET	4.7
1	H	145	THR	4.7
1	C	143	LEU	4.7
1	F	77	LEU	4.7
1	F	260	SER	4.6
1	A	493	ARG	4.6
1	D	86	SER	4.6
1	B	162	TYR	4.6
1	F	414	SER	4.6
1	F	436	ASN	4.6
1	A	332	LYS	4.6
1	E	12	THR	4.6
1	E	239	LEU	4.6
1	A	39	ALA	4.6
1	G	321	ILE	4.6
1	E	261	LEU	4.6
1	G	94	GLY	4.6
1	C	415	LEU	4.6
1	H	104	LEU	4.6
1	B	493	ARG	4.6
1	H	383	SER	4.6
1	H	281	ALA	4.6
1	D	50	PRO	4.6
1	G	351	TYR	4.6
1	F	460	MET	4.6
1	C	340	GLY	4.6
1	F	367	PRO	4.6
1	C	17	TRP	4.6
1	F	566	LEU	4.6

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Mol	Chain	Res	Type	RSRZ
1	H	503	ILE	4.6
1	C	339	THR	4.6
1	G	466	MET	4.6
1	A	45	LEU	4.6
1	C	155	GLY	4.6
1	E	89	ILE	4.6
1	F	521	ALA	4.6
1	F	297	PRO	4.6
1	G	256	GLN	4.6
1	H	174	LEU	4.6
1	E	518	ALA	4.6
1	F	186	SER	4.6
1	C	377	ARG	4.6
1	E	160	MET	4.6
1	H	403	ASP	4.6
1	E	577	LYS	4.5
1	H	33	ALA	4.5
1	H	285	THR	4.5
1	E	154	ILE	4.5
1	H	542	ILE	4.5
1	B	409	GLU	4.5
1	C	304	VAL	4.5
1	H	229	ARG	4.5
1	H	381	GLY	4.5
1	D	118	LYS	4.5
1	C	22	PRO	4.5
1	C	311	GLY	4.5
1	A	363	ASN	4.5
1	E	445	TYR	4.5
1	B	288	PHE	4.5
1	F	366	ILE	4.5
1	C	194	LYS	4.5
1	B	141	GLY	4.5
1	A	461	ASP	4.5
1	E	21	ALA	4.5
1	H	438	ALA	4.5
1	E	112	PRO	4.5
1	A	314	ALA	4.5
1	E	240	GLN	4.5
1	E	318	LEU	4.5
1	D	374	LEU	4.5
1	D	430	ASN	4.5

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Mol	Chain	Res	Type	RSRZ
1	C	428	LEU	4.5
1	A	529	ASN	4.5
1	B	145	THR	4.5
1	B	327	GLU	4.5
1	C	543	GLU	4.5
1	E	581	GLY	4.5
1	C	214	HIS	4.5
1	E	483	GLY	4.5
1	F	82	SER	4.5
1	E	102	ARG	4.5
1	E	128	ILE	4.5
1	F	56	PHE	4.5
1	F	455	ARG	4.5
1	A	48	LEU	4.5
1	B	500	PRO	4.5
1	C	387	SER	4.5
1	F	38	ALA	4.5
1	D	464	ASN	4.5
1	D	78	ARG	4.5
1	F	354	ARG	4.5
1	H	207	ALA	4.5
1	F	389	ILE	4.5
1	C	546	ASP	4.5
1	F	109	MET	4.5
1	H	91	TRP	4.5
1	H	136	ALA	4.5
1	A	126	SER	4.5
1	A	279	LEU	4.5
1	G	31	GLY	4.5
1	A	569	ARG	4.4
1	B	574	GLN	4.4
1	E	531	THR	4.4
1	E	565	LEU	4.4
1	F	393	TYR	4.4
1	B	110	GLY	4.4
1	G	15	ARG	4.4
1	B	429	PHE	4.4
1	B	538	ARG	4.4
1	C	92	VAL	4.4
1	F	382	LYS	4.4
1	G	89	ILE	4.4
1	C	574	GLN	4.4

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Mol	Chain	Res	Type	RSRZ
1	G	240	GLN	4.4
1	G	287	VAL	4.4
1	H	77	LEU	4.4
1	A	154	ILE	4.4
1	F	515	SER	4.4
1	C	524	ASP	4.4
1	A	160	MET	4.4
1	F	486	ARG	4.4
1	G	83	TYR	4.4
1	G	300	SER	4.4
1	D	385	ILE	4.4
1	F	183	ARG	4.4
1	A	60	ASP	4.4
1	D	554	GLY	4.4
1	G	440	ALA	4.4
1	A	67	MET	4.4
1	D	492	ALA	4.4
1	F	501	ILE	4.4
1	G	402	MET	4.4
1	G	39	ALA	4.4
1	E	282	GLY	4.4
1	A	250	ILE	4.4
1	B	263	LEU	4.4
1	A	305	ASN	4.4
1	B	282	GLY	4.4
1	G	88	CYS	4.4
1	D	279	LEU	4.4
1	E	436	ASN	4.4
1	A	536	ALA	4.4
1	H	137	SER	4.3
1	D	526	LEU	4.3
1	D	12	THR	4.3
1	D	306	ALA	4.3
1	B	218	LEU	4.3
1	C	554	GLY	4.3
1	D	475	GLY	4.3
1	F	89	ILE	4.3
1	G	482	SER	4.3
1	F	270	ALA	4.3
1	B	465	LYS	4.3
1	F	192	ILE	4.3
1	E	508	THR	4.3

