



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 15, 2017 – 06:56 am GMT

PDB ID : 1WCE
Title : Crystal structure of the T13 IBDV viral particle reveals a missing link in icosahedral viruses evolution
Authors : Coulibaly, F.; Chevalier, C.; Gutsche, I.; Pous, J.; Bressanelli, S.; Navaza, J.; Delmas, B.; Rey, F.A.
Deposited on : 2004-11-12
Resolution : 7.00 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

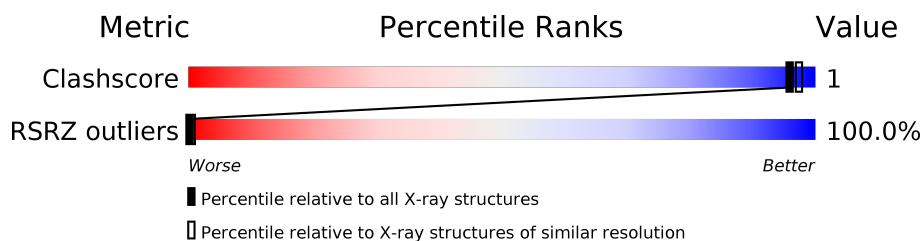
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 7.00 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))
Clashscore	112137	1035 (10.00-3.80)
RSRZ outliers	101464	1003 (10.00-3.72)

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	441	<div> <div>96%</div> <div> <div></div> <div>96%</div> <div>96%</div> </div> </div>
1	B	441	<div> <div>98%</div> <div> <div></div> <div>97%</div> <div>97%</div> </div> </div>
1	C	441	<div> <div>98%</div> <div> <div></div> <div>98%</div> <div>98%</div> </div> </div>
1	D	441	<div> <div>96%</div> <div> <div></div> <div>96%</div> <div>96%</div> </div> </div>
1	E	441	<div> <div>97%</div> <div> <div></div> <div>97%</div> <div>97%</div> </div> </div>
1	F	441	<div> <div>99%</div> <div> <div></div> <div>98%</div> <div>98%</div> </div> </div>
1	G	441	<div> <div>97%</div> <div> <div></div> <div>96%</div> <div>96%</div> </div> </div>
1	H	441	<div> <div>96%</div> <div> <div></div> <div>96%</div> <div>96%</div> </div> </div>
1	I	441	<div> <div>95%</div> <div> <div></div> <div>95%</div> <div>5%</div> </div> </div>

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Mol	Chain	Length	Quality of chain
1	J	441	<div><div></div><div>96%</div><div></div></div>
1	K	441	<div><div></div><div>94%</div><div>6%</div></div>
1	L	441	<div><div></div><div>97%</div><div></div></div>
1	M	441	<div><div></div><div>96%</div><div></div></div>

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 5533 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 MAJOR STRUCTURAL PROTEIN VP2.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	Trace
1	A	425	Total C 425 425	0	0	425
1	B	430	Total C 430 430	0	0	430
1	C	430	Total C 430 430	0	0	430
1	D	424	Total C 424 424	0	0	424
1	E	429	Total C 429 429	0	0	429
1	F	436	Total C 436 436	0	0	436
1	G	426	Total C 426 426	0	0	426
1	H	423	Total C 423 423	0	0	423
1	I	417	Total C 417 417	0	0	417
1	J	423	Total C 423 423	0	0	423
1	K	416	Total C 416 416	0	0	416
1	L	429	Total C 429 429	0	0	429
1	M	425	Total C 425 425	0	0	425

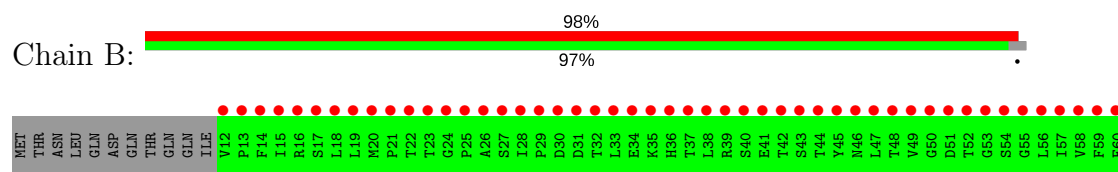
3 Residue-property plots

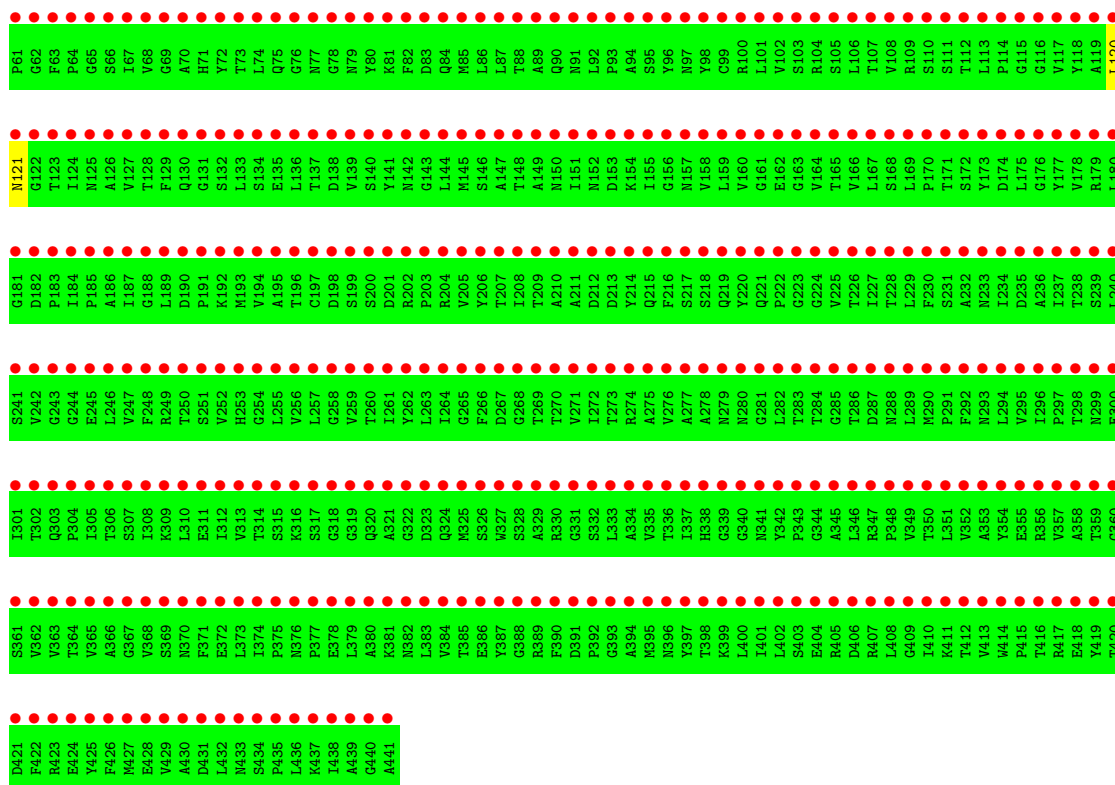
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: MAJOR STRUCTURAL PROTEIN VP2

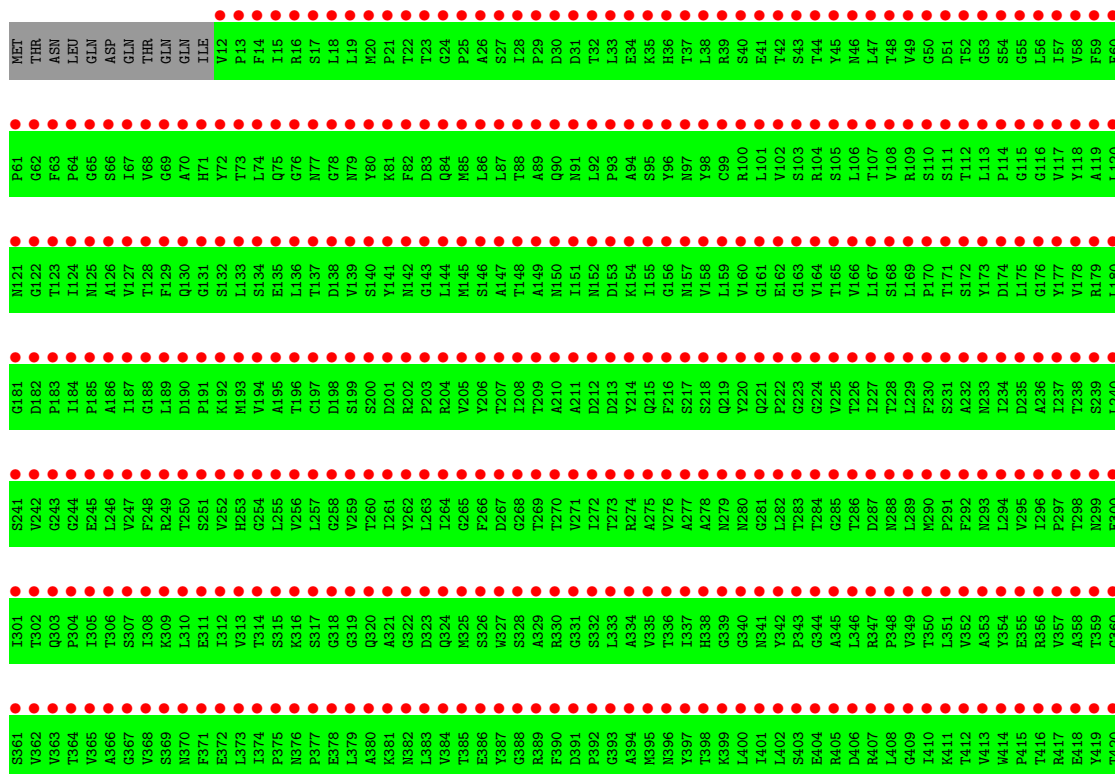
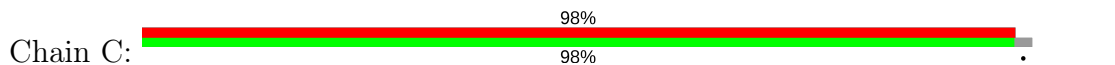


• Molecule 1: MAJOR STRUCTURAL PROTEIN VP2





• Molecule 1: MAJOR STRUCTURAL PROTEIN VP2



D421
 F422
 R423
 E424
 Y425
 F426
 M427
 E428
 V429
 A430
 D431
 L432
 N433
 S434
 P435
 L436
 K437
 I438
 A439
 G440
 A441

• Molecule 1: MAJOR STRUCTURAL PROTEIN VP2

Chain D: 

MET THR ASN LEU GLN THR GLN ILE VAL P13 P14 P15 P16 P17 P18 P19 P20 P21 P22 P23 P24 P25 P26 P27 P28 P29 P30 P31 P32 P33 P34 P35 P36 P37 P38 P39 P40 P41 P42 P43 P44 P45 P46 P47 P48 P49 P50 P51 P52 P53 P54 P55 P56 P57 P58 P59 P60
 P61 P62 P63 P64 P65 P66 P67 P68 P69 P70 P71 P72 P73 P74 P75 P76 P77 P78 P79 P80 P81 P82 P83 P84 P85 P86 P87 P88 P89 P90 P91 P92 P93 P94 P95 P96 P97 P98 P99 C00 C01 C02 C03 C04 C05 C06 C07 C08 C09 C10 C11 C12 C13 C14 C15 C16 C17 C18 C19 C20 C21 C22 C23 C24 C25 C26 C27 C28 C29 C30 C31 C32 C33 C34 C35 C36 C37 C38 C39 C40 C41 C42 C43 C44 C45 C46 C47 C48 C49 C50 C51 C52 C53 C54 C55 C56 C57 C58 C59 C60
 M121 G122 G123 G124 G125 G126 G127 G128 G129 G130 G131 G132 G133 G134 G135 G136 G137 G138 G139 G140 G141 G142 G143 G144 G145 G146 G147 G148 G149 G150 G151 G152 G153 G154 G155 G156 G157 G158 G159 G160 G161 G162 G163 G164 G165 G166 G167 G168 G169 G170 G171 G172 G173 G174 G175 G176 G177 G178 G179 G180
 G181 D182 P183 I184 P185 A186 I187 G188 L189 D190 P191 K192 K193 V194 V195 T196 T197 L198 L199 S200 S201 D202 R203 P204 R205 V206 V207 V208 V209 V210 V211 V212 V213 V214 V215 V216 V217 V218 V219 V220 V221 V222 V223 V224 V225 V226 V227 V228 V229 V230 V231 V232 V233 V234 V235 V236 V237 V238 V239 V240
 S241 V242 G243 G244 G245 L246 L247 V248 F249 F250 F251 F252 F253 F254 F255 F256 F257 F258 F259 F260 F261 F262 F263 F264 F265 F266 F267 F268 F269 F270 F271 F272 F273 F274 F275 F276 F277 F278 F279 F280 F281 F282 F283 F284 F285 F286 F287 F288 F289 F290 F291 F292 F293 F294 F295 F296 F297 F298 F299 F300
 I301 T302 Q303 P304 I305 T306 T307 I308 K309 K310 L311 E312 I313 I314 T315 S316 P317 P318 G319 G320 Q321 A322 G323 D324 Q325 M326 M327 W328 S329 A330 R331 R332 S333 L334 A335 A336 M337 T338 N339 Y340 Y341 I401 I402 L403 S404 E405 R406 R407 L408 G409 I410 K411 T412 V413 W414 P415 T416 R417 E418 T419 S420 T421
 D421 F422 R423 E424 Y425 F426 M427 E428 V429 A430 D431 L432 L433 S434 P435 L436 LYS ILE THR ALA GLY ALA

• Molecule 1: MAJOR STRUCTURAL PROTEIN VP2

Chain E: 

MET THR ASN GLN ASP GLN THR GLN ILE VAL P13 P14 P15 P16 P17 P18 P19 P20 P21 P22 P23 P24 P25 P26 P27 P28 P29 P30 P31 P32 P33 P34 P35 P36 P37 P38 P39 P40 P41 P42 P43 P44 P45 P46 P47 P48 P49 P50 P51 P52 P53 P54 P55 P56 P57 P58 P59 P60
 P61 P62 P63 P64 P65 P66 P67 P68 P69 P70 P71 P72 P73 P74 P75 P76 P77 P78 P79 P80 P81 P82 P83 P84 P85 P86 P87 P88 P89 P90 P91 P92 P93 P94 P95 P96 P97 P98 P99 C00 C01 C02 C03 C04 C05 C06 C07 C08 C09 C10 C11 C12 C13 C14 C15 C16 C17 C18 C19 C20 C21 C22 C23 C24 C25 C26 C27 C28 C29 C30 C31 C32 C33 C34 C35 C36 C37 C38 C39 C40 C41 C42 C43 C44 C45 C46 C47 C48 C49 C50 C51 C52 C53 C54 C55 C56 C57 C58 C59 C60
 M121 G122 G123 G124 G125 G126 G127 G128 G129 G130 G131 G132 G133 G134 G135 G136 G137 G138 G139 G140 G141 G142 G143 G144 G145 G146 G147 G148 G149 G150 G151 G152 G153 G154 G155 G156 G157 G158 G159 G160 G161 G162 G163 G164 G165 G166 G167 G168 G169 G170 G171 G172 G173 G174 G175 G176 G177 G178 G179 G180
 G181 D182 P183 I184 P185 A186 I187 G188 L189 D190 P191 K192 K193 V194 V195 T196 T197 L198 L199 S200 S201 D202 R203 P204 R205 V206 V207 V208 V209 V210 V211 V212 V213 V214 V215 V216 V217 V218 V219 V220 V221 V222 V223 V224 V225 V226 V227 V228 V229 V230 V231 V232 V233 V234 V235 V236 V237 V238 V239 V240
 I301 T302 Q303 P304 I305 T306 T307 I308 K309 K310 L311 E312 I313 I314 T315 S316 P317 P318 G319 G320 Q321 A322 G323 D324 Q325 M326 M327 W328 S329 A330 R331 R332 S333 L334 A335 A336 M337 T338 N339 Y340 Y341 I401 I402 L403 S404 E405 R406 R407 L408 G409 I410 K411 T412 V413 W414 P415 T416 R417 E418 T419 S420 T421
 D421 F422 R423 E424 Y425 F426 M427 E428 V429 A430 D431 L432 L433 S434 P435 L436 LYS ILE THR ALA GLY ALA

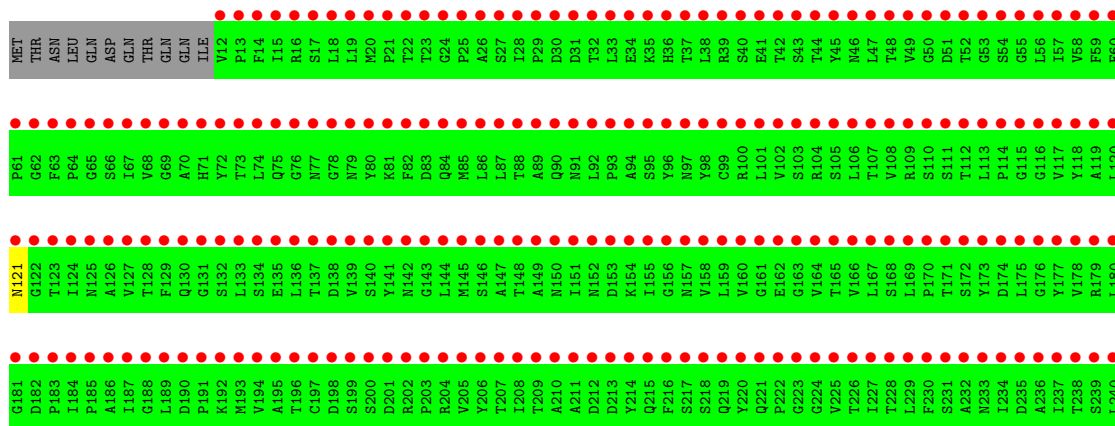


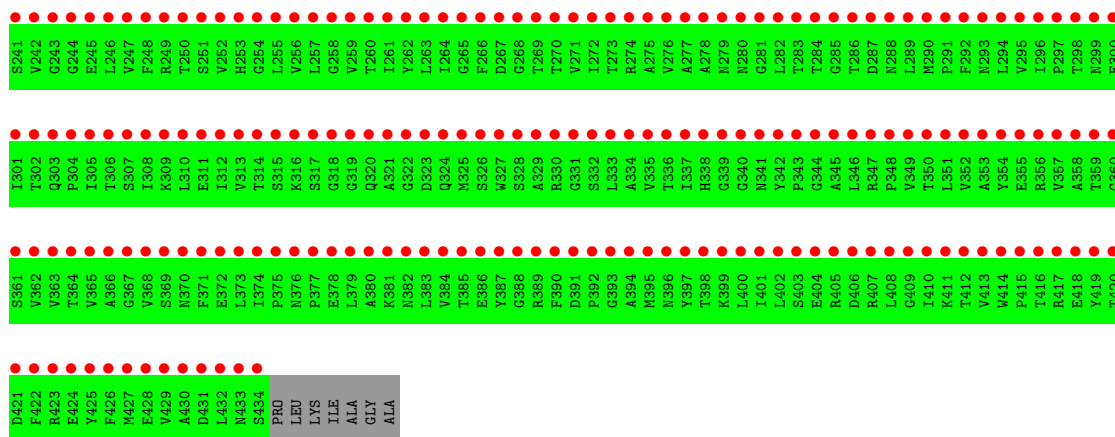
D421 F422 R423 E424 A425 F426 M427 E428 V429 K429 A430 D431 L432 M433 S434 P435 L436 K437	S361	I301	S241	G181	N121	P61
	V362	Q302	V242	D182	G122	G62
	V363	T303	G243	P183	T123	F63
	T364	P304	E244	I184	N124	P64
	V365	T305	G245	P185	N125	G65
	A366	T306	L246	A186	A126	S66
	G367	S307	V247	I187	V127	I67
	V368	L308	F248	G188	T128	V68
	S369	K309	R249	L189	F129	G69
	N370	L310	T250	D190	Q130	A70
F371	E311	S251	P191	G131	H71	
E372	T312	V252	K192	S132	Y72	
L373	V313	H253	K193	L133	T73	
I374	T314	G254	V194	S134	L74	
P375	S315	L255	A195	E135	Q75	
N376	G316	V256	L196	L136	G76	
P377	P317	L257	C197	T137	N77	
E378	G318	G258	D198	D138	G78	
L379	G319	V259	S199	V139	N79	
A380	Q320	T260	S200	S140	Y80	
K381	D321	T261	D201	Y141	K81	
N382	G322	V262	R202	N142	F82	
L383	Q323	L263	P203	G143	D83	
V384	Q324	T264	R204	L144	Q84	
T385	K325	G265	V205	N145	M85	
E386	S326	F266	Y206	S146	L86	
T387	W327	T267	T207	A147	L87	
G388	S328	G268	L208	T148	T88	
R389	A329	T269	I209	A149	A89	
F390	R330	T270	A210	N150	Q90	
D391	G331	T271	D211	L151	N91	
P392	S332	L272	D212	N152	L92	
G393	L333	T273	D213	D153	P93	
A394	A334	R274	Y214	K154	A94	
M395	V335	A275	Q215	I155	S95	
N396	T336	V276	F216	G156	Y96	
T397	I337	A277	S217	N157	N97	
T398	H338	A278	S218	V158	Y98	
K399	G339	N279	Q219	L159	C99	
L400	N340	N280	Y220	V160	R100	
I401	G341	G281	Q221	G161	L101	
L402	Y342	L282	P222	E162	V102	
S403	P343	T283	G223	G163	S103	
E404	G344	T284	G224	V164	R104	
R405	A345	G285	V225	T165	S105	
D406	L346	T286	T226	V166	L106	
R407	R347	D287	I227	L167	T107	
L408	P348	N288	T228	S168	V108	
G409	V349	L289	L229	R169	R109	
I410	T350	M290	F230	P170	S110	
K411	L351	P291	S231	T171	S111	
T412	V352	F292	A232	S172	T112	
V413	A353	N293	N233	Y173	L113	
W414	Y354	L294	I234	D174	P114	
P415	F415	V295	D235	L175	G115	
T416	R356	L296	A236	G176	G116	
R417	V357	P297	I237	Y177	V117	
E418	A358	T298	T238	V178	Y118	
Y419	T359	N299	S239	R179	A119	
T420	G360	F299	L240	L180	L120	