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Mol	Chain	Res	Type	RSRZ
1	C	146	VAL	4.3
1	A	298	LEU	4.3
1	C	436	ASN	4.3
1	G	216	GLU	4.3
1	F	286	VAL	4.3
1	G	569	ARG	4.3
1	E	474	ILE	4.3
1	H	397	GLU	4.3
1	F	580	PHE	4.3
1	A	395	ILE	4.3
1	C	364	LEU	4.3
1	D	294	LEU	4.3
1	E	541	THR	4.3
1	B	236	ARG	4.3
1	H	143	LEU	4.3
1	D	519	ILE	4.3
1	H	524	ASP	4.3
1	H	564	ASP	4.3
1	G	536	ALA	4.3
1	B	272	PHE	4.3
1	B	405	HIS	4.3
1	F	242	MET	4.3
1	H	513	THR	4.3
1	F	271	SER	4.3
1	A	544	LYS	4.3
1	G	255	ILE	4.3
1	F	226	GLU	4.3
1	B	522	ALA	4.2
1	E	69	LEU	4.2
1	F	564	ASP	4.2
1	H	187	LYS	4.2
1	A	538	ARG	4.2
1	F	14	ARG	4.2
1	H	265	PHE	4.2
1	D	344	PHE	4.2
1	C	534	VAL	4.2
1	F	238	ARG	4.2
1	H	519	ILE	4.2
1	B	159	MET	4.2
1	H	206	SER	4.2
1	G	496	LEU	4.2
1	G	545	ALA	4.2

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Mol	Chain	Res	Type	RSRZ
1	F	255	ILE	4.2
1	B	281	ALA	4.2
1	E	16	LEU	4.2
1	B	292	ILE	4.2
1	F	15	ARG	4.2
1	F	356	VAL	4.2
1	C	215	LYS	4.2
1	C	226	GLU	4.2
1	F	450	ILE	4.2
1	F	503	ILE	4.2
1	C	506	GLU	4.2
1	H	345	ARG	4.2
1	D	199	THR	4.2
1	A	264	ALA	4.2
1	E	534	VAL	4.2
1	D	562	HIS	4.2
1	F	394	ASP	4.2
1	H	432	THR	4.2
1	C	309	GLN	4.2
1	E	60	ASP	4.2
1	B	118	LYS	4.2
1	C	113	VAL	4.2
1	E	320	THR	4.2
1	H	526	LEU	4.2
1	E	233	VAL	4.2
1	E	428	LEU	4.2
1	H	107	HIS	4.2
1	C	438	ALA	4.2
1	D	64	LEU	4.2
1	H	375	VAL	4.2
1	D	169	ILE	4.2
1	C	422	VAL	4.2
1	E	75	MET	4.1
1	G	422	VAL	4.1
1	D	88	CYS	4.1
1	B	412	LEU	4.1
1	F	381	GLY	4.1
1	D	486	ARG	4.1
1	C	379	GLY	4.1
1	F	427	HIS	4.1
1	B	146	VAL	4.1
1	D	159	MET	4.1

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Mol	Chain	Res	Type	RSRZ
1	D	335	ILE	4.1
1	F	546	ASP	4.1
1	H	158	ILE	4.1
1	D	116	PHE	4.1
1	B	449	GLN	4.1
1	E	365	LYS	4.1
1	G	429	PHE	4.1
1	G	373	ALA	4.1
1	D	283	THR	4.1
1	F	199	THR	4.1
1	C	21	ALA	4.1
1	E	62	SER	4.1
1	A	293	ALA	4.1
1	G	465	LYS	4.1
1	A	157	PHE	4.1
1	E	524	ASP	4.1
1	E	373	ALA	4.1
1	B	422	VAL	4.1
1	B	254	ILE	4.1
1	E	33	ALA	4.1
1	B	302	THR	4.1
1	A	398	GLY	4.1
1	F	469	GLY	4.1
1	A	34	LEU	4.1
1	C	188	ARG	4.1
1	A	550	VAL	4.0
1	F	45	LEU	4.0
1	G	58	LYS	4.0
1	B	312	MET	4.0
1	H	558	GLU	4.0
1	F	433	VAL	4.0
1	G	203	VAL	4.0
1	C	83	TYR	4.0
1	F	254	ILE	4.0
1	G	362	ILE	4.0
1	G	269	ALA	4.0
1	C	139	SER	4.0
1	E	234	SER	4.0
1	E	252	ASP	4.0
1	E	196	MET	4.0
1	G	279	LEU	4.0
1	H	533	LEU	4.0