• Molecule 1: MAJOR STRUCTURAL PROTEIN VP2

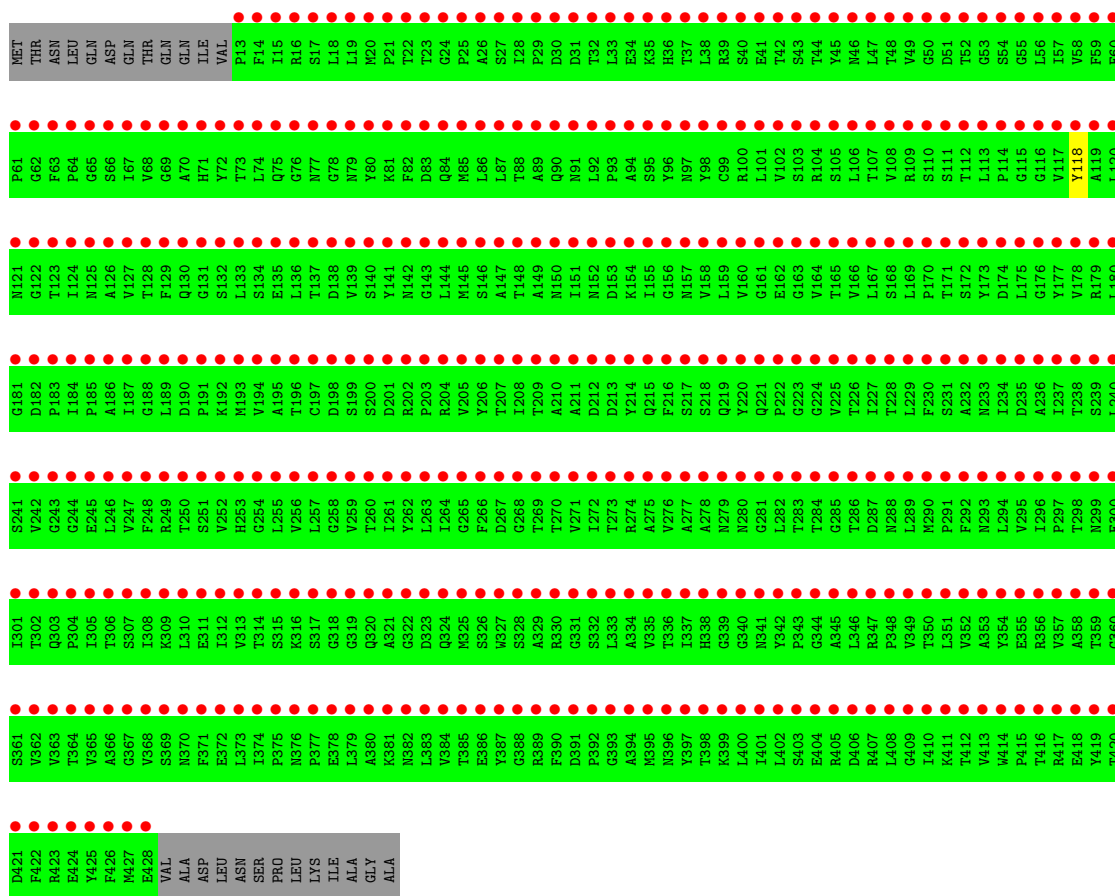


MET		THR		ASN		LEU		GLN		ASP		GLN		THR		GLN		GLN		ILE		VAL		P13		F14		I15		R16		S17		L18		L19		M20		P21		T22		T23		G24		P25		A26		S27		L28		P29		D30		N31		D32		L33		E34		K35		H36		T37		L38		R39		S40		E41		T42		S43		T44		Y45		N46		L47		T48		V49		G50		D51		T52		G53		S54		G55		L56		I57		V58		F59		F60	
P61		G62		F63		P64		G65		S66		I67		V68		G69		H70		H71		Y72		Y73		L74		Q75		G76		N77		G78		N79		K80		K81		F82		D83		Q84		N85		L86		L87		L88		A89		Q90		N91		L92		P93		A94		S95		Y96		N97		Y98		C99		R100		L101		V102		S103		S104		S105		L106		T107		S108		R109		S110		S111		T112		L113		P114		G115		V116		V117		A118		N119		L120	
N121		G122		T123		I124		P125		A126		V127		T128		F129		Q130		G131		S132		L133		S134		E135		L136		T137		D138		V139		S140		D141		Y142		M143		M144		M145		S146		A147		T148		A149		N150		D151		D152		D153		K154		Y155		G156		N157		V158		Q159		Y160		G161		P162		E163		G164		T165		V166		L167		S168		L169		L170		P171		T172		S173		Y174		D175		L176		G177		Y178		T179		L180	
G181		D182		P183		I184		P185		A186		I187		G188		L189		D190		P191		K192		K193		V194		A195		L196		C197		G198		S199		S200		D201		R202		P203		R204		V205		Y206		T207		L208		T209		A210		D211		D212		D213		Y214		L215		Q216		F217		S218		Q219		Y220		V221		P222		G223		G224		V225		T226		L227		T228		L229		F230		S231		A232		N233		I234		V235		L236		G237		T238		N239		L240	
S241		V242		G243		G244		E245		L246		V247		F248		R249		T250		S251		Y252		H253		G254		L255		V256		L257		G258		V259		T260		D261		R262		P263		R264		V265		Y266		T267		G268		R269		T270		D271		L272		L273		A274		V275		V276		A277		H278		G279		L280		N281		L282		T283		G284		A285		L286		R287		L288		V289		T290		P291		Y292		N293		L294		V295		L296		P297		T298		N299		E300	
I301		T302		Q303		P304		I305		T306		S307		L308		K309		L310		E311		T312		V313		T314		S315		G316		P317		G318		G319		Q320		A321		G322		D323		Q324		K325		S326		W327		G328		R329		A330		D331		S332		L333		A334		V335		T336		I337		H338		G339		L340		N341		Y342		P343		G344		A345		L346		R347		P348		V349		T350		L351		V352		A353		V354		E355		R356		V357		A358		Y359		G360	
S361		V362		P363		E364		V365		A366		G367		V368		S369		N370		F371		E372		L373		I374		P375		N376		P377		E378		L379		A380		K381		N382		L383		V384		T385		E386		T387		G388		R389		F390		D391		P392		G393		A394		M395		N396		Y397		T398		K399		L400		I401		L402		S403		E404		R405		D406		R407		L408		G409		I410		K411		T412		V413		W414		P415		T416		R417		E418		Y419		T420	

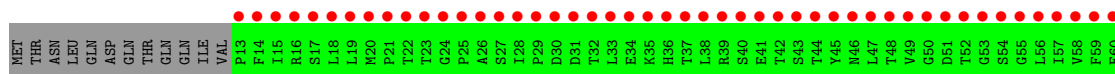


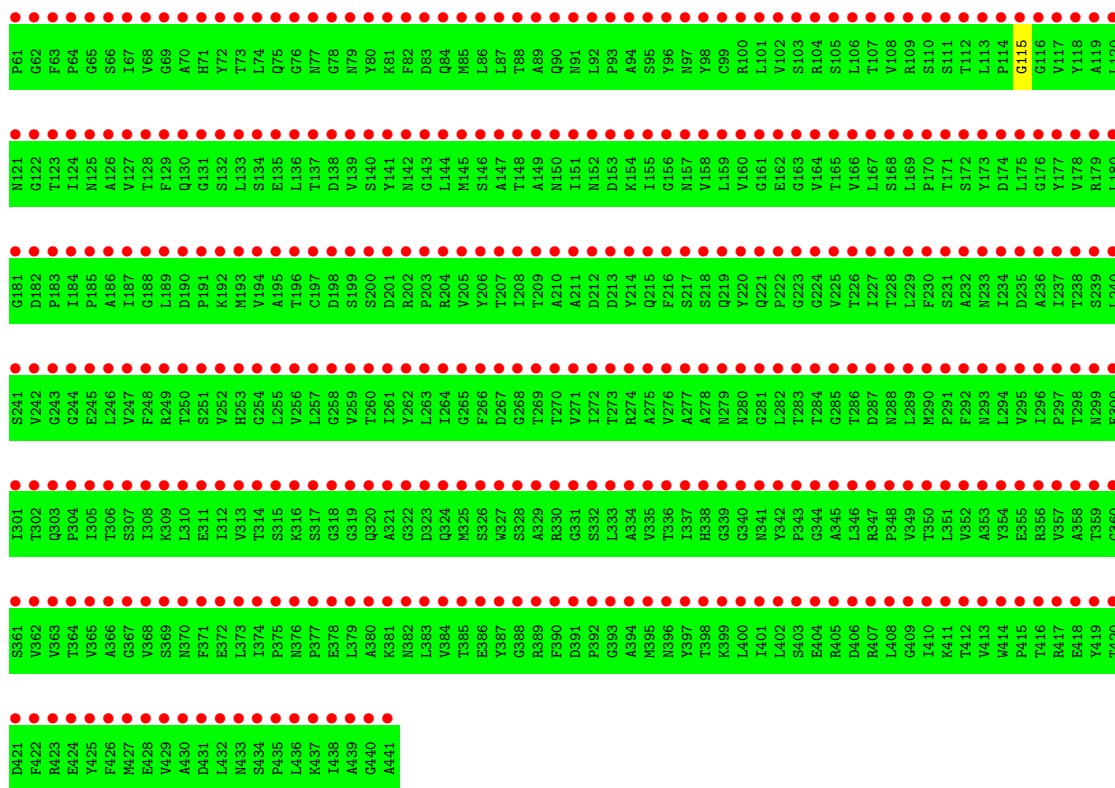


- Molecule 1: MAJOR STRUCTURAL PROTEIN VP2



- Molecule 1: MAJOR STRUCTURAL PROTEIN VP2





D421	•
F422	•
R423	•
E424	•
Y425	•
F426	•
M427	•
E428	•
V429	•
A430	•
D431	•
L432	•
N433	•
S434	•
P435	•
L436	•
LYS	
ILE	
A441	•
GLY	
ALA	

4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	854.01Å 692.23Å 792.41Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 7.00 49.86 – 6.97	Depositor EDS
% Data completeness (in resolution range)	75.1 (50.00-7.00) 74.7 (49.86-6.97)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.90 (at 6.68Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	(Not available) , (Not available) 0.411 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	DCC
Wilson B-factor (Å ²)	190.2	Xtriage
Anisotropy	0.155	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	1.78 , 49.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.27$	Xtriage
Estimated twinning fraction	0.327 for -h,-k,l	Xtriage
F_o, F_c correlation	0.67	EDS
Total number of atoms	5533	wwPDB-VP
Average B, all atoms (Å ²)	52.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.97% 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	425	0	0	2	0
1	B	430	0	0	2	0
1	C	430	0	0	0	0
1	D	424	0	0	1	0
1	E	429	0	0	1	0
1	F	436	0	0	1	0
1	G	426	0	0	1	0
1	H	423	0	0	0	0
1	I	417	0	0	0	0
1	J	423	0	0	1	0
1	K	416	0	0	1	0
1	L	429	0	0	1	0
1	M	425	0	0	1	0
All	All	5533	0	0	7	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 1.

All (7) close contacts within the same asymmetric unit are listed below, sorted by their clash

magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:111:SER:CA	1:D:112:THR:CA	1.85	1.51
1:E:117:VAL:CA	1:M:115:GLY:CA	2.26	1.13
1:A:112:THR:CA	1:B:121:ASN:CA	2.64	0.76
1:K:118:TYR:CA	1:L:115:GLY:CA	2.82	0.58
1:A:112:THR:CA	1:B:120:LEU:CA	2.96	0.43
1:F:426:PHE:CA	1:F:429:VAL:CA	3.00	0.40
1:G:112:THR:CA	1:J:121:ASN:CA	2.99	0.40

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	425/441 (96%)	19.75	425 (100%) 0 0	20, 47, 95, 99	0
1	B	430/441 (97%)	18.85	430 (100%) 0 0	20, 47, 95, 99	0
1	C	430/441 (97%)	20.28	430 (100%) 0 0	20, 47, 95, 99	0
1	D	424/441 (96%)	19.43	424 (100%) 0 0	20, 47, 95, 99	0
1	E	429/441 (97%)	18.23	429 (100%) 0 0	20, 47, 95, 99	0
1	F	436/441 (98%)	18.20	435 (99%) 0 0	20, 46, 95, 99	0
1	G	426/441 (96%)	20.65	426 (100%) 0 0	20, 47, 95, 99	0
1	H	423/441 (95%)	19.29	423 (100%) 0 0	20, 47, 95, 99	0
1	I	417/441 (94%)	20.03	417 (100%) 0 0	20, 47, 96, 99	0
1	J	423/441 (95%)	19.81	423 (100%) 0 0	20, 47, 95, 99	0
1	K	416/441 (94%)	20.36	416 (100%) 0 0	20, 47, 96, 99	0
1	L	429/441 (97%)	20.66	429 (100%) 0 0	20, 47, 95, 99	0
1	M	425/441 (96%)	19.58	425 (100%) 0 0	20, 47, 95, 99	0
All	All	5533/5733 (96%)	19.62	5532 (99%) 0 0	20, 47, 96, 99	0

All (5532) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	M	291	PRO	73.6
1	D	331	GLY	72.6
1	G	203	PRO	72.4
1	H	418	GLU	71.9
1	G	341	ASN	70.8
1	F	217	SER	69.8
1	K	406	ASP	68.5
1	M	123	THR	63.6
1	L	324	GLN	62.6

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Mol	Chain	Res	Type	RSRZ
1	D	209	THR	61.2
1	H	398	THR	60.3
1	B	396	ASN	58.5
1	A	128	THR	58.2
1	K	379	LEU	57.2
1	A	290	MET	55.7
1	H	399	LYS	55.1
1	A	396	ASN	55.0
1	A	78	GLY	54.5
1	G	401	ILE	54.4
1	D	399	LYS	54.3
1	K	173	TYR	53.8
1	M	290	MET	53.4
1	J	339	GLY	53.2
1	D	216	PHE	52.9
1	A	291	PRO	52.3
1	J	224	GLY	52.1
1	M	273	THR	51.6
1	I	420	THR	51.6
1	A	228	THR	51.0
1	G	386	GLU	51.0
1	A	320	GLN	50.6
1	I	213	ASP	49.5
1	C	228	THR	49.4
1	M	378	GLU	49.2
1	L	416	THR	49.1
1	I	206	TYR	48.8
1	G	48	THR	48.7
1	L	217	SER	48.7
1	C	398	THR	48.5
1	C	290	MET	48.4
1	K	405	ARG	48.4
1	A	380	ALA	48.0
1	A	111	SER	47.7
1	G	423	ARG	47.5
1	A	318	GLY	47.4
1	B	217	SER	47.4
1	H	396	ASN	47.3
1	K	375	PRO	47.3
1	M	406	ASP	47.1
1	J	309	LYS	46.9
1	A	79	ASN	46.9

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Mol	Chain	Res	Type	RSRZ
1	F	218	SER	46.8
1	G	251	SER	46.8
1	H	332	SER	46.5
1	C	285	GLY	46.2
1	C	227	ILE	45.9
1	C	420	THR	45.6
1	G	418	GLU	45.6
1	I	212	ASP	45.5
1	G	385	THR	45.3
1	K	418	GLU	45.3
1	E	294	LEU	45.1
1	D	208	ILE	45.1
1	M	361	SER	44.9
1	M	270	THR	44.9
1	C	314	THR	44.7
1	K	397	TYR	44.5
1	K	409	GLY	44.5
1	M	218	SER	44.5
1	I	78	GLY	44.4
1	K	315	SER	44.4
1	H	48	THR	44.4
1	I	424	GLU	44.4
1	E	423	ARG	44.2
1	D	326	SER	44.2
1	B	273	THR	44.1
1	D	222	PRO	44.0
1	A	400	LEU	43.9
1	B	378	GLU	43.8
1	D	321	ALA	43.8
1	C	363	VAL	43.8
1	L	219	GLN	43.6
1	J	251	SER	43.6
1	B	405	ARG	43.6
1	D	268	GLY	43.6
1	K	314	THR	43.5
1	B	55	GLY	43.5
1	D	330	ARG	43.3
1	C	269	THR	43.2
1	F	51	ASP	43.2
1	E	55	GLY	43.0
1	L	421	ASP	43.0
1	L	69	GLY	42.6

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Mol	Chain	Res	Type	RSRZ
1	K	172	SER	42.5
1	I	293	ASN	42.4
1	L	93	PRO	42.4
1	I	253	HIS	42.4
1	A	112	THR	42.4
1	F	35	LYS	42.3
1	I	95	SER	42.3
1	M	269	THR	42.3
1	J	350	THR	42.2
1	D	219	GLN	42.2
1	L	398	THR	42.1
1	F	78	GLY	42.0
1	D	341	ASN	42.0
1	I	299	ASN	41.9
1	E	228	THR	41.9
1	G	340	GLY	41.8
1	K	203	PRO	41.8
1	M	323	ASP	41.5
1	H	217	SER	41.5
1	C	334	ALA	41.5
1	C	157	ASN	41.4
1	K	270	THR	41.3
1	E	332	SER	41.2
1	C	270	THR	41.2
1	C	382	ASN	41.2
1	I	243	GLY	41.1
1	I	77	ASN	41.1
1	K	48	THR	41.0
1	G	215	GLN	40.9
1	J	323	ASP	40.9
1	I	302	THR	40.8
1	A	269	THR	40.8
1	G	255	LEU	40.7
1	J	277	ALA	40.6
1	M	322	GLY	40.6
1	G	417	ARG	40.6
1	I	228	THR	40.5
1	K	251	SER	40.4
1	L	196	THR	40.3
1	A	117	VAL	40.3
1	J	196	THR	40.2
1	L	405	ARG	40.1

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Mol	Chain	Res	Type	RSRZ
1	C	156	GLY	40.1
1	J	227	ILE	40.1
1	F	323	ASP	40.1
1	C	274	ARG	40.1
1	A	116	GLY	40.0
1	L	299	ASN	40.0
1	D	356	ARG	39.9
1	K	253	HIS	39.8
1	I	314	THR	39.8
1	L	420	THR	39.7
1	L	367	GLY	39.6
1	E	293	ASN	39.6
1	K	380	ALA	39.6
1	K	215	GLN	39.5
1	G	308	ILE	39.5
1	I	339	GLY	39.5
1	C	192	LYS	39.4
1	I	298	THR	39.3
1	J	252	VAL	39.3
1	F	224	GLY	39.3
1	L	87	LEU	39.3
1	D	320	GLN	39.2
1	G	149	ALA	39.2
1	G	394	ALA	39.1
1	K	419	TYR	39.1
1	E	192	LYS	39.0
1	M	392	PRO	38.9
1	I	359	THR	38.9
1	B	231	SER	38.8
1	D	325	MET	38.8
1	C	409	GLY	38.8
1	G	402	LEU	38.7
1	A	319	GLY	38.7
1	C	231	SER	38.6
1	C	105	SER	38.6
1	H	420	THR	38.6
1	L	407	ARG	38.6
1	C	320	GLN	38.6
1	B	328	SER	38.5
1	A	399	LYS	38.5
1	H	206	TYR	38.5
1	B	83	ASP	38.4

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Mol	Chain	Res	Type	RSRZ
1	C	315	SER	38.3
1	K	307	SER	38.3
1	L	409	GLY	38.3
1	B	270	THR	38.2
1	M	151	ILE	38.2
1	M	267	ASP	38.1
1	M	239	SER	38.1
1	A	284	THR	38.1
1	D	402	LEU	38.0
1	A	408	LEU	37.9
1	A	415	PRO	37.9
1	C	166	VAL	37.8
1	M	341	ASN	37.7
1	F	299	ASN	37.7
1	M	217	SER	37.6
1	H	121	ASN	37.5
1	J	322	GLY	37.5
1	I	215	GLN	37.5
1	C	190	ASP	37.4
1	I	297	PRO	37.4
1	G	267	ASP	37.4
1	E	215	GLN	37.3
1	C	291	PRO	37.3
1	I	300	GLU	37.3
1	C	401	ILE	37.2
1	C	397	TYR	37.2
1	K	295	VAL	37.2
1	D	99	CYS	37.1
1	J	228	THR	37.1
1	L	431	ASP	37.1
1	L	323	ASP	37.0
1	B	337	ILE	37.0
1	D	80	TYR	36.8
1	M	379	LEU	36.8
1	J	229	LEU	36.8
1	E	268	GLY	36.8
1	L	356	ARG	36.7
1	M	334	ALA	36.7
1	K	135	GLU	36.7
1	G	275	ALA	36.7
1	K	273	THR	36.7
1	D	311	GLU	36.7

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Mol	Chain	Res	Type	RSRZ
1	L	266	PHE	36.7
1	A	407	ARG	36.7
1	G	285	GLY	36.6
1	H	93	PRO	36.6
1	K	382	ASN	36.6
1	E	226	THR	36.6
1	K	324	GLN	36.6
1	H	333	LEU	36.6
1	J	391	ASP	36.5
1	L	435	PRO	36.5
1	B	433	ASN	36.4
1	I	407	ARG	36.4
1	C	341	ASN	36.4
1	J	209	THR	36.4
1	J	375	PRO	36.4
1	E	123	THR	36.2
1	K	190	ASP	36.1
1	B	354	TYR	36.1
1	C	226	THR	36.1
1	H	88	THR	36.1
1	M	209	THR	36.1
1	I	216	PHE	36.0
1	J	223	GLY	36.0
1	B	248	PHE	36.0
1	A	251	SER	36.0
1	J	113	LEU	35.9
1	J	398	THR	35.9
1	A	334	ALA	35.8
1	M	295	VAL	35.8
1	M	407	ARG	35.8
1	L	197	CYS	35.7
1	H	345	ALA	35.7
1	I	214	TYR	35.7
1	L	145	MET	35.7
1	M	122	GLY	35.7
1	M	333	LEU	35.7
1	E	420	THR	35.6
1	G	227	ILE	35.6
1	M	391	ASP	35.6
1	D	396	ASN	35.6
1	A	186	ALA	35.5
1	G	420	THR	35.5

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Mol	Chain	Res	Type	RSRZ
1	E	121	ASN	35.5
1	I	330	ARG	35.5
1	G	81	LYS	35.4
1	E	422	PHE	35.4
1	L	308	ILE	35.4
1	G	307	SER	35.3
1	L	221	GLN	35.3
1	K	42	THR	35.3
1	D	223	GLY	35.3
1	G	85	MET	35.2
1	K	183	PRO	35.2
1	F	385	THR	35.2
1	L	440	GLY	35.2
1	I	187	ILE	35.1
1	D	265	GLY	35.1
1	K	112	THR	35.1
1	J	406	ASP	35.0
1	J	200	SER	35.0
1	C	379	LEU	35.0
1	J	311	GLU	35.0
1	F	417	ARG	35.0
1	I	284	THR	35.0
1	H	73	THR	35.0
1	L	406	ASP	35.0
1	I	290	MET	35.0
1	F	404	GLU	35.0
1	E	50	GLY	34.9
1	J	376	ASN	34.9
1	J	337	ILE	34.8
1	H	300	GLU	34.8
1	J	192	LYS	34.8
1	H	55	GLY	34.8
1	K	402	LEU	34.8
1	J	310	LEU	34.8
1	C	289	LEU	34.7
1	E	122	GLY	34.7
1	J	415	PRO	34.7
1	M	159	LEU	34.7
1	M	314	THR	34.7
1	E	290	MET	34.6
1	F	311	GLU	34.6
1	L	178	VAL	34.6

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Mol	Chain	Res	Type	RSRZ
1	G	280	ASN	34.6
1	K	367	GLY	34.6
1	J	86	LEU	34.6
1	F	213	ASP	34.6
1	L	415	PRO	34.6
1	D	48	THR	34.5
1	I	96	TYR	34.5
1	G	253	HIS	34.5
1	L	386	GLU	34.5
1	G	288	ASN	34.5
1	A	422	PHE	34.5
1	M	408	LEU	34.5
1	K	323	ASP	34.5
1	H	250	THR	34.4
1	L	106	LEU	34.4
1	K	313	VAL	34.4
1	G	435	PRO	34.3
1	M	419	TYR	34.3
1	D	228	THR	34.3
1	L	366	ALA	34.3
1	E	330	ARG	34.2
1	I	360	GLY	34.2
1	I	427	MET	34.2
1	E	246	LEU	34.2
1	B	408	LEU	34.2
1	G	79	ASN	34.2
1	C	386	GLU	34.1
1	H	35	LYS	34.1
1	G	228	THR	34.1
1	E	218	SER	34.1
1	M	293	ASN	34.1
1	M	393	GLY	34.0
1	H	363	VAL	34.0
1	A	126	ALA	34.0
1	A	232	ALA	34.0
1	C	69	GLY	34.0
1	G	311	GLU	34.0
1	G	241	SER	33.9
1	C	278	ALA	33.9
1	J	217	SER	33.9
1	I	392	PRO	33.9
1	A	48	THR	33.8