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Mol	Chain	Res	Type	RSRZ
1	F	465	LYS	4.0
1	A	108	MET	4.0
1	D	130	TYR	4.0
1	C	213	GLY	4.0
1	E	382	LYS	4.0
1	F	453	ALA	4.0
1	F	114	SER	4.0
1	H	101	ARG	4.0
1	B	322	LEU	4.0
1	C	254	ILE	4.0
1	E	362	ILE	4.0
1	H	67	MET	4.0
1	D	460	MET	4.0
1	E	58	LYS	4.0
1	G	190	ARG	4.0
1	G	532	SER	4.0
1	B	115	PHE	4.0
1	D	180	ILE	4.0
1	G	521	ALA	4.0
1	D	15	ARG	4.0
1	D	384	THR	4.0
1	H	49	LYS	4.0
1	H	508	THR	4.0
1	B	562	HIS	4.0
1	D	432	THR	4.0
1	D	543	GLU	4.0
1	F	55	GLY	4.0
1	G	423	SER	4.0
1	B	240	GLN	4.0
1	G	481	LEU	3.9
1	H	495	LEU	3.9
1	E	415	LEU	3.9
1	B	149	GLU	3.9
1	C	441	ARG	3.9
1	A	86	SER	3.9
1	D	437	ILE	3.9
1	A	73	GLY	3.9
1	D	578	MET	3.9
1	A	134	GLN	3.9
1	F	418	GLN	3.9
1	G	59	THR	3.9
1	H	20	ILE	3.9

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Mol	Chain	Res	Type	RSRZ
1	D	434	ALA	3.9
1	F	279	LEU	3.9
1	C	437	ILE	3.9
1	G	372	VAL	3.9
1	D	458	TYR	3.9
1	H	439	TYR	3.9
1	A	270	ALA	3.9
1	D	146	VAL	3.9
1	E	244	MET	3.9
1	H	305	ASN	3.9
1	H	502	LEU	3.9
1	C	310	ARG	3.9
1	D	404	GLY	3.9
1	A	243	LYS	3.9
1	G	346	ASN	3.9
1	H	500	PRO	3.9
1	A	364	LEU	3.9
1	E	251	SER	3.9
1	F	207	ALA	3.9
1	G	435	ASN	3.9
1	B	82	SER	3.9
1	H	404	GLY	3.9
1	E	227	THR	3.9
1	H	100	MET	3.9
1	C	221	GLY	3.9
1	E	232	LYS	3.9
1	A	408	ARG	3.9
1	H	369	GLY	3.9
1	G	260	SER	3.9
1	A	149	GLU	3.9
1	A	295	MET	3.9
1	F	121	THR	3.9
1	H	288	PHE	3.9
1	E	293	ALA	3.9
1	D	302	THR	3.9
1	G	118	LYS	3.9
1	G	492	ALA	3.9
1	A	437	ILE	3.9
1	B	143	LEU	3.9
1	F	412	LEU	3.9
1	B	194	LYS	3.9
1	F	151	ALA	3.9

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Mol	Chain	Res	Type	RSRZ
1	B	241	GLY	3.8
1	H	528	LYS	3.8
1	G	10	TRP	3.8
1	H	237	MET	3.8
1	B	368	ALA	3.8
1	D	491	ILE	3.8
1	E	347	VAL	3.8
1	F	562	HIS	3.8
1	H	384	THR	3.8
1	F	187	LYS	3.8
1	A	548	ILE	3.8
1	C	177	ILE	3.8
1	E	331	GLY	3.8
1	H	549	VAL	3.8
1	E	151	ALA	3.8
1	F	251	SER	3.8
1	G	84	VAL	3.8
1	A	102	ARG	3.8
1	C	313	ALA	3.8
1	C	174	LEU	3.8
1	C	303	ASN	3.8
1	H	286	VAL	3.8
1	C	159	MET	3.8
1	H	148	ARG	3.8
1	A	284	ILE	3.8
1	E	493	ARG	3.8
1	C	465	LYS	3.8
1	G	19	THR	3.8
1	H	246	SER	3.8
1	B	437	ILE	3.8
1	C	204	THR	3.8
1	C	206	SER	3.8
1	G	199	THR	3.8
1	F	360	ARG	3.8
1	G	68	PRO	3.8
1	C	491	ILE	3.8
1	F	435	ASN	3.8
1	A	459	ALA	3.8
1	B	161	PHE	3.7
1	C	550	VAL	3.7
1	C	365	LYS	3.7
1	F	241	GLY	3.7

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Mol	Chain	Res	Type	RSRZ
1	B	234	SER	3.7
1	D	280	THR	3.7
1	H	374	LEU	3.7
1	B	521	ALA	3.7
1	C	334	VAL	3.7
1	E	149	GLU	3.7
1	A	308	PHE	3.7
1	H	32	VAL	3.7
1	A	33	ALA	3.7
1	B	158	ILE	3.7
1	B	212	LYS	3.7
1	H	175	ALA	3.7
1	C	250	ILE	3.7
1	D	89	ILE	3.7
1	D	309	GLN	3.7
1	F	408	ARG	3.7
1	D	564	ASP	3.7
1	F	258	ILE	3.7
1	H	141	GLY	3.7
1	B	210	MET	3.7
1	E	104	LEU	3.7
1	G	104	LEU	3.7
1	G	349	PHE	3.7
1	D	433	VAL	3.7
1	G	352	PRO	3.7
1	G	109	MET	3.7
1	E	195	ASN	3.7
1	G	247	ALA	3.7
1	G	335	ILE	3.7
1	H	82	SER	3.7
1	H	376	GLY	3.7
1	F	88	CYS	3.7
1	F	29	VAL	3.7
1	F	264	ALA	3.7
1	A	324	SER	3.7
1	H	569	ARG	3.7
1	B	56	PHE	3.7
1	G	370	LYS	3.7
1	A	346	ASN	3.7
1	E	231	ASP	3.7
1	C	433	VAL	3.7
1	E	375	VAL	3.7