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Mol	Chain	Res	Type	RSRZ
1	K	206	TYR	33.8
1	D	78	GLY	33.8
1	G	328	SER	33.8
1	M	420	THR	33.8
1	J	188	GLY	33.7
1	G	269	THR	33.7
1	B	274	ARG	33.7
1	G	86	LEU	33.7
1	I	292	PHE	33.7
1	L	267	ASP	33.6
1	M	265	GLY	33.6
1	L	39	ARG	33.6
1	B	190	ASP	33.6
1	L	83	ASP	33.6
1	A	217	SER	33.6
1	D	284	THR	33.6
1	F	112	THR	33.6
1	L	218	SER	33.6
1	E	270	THR	33.5
1	M	294	LEU	33.5
1	B	216	PHE	33.5
1	D	215	GLN	33.5
1	K	428	GLU	33.5
1	D	328	SER	33.5
1	K	227	ILE	33.4
1	L	172	SER	33.4
1	A	252	VAL	33.4
1	H	385	THR	33.4
1	I	194	VAL	33.3
1	L	190	ASP	33.3
1	G	428	GLU	33.3
1	A	278	ALA	33.2
1	B	311	GLU	33.2
1	L	385	THR	33.2
1	D	340	GLY	33.2
1	B	265	GLY	33.2
1	B	255	LEU	33.1
1	D	253	HIS	33.1
1	A	247	VAL	33.1
1	G	68	VAL	33.1
1	C	313	VAL	33.1
1	L	357	VAL	33.0

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Mol	Chain	Res	Type	RSRZ
1	H	208	ILE	33.0
1	D	267	ASP	33.0
1	F	405	ARG	33.0
1	E	407	ARG	32.8
1	B	170	PRO	32.8
1	M	124	ILE	32.8
1	H	299	ASN	32.8
1	H	216	PHE	32.8
1	E	83	ASP	32.8
1	E	424	GLU	32.8
1	E	318	GLY	32.8
1	G	337	ILE	32.8
1	B	393	GLY	32.7
1	I	291	PRO	32.7
1	G	416	THR	32.7
1	J	137	THR	32.7
1	J	421	ASP	32.7
1	F	80	TYR	32.7
1	H	275	ALA	32.6
1	L	191	PRO	32.6
1	J	195	ALA	32.6
1	C	297	PRO	32.6
1	F	291	PRO	32.6
1	D	395	MET	32.6
1	K	240	LEU	32.6
1	F	406	ASP	32.5
1	J	392	PRO	32.5
1	A	192	LYS	32.5
1	D	357	VAL	32.5
1	B	397	TYR	32.5
1	G	83	ASP	32.5
1	G	49	VAL	32.5
1	M	326	SER	32.4
1	L	259	VAL	32.4
1	H	386	GLU	32.4
1	J	112	THR	32.3
1	B	336	THR	32.3
1	A	409	GLY	32.3
1	D	324	GLN	32.2
1	A	363	VAL	32.2
1	M	69	GLY	32.2
1	B	267	ASP	32.2

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Mol	Chain	Res	Type	RSRZ
1	L	381	LYS	32.2
1	M	204	ARG	32.2
1	D	250	THR	32.2
1	L	317	SER	32.2
1	E	79	ASN	32.1
1	G	431	ASP	32.1
1	F	241	SER	32.1
1	C	396	ASN	32.1
1	J	149	ALA	32.0
1	J	405	ARG	32.0
1	C	380	ALA	32.0
1	J	79	ASN	32.0
1	J	219	GLN	32.0
1	L	307	SER	32.0
1	M	156	GLY	32.0
1	K	322	GLY	32.0
1	E	345	ALA	32.0
1	F	321	ALA	32.0
1	K	338	HIS	31.9
1	A	336	THR	31.9
1	G	252	VAL	31.9
1	E	406	ASP	31.9
1	F	215	GLN	31.8
1	B	290	MET	31.8
1	I	166	VAL	31.8
1	J	183	PRO	31.8
1	C	406	ASP	31.8
1	G	82	PHE	31.8
1	F	320	GLN	31.8
1	I	205	VAL	31.8
1	H	284	THR	31.8
1	F	50	GLY	31.8
1	L	350	THR	31.8
1	C	362	VAL	31.7
1	K	396	ASN	31.7
1	A	404	GLU	31.7
1	I	423	ARG	31.7
1	A	130	GLN	31.7
1	C	399	LYS	31.7
1	L	326	SER	31.7
1	K	130	GLN	31.7
1	C	321	ALA	31.7

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Mol	Chain	Res	Type	RSRZ
1	C	225	VAL	31.7
1	I	405	ARG	31.7
1	M	337	ILE	31.7
1	G	405	ARG	31.7
1	H	42	THR	31.6
1	G	259	VAL	31.6
1	L	228	THR	31.6
1	G	415	PRO	31.6
1	L	298	THR	31.6
1	I	186	ALA	31.5
1	B	320	GLN	31.5
1	F	123	THR	31.5
1	A	362	VAL	31.5
1	L	286	THR	31.5
1	G	78	GLY	31.5
1	K	417	ARG	31.4
1	L	269	THR	31.4
1	C	99	CYS	31.4
1	D	427	MET	31.4
1	H	269	THR	31.3
1	I	185	PRO	31.3
1	G	329	ALA	31.3
1	H	313	VAL	31.3
1	G	35	LYS	31.3
1	B	381	LYS	31.3
1	C	309	LYS	31.3
1	K	153	ASP	31.3
1	L	325	MET	31.3
1	G	375	PRO	31.3
1	M	186	ALA	31.3
1	F	196	THR	31.3
1	K	337	ILE	31.3
1	K	284	THR	31.3
1	D	385	THR	31.3
1	A	265	GLY	31.3
1	C	210	ALA	31.2
1	K	232	ALA	31.2
1	G	246	LEU	31.2
1	M	140	SER	31.2
1	M	313	VAL	31.2
1	F	208	ILE	31.2
1	A	288	ASN	31.2

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Mol	Chain	Res	Type	RSRZ
1	F	16	ARG	31.1
1	I	289	LEU	31.1
1	J	19	LEU	31.1
1	J	293	ASN	31.1
1	K	252	VAL	31.1
1	G	315	SER	31.1
1	G	399	LYS	31.1
1	M	98	TYR	31.1
1	M	59	PHE	31.1
1	E	300	GLU	31.1
1	F	418	GLU	31.0
1	L	260	THR	31.0
1	F	336	THR	31.0
1	D	392	PRO	31.0
1	F	52	THR	31.0
1	D	52	THR	31.0
1	A	262	TYR	31.0
1	B	314	THR	31.0
1	F	295	VAL	31.0
1	E	408	LEU	30.9
1	D	274	ARG	30.9
1	A	405	ARG	30.9
1	F	377	PRO	30.9
1	L	192	LYS	30.9
1	F	192	LYS	30.9
1	G	316	LYS	30.9
1	M	150	ASN	30.8
1	L	362	VAL	30.8
1	G	336	THR	30.8
1	D	119	ALA	30.8
1	L	53	GLY	30.8
1	A	300	GLU	30.7
1	H	297	PRO	30.7
1	K	296	ILE	30.7
1	G	70	ALA	30.7
1	G	404	GLU	30.7
1	I	15	ILE	30.7
1	M	222	PRO	30.7
1	I	404	GLU	30.7
1	M	120	LEU	30.7
1	K	421	ASP	30.6
1	B	386	GLU	30.6

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Mol	Chain	Res	Type	RSRZ
1	E	381	LYS	30.6
1	C	422	PHE	30.6
1	M	324	GLN	30.6
1	H	248	PHE	30.6
1	J	213	ASP	30.6
1	J	324	GLN	30.6
1	L	379	LEU	30.6
1	D	339	GLY	30.5
1	J	340	GLY	30.5
1	I	64	PRO	30.5
1	M	203	PRO	30.5
1	E	274	ARG	30.5
1	G	107	THR	30.5
1	H	397	TYR	30.5
1	J	428	GLU	30.5
1	B	50	GLY	30.5
1	H	291	PRO	30.5
1	G	204	ARG	30.5
1	K	217	SER	30.5
1	K	191	PRO	30.5
1	H	197	CYS	30.5
1	C	322	GLY	30.5
1	H	240	LEU	30.5
1	F	298	THR	30.4
1	I	391	ASP	30.4
1	K	266	PHE	30.4
1	L	419	TYR	30.4
1	E	326	SER	30.4
1	M	360	GLY	30.4
1	I	152	ASN	30.4
1	D	256	VAL	30.3
1	I	315	SER	30.3
1	F	306	THR	30.3
1	J	267	ASP	30.3
1	G	202	ARG	30.3
1	C	367	GLY	30.3
1	J	221	GLN	30.3
1	H	394	ALA	30.3
1	I	160	VAL	30.3
1	I	375	PRO	30.3
1	G	434	SER	30.2
1	D	213	ASP	30.2

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Mol	Chain	Res	Type	RSRZ
1	I	244	GLY	30.2
1	K	400	LEU	30.2
1	D	37	THR	30.2
1	J	336	THR	30.2
1	J	40	SER	30.2
1	F	36	HIS	30.2
1	K	316	LYS	30.2
1	C	286	THR	30.2
1	J	35	LYS	30.2
1	L	418	GLU	30.2
1	B	146	SER	30.2
1	H	270	THR	30.2
1	I	267	ASP	30.2
1	L	210	ALA	30.1
1	M	397	TYR	30.1
1	D	36	HIS	30.1
1	A	163	GLY	30.1
1	D	290	MET	30.1
1	K	339	GLY	30.1
1	A	392	PRO	30.1
1	B	334	ALA	30.0
1	B	203	PRO	30.0
1	I	79	ASN	30.0
1	L	166	VAL	30.0
1	J	302	THR	30.0
1	J	329	ALA	30.0
1	M	245	GLU	30.0
1	F	296	ILE	30.0
1	C	311	GLU	30.0
1	A	350	THR	30.0
1	M	315	SER	30.0
1	L	250	THR	29.9
1	K	226	THR	29.9
1	L	47	LEU	29.9
1	C	279	ASN	29.9
1	H	80	TYR	29.9
1	K	196	THR	29.9
1	C	364	THR	29.9
1	H	230	PHE	29.8
1	I	311	GLU	29.8
1	E	73	THR	29.8
1	A	299	ASN	29.8

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Mol	Chain	Res	Type	RSRZ
1	F	407	ARG	29.8
1	M	339	GLY	29.8
1	K	381	LYS	29.7
1	K	341	ASN	29.7
1	C	112	THR	29.7
1	M	376	ASN	29.7
1	G	98	TYR	29.7
1	K	184	ILE	29.7
1	D	59	PHE	29.7
1	H	47	LEU	29.7
1	J	83	ASP	29.7
1	L	14	PHE	29.7
1	F	209	THR	29.7
1	K	205	VAL	29.6
1	F	340	GLY	29.6
1	L	42	THR	29.6
1	H	247	VAL	29.6
1	K	269	THR	29.6
1	L	297	PRO	29.6
1	D	391	ASP	29.6
1	F	47	LEU	29.6
1	M	362	VAL	29.6
1	C	251	SER	29.6
1	D	254	GLY	29.6
1	G	214	TYR	29.6
1	K	192	LYS	29.6
1	I	209	THR	29.5
1	J	212	ASP	29.5
1	B	313	VAL	29.5
1	C	250	THR	29.5
1	B	316	LYS	29.5
1	I	353	ALA	29.5
1	H	149	ALA	29.5
1	B	171	THR	29.5
1	H	253	HIS	29.5
1	B	395	MET	29.4
1	B	35	LYS	29.4
1	F	376	ASN	29.4
1	G	356	ARG	29.4
1	J	216	PHE	29.4
1	F	347	ARG	29.4
1	D	187	ILE	29.4

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Mol	Chain	Res	Type	RSRZ
1	L	121	ASN	29.4
1	K	422	PHE	29.3
1	A	89	ALA	29.3
1	A	322	GLY	29.3
1	F	255	LEU	29.3
1	C	387	TYR	29.3
1	G	321	ALA	29.3
1	J	184	ILE	29.3
1	C	323	ASP	29.3
1	E	273	THR	29.3
1	H	41	GLU	29.3
1	B	407	ARG	29.3
1	B	272	ILE	29.3
1	H	264	ILE	29.3
1	H	314	THR	29.3
1	E	203	PRO	29.3
1	M	320	GLN	29.3
1	C	130	GLN	29.3
1	D	273	THR	29.3
1	K	216	PHE	29.3
1	A	110	SER	29.2
1	F	111	SER	29.2
1	J	82	PHE	29.2
1	F	337	ILE	29.2
1	B	284	THR	29.2
1	C	116	GLY	29.2
1	G	188	GLY	29.2
1	E	140	SER	29.2
1	C	336	THR	29.2
1	K	398	THR	29.1
1	A	176	GLY	29.1
1	B	226	THR	29.1
1	G	427	MET	29.1
1	B	112	THR	29.1
1	L	165	THR	29.1
1	G	397	TYR	29.1
1	M	252	VAL	29.1
1	G	396	ASN	29.1
1	E	396	ASN	29.1
1	D	361	SER	29.0
1	A	83	ASP	29.0
1	L	216	PHE	29.0

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Mol	Chain	Res	Type	RSRZ
1	H	39	ARG	29.0
1	D	53	GLY	29.0
1	B	406	ASP	29.0
1	C	258	GLY	29.0
1	B	341	ASN	29.0
1	C	268	GLY	29.0
1	B	322	GLY	29.0
1	L	318	GLY	28.9
1	C	265	GLY	28.9
1	A	331	GLY	28.9
1	H	123	THR	28.9
1	A	173	TYR	28.9
1	H	416	THR	28.9
1	A	264	ILE	28.9
1	G	289	LEU	28.9
1	I	378	GLU	28.9
1	K	317	SER	28.9
1	L	94	ALA	28.9
1	L	20	MET	28.9
1	B	400	LEU	28.8
1	L	111	SER	28.8
1	E	329	ALA	28.8
1	H	342	TYR	28.8
1	J	18	LEU	28.8
1	A	317	SER	28.8
1	E	328	SER	28.8
1	D	373	LEU	28.8
1	J	245	GLU	28.8
1	L	43	SER	28.7
1	I	421	ASP	28.7
1	B	434	SER	28.7
1	C	247	VAL	28.7
1	E	253	HIS	28.7
1	G	247	VAL	28.7
1	C	224	GLY	28.7
1	E	416	THR	28.7
1	C	244	GLY	28.7
1	I	183	PRO	28.7
1	J	84	GLN	28.7
1	J	259	VAL	28.7
1	D	262	TYR	28.7
1	H	260	THR	28.7

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Mol	Chain	Res	Type	RSRZ
1	D	231	SER	28.7
1	G	302	THR	28.7
1	M	246	LEU	28.7
1	F	360	GLY	28.7
1	A	77	ASN	28.6
1	M	299	ASN	28.6
1	B	123	THR	28.6
1	K	350	THR	28.6
1	H	382	ASN	28.6
1	G	244	GLY	28.6
1	I	203	PRO	28.6
1	J	74	LEU	28.6
1	J	334	ALA	28.6
1	F	216	PHE	28.5
1	K	149	ALA	28.5
1	L	258	GLY	28.5
1	H	244	GLY	28.5
1	B	185	PRO	28.5
1	L	246	LEU	28.5
1	I	176	GLY	28.4
1	J	291	PRO	28.4
1	H	327	TRP	28.4
1	G	94	ALA	28.4
1	L	441	ALA	28.4
1	C	15	ILE	28.4
1	F	396	ASN	28.4
1	C	300	GLU	28.4
1	H	404	GLU	28.4
1	M	316	LYS	28.4
1	E	222	PRO	28.4
1	K	370	ASN	28.4
1	C	413	VAL	28.3
1	D	194	VAL	28.3
1	J	298	THR	28.3
1	C	154	LYS	28.3
1	J	15	ILE	28.3
1	H	421	ASP	28.3
1	E	265	GLY	28.3
1	G	262	TYR	28.3
1	K	171	THR	28.3
1	F	341	ASN	28.3
1	M	336	THR	28.3

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Mol	Chain	Res	Type	RSRZ
1	E	317	SER	28.2
1	K	327	TRP	28.2
1	J	233	ASN	28.2
1	K	179	ARG	28.2
1	E	244	GLY	28.2
1	M	241	SER	28.2
1	I	341	ASN	28.2
1	E	231	SER	28.2
1	A	208	ILE	28.2
1	D	46	ASN	28.2
1	H	377	PRO	28.2
1	I	196	THR	28.2
1	K	247	VAL	28.2
1	G	395	MET	28.2
1	I	46	ASN	28.2
1	A	121	ASN	28.1
1	I	92	LEU	28.1
1	E	418	GLU	28.1
1	I	165	THR	28.1
1	E	245	GLU	28.1
1	A	171	THR	28.1
1	B	329	ALA	28.1
1	I	320	GLN	28.1
1	F	307	SER	28.1
1	M	54	SER	28.1
1	F	334	ALA	28.1
1	M	191	PRO	28.0
1	C	400	LEU	28.0
1	D	196	THR	28.0
1	H	255	LEU	28.0
1	I	343	PRO	28.0
1	K	248	PHE	28.0
1	I	71	HIS	28.0
1	C	123	THR	28.0
1	B	251	SER	28.0
1	I	326	SER	28.0
1	I	327	TRP	28.0
1	E	94	ALA	28.0
1	G	320	GLN	28.0
1	A	256	VAL	27.9
1	L	295	VAL	27.9
1	A	341	ASN	27.9

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Mol	Chain	Res	Type	RSRZ
1	K	96	TYR	27.9
1	C	49	VAL	27.9
1	I	342	TYR	27.9
1	B	73	THR	27.9
1	M	409	GLY	27.9
1	L	261	ILE	27.9
1	C	189	LEU	27.9
1	A	207	THR	27.9
1	J	379	LEU	27.9
1	H	189	LEU	27.8
1	M	359	THR	27.8
1	A	231	SER	27.8
1	E	160	VAL	27.8
1	D	50	GLY	27.8
1	F	251	SER	27.8
1	H	202	ARG	27.8
1	H	120	LEU	27.8
1	G	226	THR	27.8
1	M	251	SER	27.8
1	B	230	PHE	27.8
1	I	362	VAL	27.8
1	C	158	VAL	27.8
1	A	164	VAL	27.8
1	C	254	GLY	27.8
1	D	247	VAL	27.7
1	J	253	HIS	27.7
1	C	416	THR	27.7
1	L	320	GLN	27.7
1	B	376	ASN	27.7
1	G	196	THR	27.7
1	I	14	PHE	27.7
1	A	98	TYR	27.7
1	C	239	SER	27.7
1	F	331	GLY	27.7
1	H	188	GLY	27.7
1	G	200	SER	27.7
1	J	218	SER	27.7
1	K	51	ASP	27.7
1	A	352	VAL	27.7
1	C	284	THR	27.7
1	D	393	GLY	27.7
1	D	332	SER	27.7

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Mol	Chain	Res	Type	RSRZ
1	H	16	ARG	27.6
1	L	436	LEU	27.6
1	B	81	LYS	27.6
1	F	37	THR	27.6
1	D	35	LYS	27.6
1	I	200	SER	27.6
1	B	202	ARG	27.6
1	D	249	ARG	27.6
1	H	378	GLU	27.6
1	F	231	SER	27.6
1	A	357	VAL	27.6
1	E	429	VAL	27.6
1	F	318	GLY	27.6
1	B	157	ASN	27.6
1	J	69	GLY	27.6
1	C	128	THR	27.6
1	M	93	PRO	27.6
1	K	233	ASN	27.5
1	K	326	SER	27.5
1	D	299	ASN	27.5
1	A	302	THR	27.5
1	F	203	PRO	27.5
1	H	415	PRO	27.5
1	E	80	TYR	27.5
1	D	400	LEU	27.5
1	E	217	SER	27.5
1	D	246	LEU	27.5
1	H	323	ASP	27.4
1	H	36	HIS	27.4
1	B	340	GLY	27.4
1	L	57	ILE	27.4
1	E	302	THR	27.4
1	E	53	GLY	27.4
1	A	307	SER	27.4
1	L	300	GLU	27.4
1	A	287	ASP	27.4
1	I	425	TYR	27.4
1	C	208	ILE	27.4
1	A	257	LEU	27.4
1	F	326	SER	27.4
1	B	33	LEU	27.4
1	C	415	PRO	27.4

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Mol	Chain	Res	Type	RSRZ
1	I	416	THR	27.4
1	E	240	LEU	27.3
1	D	245	GLU	27.3
1	L	384	VAL	27.3
1	K	404	GLU	27.3
1	H	319	GLY	27.3
1	B	315	SER	27.3
1	F	343	PRO	27.3
1	M	240	LEU	27.3
1	G	433	ASN	27.3
1	B	115	GLY	27.2
1	C	245	GLU	27.2
1	F	314	THR	27.2
1	H	229	LEU	27.1
1	C	392	PRO	27.1
1	G	290	MET	27.1
1	L	310	LEU	27.1
1	L	135	GLU	27.1
1	H	401	ILE	27.1
1	B	140	SER	27.1
1	A	351	LEU	27.1
1	E	241	SER	27.0
1	H	318	GLY	27.0
1	J	55	GLY	27.0
1	J	203	PRO	27.0
1	B	233	ASN	27.0
1	H	336	THR	27.0
1	K	123	THR	27.0
1	F	322	GLY	27.0
1	G	243	GLY	27.0
1	B	330	ARG	27.0
1	K	318	GLY	27.0
1	H	196	THR	27.0
1	J	80	TYR	27.0
1	J	244	GLY	27.0
1	A	355	GLU	27.0
1	G	69	GLY	27.0
1	C	385	THR	26.9
1	B	142	ASN	26.9
1	K	306	THR	26.9
1	H	417	ARG	26.9
1	L	270	THR	26.9

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Mol	Chain	Res	Type	RSRZ
1	K	35	LYS	26.9
1	C	375	PRO	26.9
1	B	300	GLU	26.9
1	H	59	PHE	26.9
1	J	246	LEU	26.9
1	H	90	GLN	26.8
1	F	83	ASP	26.8
1	M	292	PHE	26.8
1	A	250	THR	26.8
1	H	320	GLN	26.8
1	J	155	ILE	26.8
1	B	98	TYR	26.7
1	H	191	PRO	26.7
1	C	131	GLY	26.7
1	C	344	GLY	26.7
1	M	224	GLY	26.7
1	F	325	MET	26.7
1	I	399	LYS	26.7
1	J	56	LEU	26.7
1	A	73	THR	26.7
1	L	316	LYS	26.7
1	A	226	THR	26.7
1	H	273	THR	26.7
1	H	283	THR	26.6
1	A	395	MET	26.6
1	D	123	THR	26.6
1	F	207	THR	26.6
1	G	219	GLN	26.6
1	E	54	SER	26.6
1	L	233	ASN	26.6
1	G	279	ASN	26.6
1	D	232	ALA	26.5
1	K	218	SER	26.5
1	L	200	SER	26.5
1	M	138	ASP	26.5
1	G	300	GLU	26.5
1	E	295	VAL	26.5
1	A	398	THR	26.5
1	L	428	GLU	26.5
1	B	317	SER	26.5
1	A	249	ARG	26.5
1	J	317	SER	26.5