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Mol	Chain	Res	Type	RSRZ
1	F	525	GLU	3.7
1	C	98	MET	3.7
1	D	310	ARG	3.7
1	H	57	GLY	3.7
1	A	238	ARG	3.6
1	H	16	LEU	3.6
1	D	213	GLY	3.6
1	G	184	VAL	3.6
1	E	384	THR	3.6
1	F	299	LYS	3.6
1	G	265	PHE	3.6
1	A	486	ARG	3.6
1	C	577	LYS	3.6
1	D	194	LYS	3.6
1	G	138	SER	3.6
1	F	484	GLY	3.6
1	E	545	ALA	3.6
1	E	485	GLN	3.6
1	C	403	ASP	3.6
1	E	135	VAL	3.6
1	A	354	ARG	3.6
1	A	522	ALA	3.6
1	H	382	LYS	3.6
1	E	143	LEU	3.6
1	E	26	GLY	3.6
1	A	239	LEU	3.6
1	A	38	ALA	3.6
1	B	510	ALA	3.6
1	C	509	SER	3.6
1	C	545	ALA	3.6
1	B	266	VAL	3.6
1	F	506	GLU	3.6
1	E	24	LYS	3.6
1	H	302	THR	3.6
1	H	119	GLN	3.6
1	A	141	GLY	3.6
1	H	449	GLN	3.6
1	C	523	LEU	3.6
1	D	54	ASP	3.6
1	A	280	THR	3.6
1	C	277	ASP	3.6
1	F	132	SER	3.5

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Mol	Chain	Res	Type	RSRZ
1	C	245	VAL	3.5
1	E	319	PHE	3.5
1	A	517	ARG	3.5
1	C	220	PHE	3.5
1	B	26	GLY	3.5
1	G	319	PHE	3.5
1	F	531	THR	3.5
1	F	520	GLN	3.5
1	A	195	ASN	3.5
1	H	316	GLN	3.5
1	D	322	LEU	3.5
1	G	400	ILE	3.5
1	H	540	SER	3.5
1	A	429	PHE	3.5
1	E	211	LEU	3.5
1	F	480	LEU	3.5
1	F	168	SER	3.5
1	G	65	VAL	3.5
1	D	436	ASN	3.5
1	G	524	ASP	3.5
1	G	69	LEU	3.5
1	A	306	ALA	3.5
1	E	39	ALA	3.5
1	A	183	ARG	3.5
1	C	130	TYR	3.5
1	D	292	ILE	3.5
1	F	523	LEU	3.5
1	G	462	PHE	3.5
1	E	126	SER	3.5
1	D	71	VAL	3.5
1	H	545	ALA	3.5
1	D	575	LEU	3.5
1	F	530	ARG	3.5
1	B	415	LEU	3.5
1	H	416	ARG	3.5
1	E	444	GLN	3.4
1	D	534	VAL	3.4
1	H	24	LYS	3.4
1	H	319	PHE	3.4
1	H	287	VAL	3.4
1	B	450	ILE	3.4
1	G	344	PHE	3.4

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Mol	Chain	Res	Type	RSRZ
1	A	316	GLN	3.4
1	A	260	SER	3.4
1	C	343	GLU	3.4
1	D	547	GLU	3.4
1	D	228	LYS	3.4
1	G	382	LYS	3.4
1	G	506	GLU	3.4
1	A	266	VAL	3.4
1	A	272	PHE	3.4
1	C	64	LEU	3.4
1	C	127	ARG	3.4
1	C	493	ARG	3.4
1	G	578	MET	3.4
1	G	486	ARG	3.4
1	D	381	GLY	3.4
1	A	402	MET	3.4
1	E	109	MET	3.4
1	F	466	MET	3.4
1	F	178	VAL	3.4
1	D	270	ALA	3.4
1	G	90	SER	3.4
1	B	40	SER	3.4
1	E	297	PRO	3.4
1	G	477	ASN	3.4
1	H	463	ILE	3.4
1	D	438	ALA	3.4
1	F	90	SER	3.4
1	G	241	GLY	3.4
1	H	250	ILE	3.4
1	F	43	PHE	3.3
1	F	553	ASP	3.3
1	C	192	ILE	3.3
1	E	506	GLU	3.3
1	F	198	ASN	3.3
1	E	150	GLY	3.3
1	F	429	PHE	3.3
1	H	478	GLY	3.3
1	B	290	SER	3.3
1	F	193	SER	3.3
1	H	307	GLN	3.3
1	H	511	LEU	3.3
1	H	262	ALA	3.3

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Mol	Chain	Res	Type	RSRZ
1	F	371	THR	3.3
1	C	112	PRO	3.3
1	E	298	LEU	3.3
1	B	298	LEU	3.3
1	G	173	VAL	3.3
1	F	293	ALA	3.3
1	G	428	LEU	3.3
1	F	108	MET	3.3
1	F	475	GLY	3.3
1	E	469	GLY	3.3
1	H	232	LYS	3.3
1	C	140	SER	3.3
1	E	220	PHE	3.3
1	F	409	GLU	3.3
1	H	267	LEU	3.3
1	H	271	SER	3.3
1	G	526	LEU	3.3
1	F	561	THR	3.3
1	A	409	GLU	3.3
1	A	365	LYS	3.3
1	D	520	GLN	3.3
1	C	203	VAL	3.3
1	H	373	ALA	3.3
1	E	499	SER	3.3
1	F	545	ALA	3.3
1	E	48	LEU	3.3
1	G	442	THR	3.3
1	A	120	SER	3.3
1	A	379	GLY	3.3
1	C	84	VAL	3.3
1	C	239	LEU	3.3
1	G	292	ILE	3.3
1	A	475	GLY	3.3
1	C	530	ARG	3.3
1	H	560	GLY	3.3
1	B	491	ILE	3.3
1	G	502	LEU	3.3
1	G	95	LYS	3.2
1	A	404	GLY	3.2
1	E	453	ALA	3.2
1	D	287	VAL	3.2
1	D	339	THR	3.2

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Mol	Chain	Res	Type	RSRZ
1	E	438	ALA	3.2
1	B	507	ALA	3.2
1	E	86	SER	3.2
1	F	87	TYR	3.2
1	G	17	TRP	3.2
1	G	374	LEU	3.2
1	H	140	SER	3.2
1	C	195	ASN	3.2
1	B	237	MET	3.2
1	G	55	GLY	3.2
1	G	106	GLY	3.2
1	G	472	THR	3.2
1	F	110	GLY	3.2
1	G	232	LYS	3.2
1	H	54	ASP	3.2
1	H	299	LYS	3.2
1	D	527	GLN	3.2
1	E	214	HIS	3.2
1	E	446	SER	3.2
1	F	554	GLY	3.2
1	B	387	SER	3.2
1	C	54	ASP	3.2
1	F	495	LEU	3.2
1	G	100	MET	3.2
1	B	543	GLU	3.2
1	A	491	ILE	3.2
1	G	14	ARG	3.2
1	H	236	ARG	3.2
1	D	409	GLU	3.2
1	H	202	GLN	3.2
1	H	26	GLY	3.2
1	F	40	SER	3.2
1	E	258	ILE	3.2
1	B	50	PRO	3.1
1	D	183	ARG	3.2
1	B	504	LEU	3.1
1	E	192	ILE	3.1
1	B	283	THR	3.1
1	F	451	GLU	3.1
1	D	119	GLN	3.1
1	D	555	VAL	3.1
1	A	82	SER	3.1

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Mol	Chain	Res	Type	RSRZ
1	D	440	ALA	3.1
1	F	468	ASN	3.1
1	G	505	ASP	3.1
1	F	75	MET	3.1
1	E	161	PHE	3.1
1	B	372	VAL	3.1
1	E	352	PRO	3.1
1	F	161	PHE	3.1
1	H	441	ARG	3.1
1	C	384	THR	3.1
1	H	284	ILE	3.1
1	B	573	ALA	3.1
1	H	358	ALA	3.1
1	G	371	THR	3.1
1	E	549	VAL	3.1
1	B	579	GLN	3.1
1	E	548	ILE	3.1
1	F	423	SER	3.1
1	G	108	MET	3.1
1	C	507	ALA	3.1
1	A	443	GLU	3.1
1	H	553	ASP	3.1
1	E	405	HIS	3.1
1	F	309	GLN	3.1
1	A	28	ILE	3.1
1	A	97	VAL	3.1
1	C	372	VAL	3.1
1	G	28	ILE	3.1
1	D	68	PRO	3.1
1	G	417	ASN	3.1
1	F	373	ALA	3.1
1	H	539	LEU	3.1
1	G	449	GLN	3.1
1	D	225	VAL	3.1
1	G	507	ALA	3.1
1	C	212	LYS	3.1
1	G	342	VAL	3.1
1	A	101	ARG	3.1
1	A	159	MET	3.1
1	D	85	SER	3.0
1	C	307	GLN	3.0
1	C	429	PHE	3.0