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Mol	Chain	Res	Type	RSRZ
1	B	306	THR	26.5
1	D	306	THR	26.5
1	G	183	PRO	26.5
1	D	394	ALA	26.5
1	J	407	ARG	26.5
1	I	417	ARG	26.4
1	D	159	LEU	26.4
1	G	309	LYS	26.4
1	D	355	GLU	26.4
1	I	379	LEU	26.4
1	J	364	THR	26.4
1	D	94	ALA	26.4
1	F	354	TYR	26.4
1	F	73	THR	26.4
1	I	98	TYR	26.4
1	J	381	LYS	26.4
1	G	212	ASP	26.3
1	L	311	GLU	26.3
1	D	316	LYS	26.3
1	B	219	GLN	26.3
1	K	369	SER	26.3
1	F	76	GLY	26.3
1	L	184	ILE	26.3
1	A	335	VAL	26.3
1	K	424	GLU	26.3
1	G	339	GLY	26.3
1	I	286	THR	26.3
1	D	281	GLY	26.3
1	D	412	THR	26.3
1	F	359	THR	26.3
1	E	289	LEU	26.3
1	A	172	SER	26.3
1	C	356	ARG	26.3
1	M	355	GLU	26.3
1	F	15	ILE	26.3
1	E	430	ALA	26.3
1	H	54	SER	26.2
1	G	319	GLY	26.2
1	K	285	GLY	26.2
1	K	391	ASP	26.2
1	A	279	ASN	26.2
1	J	390	PHE	26.2

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Mol	Chain	Res	Type	RSRZ
1	G	432	LEU	26.2
1	C	202	ARG	26.2
1	C	308	ILE	26.2
1	D	264	ILE	26.2
1	L	348	PRO	26.2
1	C	248	PHE	26.2
1	C	272	ILE	26.2
1	C	378	GLU	26.2
1	M	380	ALA	26.1
1	D	322	GLY	26.1
1	H	249	ARG	26.1
1	L	15	ILE	26.1
1	G	73	THR	26.1
1	F	206	TYR	26.1
1	L	264	ILE	26.1
1	H	422	PHE	26.1
1	J	307	SER	26.1
1	K	427	MET	26.1
1	F	338	HIS	26.1
1	K	224	GLY	26.1
1	A	397	TYR	26.1
1	I	268	GLY	26.1
1	B	344	GLY	26.1
1	A	209	THR	26.1
1	C	137	THR	26.1
1	E	224	GLY	26.1
1	E	159	LEU	26.1
1	I	308	ILE	26.1
1	G	257	LEU	26.0
1	G	364	THR	26.0
1	H	381	LYS	26.0
1	K	410	ILE	26.0
1	H	233	ASN	26.0
1	E	333	LEU	26.0
1	G	406	ASP	26.0
1	J	230	PHE	26.0
1	G	53	GLY	26.0
1	I	192	LYS	26.0
1	L	254	GLY	26.0
1	A	177	TYR	26.0
1	L	224	GLY	26.0
1	J	187	ILE	26.0

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Mol	Chain	Res	Type	RSRZ
1	K	244	GLY	26.0
1	G	84	GLN	26.0
1	J	402	LEU	26.0
1	B	264	ILE	26.0
1	I	57	ILE	26.0
1	L	226	THR	26.0
1	A	99	CYS	26.0
1	F	293	ASN	25.9
1	G	90	GLN	25.9
1	F	93	PRO	25.9
1	K	399	LYS	25.9
1	M	418	GLU	25.9
1	H	391	ASP	25.9
1	G	91	ASN	25.9
1	L	164	VAL	25.9
1	M	158	VAL	25.9
1	I	376	ASN	25.9
1	C	343	PRO	25.9
1	E	415	PRO	25.9
1	B	188	GLY	25.9
1	K	288	ASN	25.9
1	G	170	PRO	25.9
1	F	54	SER	25.9
1	H	280	ASN	25.9
1	E	48	THR	25.9
1	M	258	GLY	25.8
1	K	178	VAL	25.8
1	I	47	LEU	25.8
1	K	401	ILE	25.8
1	L	265	GLY	25.8
1	I	83	ASP	25.8
1	A	316	LYS	25.8
1	K	328	SER	25.8
1	I	70	ALA	25.8
1	L	46	ASN	25.8
1	D	433	ASN	25.8
1	M	357	VAL	25.8
1	K	166	VAL	25.8
1	C	390	PHE	25.8
1	I	230	PHE	25.8
1	F	358	ALA	25.8
1	I	61	PRO	25.8

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Mol	Chain	Res	Type	RSRZ
1	I	85	MET	25.8
1	K	121	ASN	25.7
1	J	258	GLY	25.7
1	H	46	ASN	25.7
1	I	226	THR	25.7
1	K	287	ASP	25.7
1	L	369	SER	25.7
1	A	224	GLY	25.7
1	H	387	TYR	25.6
1	L	234	ILE	25.6
1	M	311	GLU	25.6
1	J	366	ALA	25.6
1	L	403	SER	25.6
1	L	13	PRO	25.6
1	A	203	PRO	25.6
1	D	318	GLY	25.6
1	C	172	SER	25.6
1	D	344	GLY	25.6
1	D	323	ASP	25.6
1	L	327	TRP	25.6
1	F	212	ASP	25.6
1	M	119	ALA	25.6
1	C	52	THR	25.6
1	G	121	ASN	25.6
1	B	268	GLY	25.6
1	G	357	VAL	25.6
1	K	39	ARG	25.6
1	H	187	ILE	25.6
1	H	112	THR	25.6
1	C	171	THR	25.5
1	K	378	GLU	25.5
1	F	240	LEU	25.5
1	G	348	PRO	25.5
1	K	129	PHE	25.5
1	F	96	TYR	25.5
1	B	415	PRO	25.5
1	J	393	GLY	25.5
1	D	261	ILE	25.5
1	E	428	GLU	25.5
1	C	335	VAL	25.5
1	C	163	GLY	25.5
1	C	167	LEU	25.5

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Mol	Chain	Res	Type	RSRZ
1	B	215	GLN	25.5
1	F	92	LEU	25.5
1	M	157	ASN	25.5
1	G	268	GLY	25.5
1	G	201	ASP	25.4
1	M	52	THR	25.4
1	I	283	THR	25.4
1	J	308	ILE	25.4
1	A	245	GLU	25.4
1	K	160	VAL	25.4
1	F	245	GLU	25.4
1	B	269	THR	25.4
1	F	274	ARG	25.4
1	M	125	ASN	25.4
1	D	221	GLN	25.4
1	G	164	VAL	25.4
1	F	329	ALA	25.4
1	I	43	SER	25.4
1	H	364	THR	25.4
1	L	280	ASN	25.4
1	I	76	GLY	25.3
1	G	92	LEU	25.3
1	C	36	HIS	25.3
1	L	168	SER	25.3
1	E	378	GLU	25.3
1	H	311	GLU	25.3
1	B	72	TYR	25.3
1	J	335	VAL	25.3
1	G	57	ILE	25.3
1	I	159	LEU	25.3
1	F	330	ARG	25.3
1	H	82	PHE	25.3
1	G	324	GLN	25.3
1	K	204	ARG	25.3
1	C	165	THR	25.3
1	C	203	PRO	25.2
1	A	376	ASN	25.2
1	D	327	TRP	25.2
1	K	263	LEU	25.2
1	G	424	GLU	25.2
1	E	354	TYR	25.2
1	H	254	GLY	25.2

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Mol	Chain	Res	Type	RSRZ
1	L	173	TYR	25.2
1	A	270	THR	25.2
1	H	37	THR	25.2
1	E	291	PRO	25.2
1	E	316	LYS	25.2
1	A	420	THR	25.2
1	B	307	SER	25.2
1	B	254	GLY	25.1
1	L	55	GLY	25.1
1	B	206	TYR	25.1
1	I	107	THR	25.1
1	M	284	THR	25.1
1	C	153	ASP	25.1
1	A	268	GLY	25.1
1	I	48	THR	25.1
1	D	203	PRO	25.1
1	D	343	PRO	25.1
1	I	318	GLY	25.1
1	E	340	GLY	25.0
1	D	386	GLU	25.0
1	I	269	THR	25.0
1	J	202	ARG	25.0
1	J	130	GLN	25.0
1	G	265	GLY	25.0
1	B	52	THR	25.0
1	M	350	THR	25.0
1	C	152	ASN	25.0
1	A	337	ILE	25.0
1	M	356	ARG	25.0
1	B	377	PRO	24.9
1	D	115	GLY	24.9
1	E	288	ASN	24.9
1	C	383	LEU	24.9
1	D	90	GLN	24.9
1	D	190	ASP	24.9
1	B	121	ASN	24.9
1	J	278	ALA	24.9
1	E	395	MET	24.9
1	I	252	VAL	24.9
1	E	400	LEU	24.9
1	D	312	ILE	24.9
1	J	85	MET	24.9

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Mol	Chain	Res	Type	RSRZ
1	M	286	THR	24.9
1	D	337	ILE	24.8
1	L	336	THR	24.8
1	K	131	GLY	24.8
1	F	98	TYR	24.8
1	L	268	GLY	24.8
1	C	373	LEU	24.8
1	B	250	THR	24.8
1	K	395	MET	24.8
1	B	339	GLY	24.8
1	L	110	SER	24.8
1	F	190	ASP	24.8
1	J	326	SER	24.8
1	E	112	THR	24.8
1	J	61	PRO	24.8
1	D	278	ALA	24.8
1	A	411	LYS	24.8
1	B	359	THR	24.8
1	B	244	GLY	24.8
1	E	252	VAL	24.8
1	H	91	ASN	24.8
1	J	362	VAL	24.7
1	G	165	THR	24.7
1	H	409	GLY	24.7
1	M	279	ASN	24.7
1	B	280	ASN	24.7
1	L	128	THR	24.7
1	C	186	ALA	24.7
1	J	226	THR	24.7
1	K	291	PRO	24.7
1	B	239	SER	24.7
1	I	119	ALA	24.7
1	B	392	PRO	24.7
1	F	335	VAL	24.7
1	L	215	GLN	24.7
1	E	331	GLY	24.7
1	F	161	GLY	24.7
1	H	268	GLY	24.7
1	F	55	GLY	24.7
1	I	294	LEU	24.7
1	B	256	VAL	24.7
1	F	77	ASN	24.7

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Mol	Chain	Res	Type	RSRZ
1	C	106	LEU	24.7
1	F	397	TYR	24.7
1	J	96	TYR	24.6
1	A	97	ASN	24.6
1	M	268	GLY	24.6
1	B	184	ILE	24.6
1	C	376	ASN	24.6
1	I	251	SER	24.6
1	G	240	LEU	24.6
1	K	426	PHE	24.6
1	D	40	SER	24.6
1	J	75	GLN	24.6
1	I	377	PRO	24.6
1	A	150	ASN	24.6
1	F	116	GLY	24.6
1	H	326	SER	24.6
1	G	122	GLY	24.6
1	M	208	ILE	24.5
1	C	331	GLY	24.5
1	A	51	ASP	24.5
1	H	289	LEU	24.5
1	H	228	THR	24.5
1	K	97	ASN	24.5
1	D	291	PRO	24.5
1	M	96	TYR	24.5
1	M	121	ASN	24.5
1	B	275	ALA	24.5
1	E	385	THR	24.5
1	L	236	ALA	24.5
1	G	430	ALA	24.5
1	G	16	ARG	24.5
1	A	343	PRO	24.5
1	L	195	ALA	24.5
1	G	233	ASN	24.5
1	E	417	ARG	24.4
1	A	140	SER	24.4
1	C	68	VAL	24.4
1	M	88	THR	24.4
1	M	416	THR	24.4
1	I	124	ILE	24.4
1	G	88	THR	24.4
1	J	197	CYS	24.4