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Mol	Chain	Res	Type	RSRZ
1	D	382	LYS	3.0
1	H	157	PHE	3.0
1	H	365	LYS	3.0
1	H	504	LEU	3.0
1	D	372	VAL	3.0
1	G	167	LEU	3.0
1	H	318	LEU	3.0
1	A	283	THR	3.0
1	H	290	SER	3.0
1	G	63	VAL	3.0
1	G	453	ALA	3.0
1	H	392	PHE	3.0
1	H	494	ALA	3.0
1	C	331	GLY	3.0
1	A	458	TYR	3.0
1	A	492	ALA	3.0
1	A	579	GLN	3.0
1	A	442	THR	3.0
1	F	369	GLY	3.0
1	H	13	PHE	3.0
1	G	82	SER	3.0
1	E	314	ALA	3.0
1	F	244	MET	3.0
1	F	472	THR	3.0
1	B	152	SER	3.0
1	C	222	GLY	3.0
1	A	285	THR	3.0
1	C	315	CYS	3.0
1	C	496	LEU	3.0
1	D	160	MET	3.0
1	D	504	LEU	3.0
1	F	257	LEU	3.0
1	G	407	LEU	3.0
1	H	254	ILE	3.0
1	B	313	ALA	3.0
1	B	123	THR	3.0
1	E	188	ARG	3.0
1	E	316	GLN	3.0
1	B	439	TYR	3.0
1	B	108	MET	3.0
1	C	495	LEU	3.0
1	F	18	PRO	3.0

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Mol	Chain	Res	Type	RSRZ
1	F	160	MET	3.0
1	C	354	ARG	3.0
1	C	409	GLU	3.0
1	H	340	GLY	3.0
1	F	507	ALA	2.9
1	H	527	GLN	2.9
1	A	118	LYS	2.9
1	D	346	ASN	2.9
1	F	411	THR	2.9
1	E	175	ALA	2.9
1	E	516	GLU	2.9
1	G	143	LEU	2.9
1	D	11	GLN	2.9
1	G	487	GLN	2.9
1	C	102	ARG	2.9
1	C	470	LEU	2.9
1	D	311	GLY	2.9
1	F	139	SER	2.9
1	B	381	GLY	2.9
1	C	120	SER	2.9
1	H	451	GLU	2.9
1	H	523	LEU	2.9
1	H	507	ALA	2.9
1	A	347	VAL	2.9
1	F	304	VAL	2.9
1	A	508	THR	2.9
1	B	458	TYR	2.9
1	B	310	ARG	2.9
1	H	61	ARG	2.9
1	G	56	PHE	2.9
1	H	159	MET	2.9
1	C	341	ASP	2.9
1	D	343	GLU	2.9
1	C	33	ALA	2.9
1	C	268	TYR	2.9
1	H	124	LEU	2.9
1	D	429	PHE	2.9
1	C	508	THR	2.9
1	E	505	ASP	2.9
1	C	450	ILE	2.9
1	E	330	GLU	2.9
1	G	178	VAL	2.9

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Mol	Chain	Res	Type	RSRZ
1	H	92	VAL	2.9
1	G	136	ALA	2.9
1	H	83	TYR	2.9
1	F	202	GLN	2.9
1	H	122	GLY	2.9
1	C	111	MET	2.9
1	B	416	ARG	2.9
1	F	101	ARG	2.9
1	C	29	VAL	2.9
1	F	196	MET	2.9
1	F	278	SER	2.9
1	G	464	ASN	2.8
1	B	222	GLY	2.8
1	D	523	LEU	2.8
1	A	405	HIS	2.8
1	B	318	LEU	2.8
1	B	395	ILE	2.8
1	E	478	GLY	2.8
1	G	387	SER	2.8
1	B	61	ARG	2.8
1	C	547	GLU	2.8
1	F	303	ASN	2.8
1	E	380	SER	2.8
1	G	53	ASP	2.8
1	C	292	ILE	2.8
1	D	291	MET	2.8
1	F	219	ILE	2.8
1	H	76	ILE	2.8
1	C	556	ILE	2.8
1	D	435	ASN	2.8
1	C	280	THR	2.8
1	F	59	THR	2.8
1	A	14	ARG	2.8
1	D	27	LEU	2.8
1	C	75	MET	2.8
1	G	11	GLN	2.8
1	A	359	LEU	2.8
1	F	315	CYS	2.8
1	G	162	TYR	2.8
1	C	373	ALA	2.8
1	F	374	LEU	2.8
1	G	385	ILE	2.8

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Mol	Chain	Res	Type	RSRZ
1	G	531	THR	2.8
1	E	25	ALA	2.8
1	F	437	ILE	2.8
1	E	406	ASP	2.8
1	A	220	PHE	2.8
1	E	442	THR	2.8
1	H	475	GLY	2.8
1	D	550	VAL	2.8
1	H	177	ILE	2.8
1	D	423	SER	2.8
1	E	173	VAL	2.8
1	A	138	SER	2.8
1	B	53	ASP	2.8
1	B	137	SER	2.8
1	E	459	ALA	2.8
1	D	462	PHE	2.8
1	F	420	ALA	2.8
1	D	184	VAL	2.7
1	B	578	MET	2.7
1	G	191	ASN	2.7
1	F	478	GLY	2.7
1	G	293	ALA	2.7
1	B	433	VAL	2.7
1	B	513	THR	2.7
1	H	575	LEU	2.7
1	A	478	GLY	2.7
1	G	192	ILE	2.7
1	B	414	SER	2.7
1	E	348	THR	2.7
1	F	81	THR	2.7
1	H	208	GLU	2.7
1	G	49	LYS	2.7
1	E	461	ASP	2.7
1	F	138	SER	2.7
1	H	258	ILE	2.7
1	H	477	ASN	2.7
1	A	551	VAL	2.7
1	H	309	GLN	2.7
1	C	40	SER	2.7
1	H	234	SER	2.7
1	C	522	ALA	2.7
1	E	201	GLY	2.7

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Mol	Chain	Res	Type	RSRZ
1	F	31	GLY	2.7
1	E	142	ALA	2.7
1	F	269	ALA	2.7
1	E	402	MET	2.7
1	H	12	THR	2.7
1	G	437	ILE	2.7
1	H	268	TYR	2.7
1	C	282	GLY	2.7
1	C	265	PHE	2.7
1	A	535	ILE	2.7
1	B	45	LEU	2.7
1	D	227	THR	2.7
1	C	344	PHE	2.7
1	D	281	ALA	2.7
1	F	474	ILE	2.7
1	G	489	ILE	2.7
1	E	43	PHE	2.7
1	F	156	LEU	2.7
1	H	195	ASN	2.7
1	H	233	VAL	2.7
1	G	365	LYS	2.7
1	D	135	VAL	2.7
1	D	415	LEU	2.7
1	A	130	TYR	2.7
1	C	85	SER	2.7
1	E	162	TYR	2.7
1	G	307	GLN	2.7
1	H	321	ILE	2.6
1	G	221	GLY	2.6
1	H	342	VAL	2.6
1	G	270	ALA	2.6
1	G	348	THR	2.6
1	H	130	TYR	2.6
1	E	129	THR	2.6
1	F	54	ASP	2.6
1	G	473	VAL	2.6
1	A	436	ASN	2.6
1	B	239	LEU	2.6
1	E	455	ARG	2.6
1	G	20	ILE	2.6
1	B	88	CYS	2.6
1	A	74	LEU	2.6

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Mol	Chain	Res	Type	RSRZ
1	B	129	THR	2.6
1	C	322	LEU	2.6
1	E	366	ILE	2.6
1	G	201	GLY	2.6
1	F	189	PHE	2.6
1	F	236	ARG	2.6
1	B	275	VAL	2.6
1	D	232	LYS	2.6
1	D	317	THR	2.6
1	E	351	TYR	2.6
1	A	342	VAL	2.6
1	A	410	TYR	2.6
1	C	81	THR	2.6
1	G	410	TYR	2.6
1	H	19	THR	2.6
1	A	570	GLY	2.5
1	F	49	LYS	2.5
1	F	197	GLN	2.5
1	D	172	ILE	2.5
1	H	410	TYR	2.5
1	D	34	LEU	2.5
1	G	301	LEU	2.5
1	C	411	THR	2.5
1	F	452	GLU	2.5
1	D	296	ARG	2.5
1	E	94	GLY	2.5
1	E	388	LEU	2.5
1	C	295	MET	2.5
1	G	122	GLY	2.5
1	C	229	ARG	2.5
1	F	370	LYS	2.5
1	H	493	ARG	2.5
1	A	474	ILE	2.5
1	C	60	ASP	2.5
1	H	247	ALA	2.5
1	F	517	ARG	2.5
1	G	445	TYR	2.5
1	E	299	LYS	2.5
1	A	385	ILE	2.5
1	D	377	ARG	2.5
1	H	407	LEU	2.5
1	B	544	LYS	2.5

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Mol	Chain	Res	Type	RSRZ
1	C	53	ASP	2.5
1	D	493	ARG	2.5
1	F	375	VAL	2.5
1	F	502	LEU	2.5
1	H	251	SER	2.5
1	H	348	THR	2.5
1	G	263	LEU	2.5
1	C	107	HIS	2.5
1	D	251	SER	2.5
1	H	532	SER	2.5
1	E	464	ASN	2.5
1	H	516	GLU	2.5
1	H	154	ILE	2.5
1	H	125	LEU	2.5
1	F	481	LEU	2.4
1	F	247	ALA	2.4
1	G	549	VAL	2.4
1	H	71	VAL	2.4
1	E	77	LEU	2.4
1	G	290	SER	2.4
1	G	476	GLU	2.4
1	B	568	HIS	2.4
1	B	371	THR	2.4
1	B	527	GLN	2.4
1	C	231	ASP	2.4
1	D	129	THR	2.4
1	C	374	LEU	2.4
1	H	266	VAL	2.4
1	F	508	THR	2.4
1	H	264	ALA	2.4
1	F	227	THR	2.4
1	H	189	PHE	2.4
1	E	484	GLY	2.4
1	F	250	ILE	2.4
1	E	477	ASN	2.4
1	H	240	GLN	2.4
1	H	301	LEU	2.4
1	D	501	ILE	2.4
1	F	438	ALA	2.4
1	G	253	PRO	2.4
1	G	320	THR	2.4
1	D	109	MET	2.4

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Mol	Chain	Res	Type	RSRZ
1	E	454	ALA	2.4
1	G	500	PRO	2.4
1	D	240	GLN	2.4
1	C	458	TYR	2.4
1	A	237	MET	2.4
1	H	200	MET	2.4
1	B	469	GLY	2.4
1	G	218	LEU	2.4
1	H	353	GLY	2.4
1	E	310	ARG	2.4
1	G	383	SER	2.4
1	A	432	THR	2.4
1	C	342	VAL	2.4
1	G	434	ALA	2.4
1	F	536	ALA	2.4
1	E	522	ALA	2.3
1	E	563	ASN	2.3
1	A	228	LYS	2.3
1	G	119	GLN	2.3
1	G	223	GLN	2.3
1	A	552	GLU	2.3
1	B	565	LEU	2.3
1	D	221	GLY	2.3
1	H	385	ILE	2.3
1	G	52	LEU	2.3
1	A	142	ALA	2.3
1	D	140	SER	2.3
1	D	250	ILE	2.3
1	F	442	THR	2.3
1	E	411	THR	2.3
1	F	509	SER	2.3
1	H	576	HIS	2.3
1	C	178	VAL	2.3
1	H	417	ASN	2.3
1	B	512	ASP	2.3
1	E	221	GLY	2.3
1	G	57	GLY	2.3
1	C	23	PHE	2.3
1	D	98	MET	2.3
1	A	526	LEU	2.3
1	D	533	LEU	2.3
1	A	198	ASN	2.3

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Mol	Chain	Res	Type	RSRZ
1	E	561	THR	2.3
1	A	575	LEU	2.3
1	C	536	ALA	2.3
1	F	172	ILE	2.3
1	B	84	VAL	2.3
1	H	274	SER	2.3
1	G	211	LEU	2.3
1	A	208	GLU	2.3
1	A	64	LEU	2.2
1	A	124	LEU	2.2
1	B	98	MET	2.2
1	D	276	MET	2.2
1	G	97	VAL	2.2
1	A	490	ALA	2.2
1	D	241	GLY	2.2
1	H	253	PRO	2.2
1	H	298	LEU	2.2
1	H	398	GLY	2.2
1	B	208	GLU	2.2
1	D	403	ASP	2.2
1	A	77	LEU	2.2
1	D	65	VAL	2.2
1	D	97	VAL	2.2
1	F	320	THR	2.2
1	D	525	GLU	2.2
1	G	306	ALA	2.2
1	G	16	LEU	2.2
1	A	18	PRO	2.2
1	F	306	ALA	2.2
1	G	251	SER	2.2
1	A	500	PRO	2.2
1	C	544	LYS	2.2
1	D	445	TYR	2.2
1	C	13	PHE	2.2
1	B	271	SER	2.2
1	E	579	GLN	2.2
1	D	399	GLU	2.2
1	D	264	ALA	2.2
1	A	244	MET	2.2
1	C	565	LEU	2.2
1	F	13	PHE	2.2
1	E	465	LYS	2.2

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Mol	Chain	Res	Type	RSRZ
1	H	462	PHE	2.2
1	A	422	VAL	2.2
1	H	552	GLU	2.2
1	E	288	PHE	2.2
1	G	217	VAL	2.1
1	H	561	THR	2.1
1	E	470	LEU	2.1
1	C	43	PHE	2.1
1	D	450	ILE	2.1
1	F	246	SER	2.1
1	C	366	ILE	2.1
1	A	59	THR	2.1
1	E	312	MET	2.1
1	A	411	THR	2.1
1	B	346	ASN	2.1
1	F	477	ASN	2.1
1	C	381	GLY	2.1
1	H	354	ARG	2.1
1	H	474	ILE	2.1
1	B	523	LEU	2.1
1	B	306	ALA	2.1
1	E	360	ARG	2.1
1	G	27	LEU	2.1
1	C	288	PHE	2.1
1	G	274	SER	2.1
1	C	67	MET	2.1
1	H	259	ALA	2.1
1	C	451	GLU	2.1
1	H	415	LEU	2.1
1	E	422	VAL	2.1
1	H	45	LEU	2.1
1	H	133	GLU	2.1
1	E	364	LEU	2.1
1	E	236	ARG	2.1
1	D	257	LEU	2.1
1	H	263	LEU	2.1
1	D	478	GLY	2.1
1	A	240	GLN	2.1
1	C	312	MET	2.1
1	E	101	ARG	2.1
1	D	205	THR	2.0
1	E	145	THR	2.0

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Mol	Chain	Res	Type	RSRZ
1	A	56	PHE	2.0
1	E	460	MET	2.0
1	E	530	ARG	2.0
1	H	112	PRO	2.0
1	A	311	GLY	2.0
1	B	52	LEU	2.0
1	B	116	PHE	2.0
1	H	88	CYS	2.0
1	G	367	PRO	2.0
1	C	187	LYS	2.0
1	B	536	ALA	2.0
1	D	21	ALA	2.0
1	E	557	VAL	2.0
1	B	221	GLY	2.0
1	E	451	GLU	2.0
1	H	63	VAL	2.0
1	F	565	LEU	2.0
1	G	364	LEU	2.0
1	B	107	HIS	2.0
1	G	110	GLY	2.0
1	G	98	MET	2.0
1	C	168	SER	2.0
1	D	470	LEU	2.0
1	F	398	GLY	2.0
1	F	16	LEU	2.0
1	B	528	LYS	2.0
1	F	92	VAL	2.0
1	A	307	GLN	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.