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Mol	Chain	Res	Type	RSRZ
1	D	378	GLU	24.4
1	E	260	THR	24.4
1	B	116	GLY	24.4
1	K	366	ALA	24.4
1	J	194	VAL	24.4
1	E	359	THR	24.4
1	G	260	THR	24.4
1	D	224	GLY	24.4
1	H	355	GLU	24.4
1	A	34	GLU	24.3
1	H	81	LYS	24.3
1	E	225	VAL	24.3
1	E	292	PHE	24.3
1	J	78	GLY	24.3
1	F	226	THR	24.3
1	M	250	THR	24.3
1	A	143	GLY	24.3
1	L	35	LYS	24.3
1	J	342	TYR	24.3
1	E	78	GLY	24.3
1	C	332	SER	24.3
1	I	307	SER	24.3
1	I	309	LYS	24.3
1	C	164	VAL	24.3
1	K	142	ASN	24.3
1	B	347	ARG	24.3
1	L	130	GLN	24.3
1	A	80	TYR	24.3
1	C	437	LYS	24.3
1	G	398	THR	24.3
1	D	195	ALA	24.2
1	D	404	GLU	24.2
1	K	169	LEU	24.2
1	C	407	ARG	24.2
1	G	258	GLY	24.2
1	H	259	VAL	24.2
1	D	347	ARG	24.2
1	F	222	PRO	24.2
1	E	431	ASP	24.2
1	J	105	SER	24.2
1	I	279	ASN	24.2
1	D	210	ALA	24.2

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Mol	Chain	Res	Type	RSRZ
1	F	386	GLU	24.2
1	K	385	THR	24.2
1	I	390	PHE	24.2
1	L	179	ARG	24.2
1	G	15	ILE	24.1
1	K	255	LEU	24.1
1	C	318	GLY	24.1
1	M	135	GLU	24.1
1	H	335	VAL	24.1
1	M	91	ASN	24.1
1	I	323	ASP	24.1
1	F	79	ASN	24.1
1	K	185	PRO	24.1
1	M	304	PRO	24.1
1	C	372	GLU	24.1
1	H	218	SER	24.1
1	M	375	PRO	24.1
1	B	364	THR	24.1
1	L	223	GLY	24.1
1	M	247	VAL	24.1
1	I	374	ILE	24.1
1	D	226	THR	24.1
1	I	418	GLU	24.1
1	C	61	PRO	24.1
1	J	156	GLY	24.0
1	M	228	THR	24.0
1	C	298	THR	24.0
1	B	131	GLY	24.0
1	E	425	TYR	24.0
1	E	161	GLY	24.0
1	G	250	THR	24.0
1	E	93	PRO	24.0
1	D	116	GLY	24.0
1	A	76	GLY	24.0
1	K	162	GLU	24.0
1	J	387	TYR	24.0
1	G	361	SER	24.0
1	G	192	LYS	24.0
1	L	253	HIS	24.0
1	F	380	ALA	24.0
1	L	107	THR	24.0
1	A	267	ASP	24.0

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Mol	Chain	Res	Type	RSRZ
1	D	279	ASN	23.9
1	B	100	ARG	23.9
1	H	87	LEU	23.9
1	G	77	ASN	23.9
1	M	302	THR	23.9
1	B	431	ASP	23.9
1	K	136	LEU	23.9
1	D	354	TYR	23.9
1	E	84	GLN	23.9
1	K	71	HIS	23.9
1	G	379	LEU	23.9
1	L	73	THR	23.9
1	B	304	PRO	23.9
1	K	268	GLY	23.9
1	G	222	PRO	23.9
1	K	265	GLY	23.9
1	L	119	ALA	23.9
1	L	284	THR	23.9
1	J	338	HIS	23.9
1	C	431	ASP	23.8
1	F	114	PRO	23.8
1	A	240	LEU	23.8
1	H	221	GLN	23.8
1	G	287	ASP	23.8
1	A	353	ALA	23.8
1	B	152	ASN	23.8
1	D	317	SER	23.8
1	M	178	VAL	23.8
1	H	108	VAL	23.8
1	I	207	THR	23.8
1	I	16	ARG	23.8
1	M	399	LYS	23.8
1	A	206	TYR	23.8
1	E	209	THR	23.8
1	L	434	SER	23.7
1	E	157	ASN	23.7
1	M	171	THR	23.7
1	F	20	MET	23.7
1	B	285	GLY	23.7
1	G	119	ALA	23.7
1	I	135	GLU	23.7
1	K	407	ARG	23.7

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Mol	Chain	Res	Type	RSRZ
1	M	179	ARG	23.7
1	F	131	GLY	23.7
1	H	405	ARG	23.7
1	A	178	VAL	23.7
1	H	337	ILE	23.7
1	J	179	ARG	23.7
1	J	416	THR	23.7
1	H	43	SER	23.7
1	D	436	LEU	23.7
1	D	266	PHE	23.7
1	K	393	GLY	23.7
1	I	413	VAL	23.7
1	D	263	LEU	23.7
1	H	246	LEU	23.7
1	F	202	ARG	23.7
1	A	158	VAL	23.7
1	A	141	TYR	23.7
1	F	273	THR	23.7
1	F	191	PRO	23.7
1	A	364	THR	23.7
1	H	110	SER	23.6
1	I	331	GLY	23.6
1	F	333	LEU	23.6
1	B	183	PRO	23.6
1	L	393	GLY	23.6
1	C	377	PRO	23.6
1	K	283	THR	23.6
1	E	47	LEU	23.6
1	L	304	PRO	23.6
1	A	356	ARG	23.6
1	E	380	ALA	23.6
1	H	331	GLY	23.6
1	G	274	ARG	23.6
1	I	254	GLY	23.6
1	H	94	ALA	23.6
1	L	40	SER	23.6
1	A	131	GLY	23.6
1	C	78	GLY	23.6
1	B	245	GLU	23.6
1	B	205	VAL	23.6
1	K	415	PRO	23.6
1	D	270	THR	23.6

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Mol	Chain	Res	Type	RSRZ
1	H	334	ALA	23.5
1	J	268	GLY	23.5
1	I	316	LYS	23.5
1	H	287	ASP	23.5
1	M	338	HIS	23.5
1	M	29	PRO	23.5
1	G	171	THR	23.5
1	J	318	GLY	23.5
1	I	317	SER	23.5
1	D	207	THR	23.5
1	L	229	LEU	23.5
1	K	336	THR	23.5
1	D	348	PRO	23.5
1	H	322	GLY	23.5
1	F	244	GLY	23.5
1	H	52	THR	23.5
1	L	212	ASP	23.5
1	B	342	TYR	23.5
1	E	162	GLU	23.5
1	M	262	TYR	23.5
1	J	261	ILE	23.5
1	L	404	GLU	23.5
1	I	287	ASP	23.5
1	K	152	ASN	23.5
1	J	199	SER	23.5
1	F	110	SER	23.4
1	I	306	THR	23.4
1	H	312	ILE	23.4
1	B	247	VAL	23.4
1	D	79	ASN	23.4
1	C	207	THR	23.4
1	L	240	LEU	23.4
1	B	260	THR	23.4
1	G	134	SER	23.4
1	G	330	ARG	23.4
1	A	255	LEU	23.4
1	L	225	VAL	23.4
1	A	344	GLY	23.4
1	H	347	ARG	23.4
1	F	46	ASN	23.4
1	G	296	ILE	23.4
1	D	114	PRO	23.3

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Mol	Chain	Res	Type	RSRZ
1	C	435	PRO	23.3
1	D	93	PRO	23.3
1	G	104	ARG	23.3
1	A	127	VAL	23.3
1	D	197	CYS	23.3
1	G	344	GLY	23.3
1	G	27	SER	23.3
1	G	304	PRO	23.3
1	L	429	VAL	23.3
1	D	184	ILE	23.3
1	E	52	THR	23.3
1	E	286	THR	23.3
1	B	195	ALA	23.3
1	C	430	ALA	23.3
1	A	185	PRO	23.3
1	F	372	GLU	23.3
1	D	13	PRO	23.3
1	L	209	THR	23.3
1	F	401	ILE	23.3
1	C	232	ALA	23.3
1	I	263	LEU	23.3
1	L	68	VAL	23.3
1	J	330	ARG	23.3
1	I	84	GLN	23.3
1	E	264	ILE	23.2
1	A	253	HIS	23.2
1	M	184	ILE	23.2
1	M	187	ILE	23.2
1	M	225	VAL	23.2
1	C	87	LEU	23.2
1	C	333	LEU	23.2
1	E	338	HIS	23.2
1	C	273	THR	23.2
1	L	328	SER	23.2
1	J	171	THR	23.2
1	A	418	GLU	23.2
1	G	191	PRO	23.2
1	M	417	ARG	23.2
1	I	280	ASN	23.2
1	B	428	GLU	23.1
1	K	59	PHE	23.1
1	J	165	THR	23.1

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Mol	Chain	Res	Type	RSRZ
1	D	83	ASP	23.1
1	E	51	ASP	23.1
1	E	251	SER	23.1
1	J	193	MET	23.1
1	E	230	PHE	23.1
1	E	30	ASP	23.1
1	K	168	SER	23.1
1	I	50	GLY	23.1
1	L	322	GLY	23.1
1	L	376	ASN	23.1
1	J	386	GLU	23.1
1	I	239	SER	23.1
1	D	398	THR	23.1
1	A	153	ASP	23.1
1	C	319	GLY	23.1
1	G	153	ASP	23.1
1	G	355	GLU	23.1
1	I	234	ILE	23.1
1	B	164	VAL	23.1
1	D	329	ALA	23.1
1	M	243	GLY	23.1
1	M	254	GLY	23.1
1	E	216	PHE	23.1
1	F	254	GLY	23.1
1	L	241	SER	23.1
1	K	230	PHE	23.1
1	D	413	VAL	23.0
1	M	155	ILE	23.0
1	J	191	PRO	23.0
1	J	290	MET	23.0
1	F	392	PRO	23.0
1	I	145	MET	23.0
1	L	231	SER	23.0
1	J	395	MET	23.0
1	F	113	LEU	23.0
1	J	118	TYR	23.0
1	J	429	VAL	23.0
1	B	228	THR	23.0
1	H	119	ALA	23.0
1	L	337	ILE	23.0
1	B	258	GLY	23.0
1	C	201	ASP	23.0

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Mol	Chain	Res	Type	RSRZ
1	C	417	ARG	23.0
1	F	423	ARG	23.0
1	I	146	SER	23.0
1	J	189	LEU	23.0
1	I	336	THR	22.9
1	K	320	GLN	22.9
1	F	38	LEU	22.9
1	L	127	VAL	22.9
1	J	17	SER	22.9
1	J	285	GLY	22.9
1	C	424	GLU	22.9
1	D	212	ASP	22.9
1	M	99	CYS	22.9
1	M	422	PHE	22.9
1	G	190	ASP	22.9
1	F	263	LEU	22.9
1	C	393	GLY	22.9
1	G	314	THR	22.9
1	C	223	GLY	22.9
1	E	227	ILE	22.9
1	E	223	GLY	22.9
1	C	350	THR	22.9
1	I	126	ALA	22.9
1	B	253	HIS	22.9
1	C	111	SER	22.9
1	E	266	PHE	22.9
1	K	231	SER	22.9
1	L	319	GLY	22.9
1	M	288	ASN	22.9
1	A	211	ALA	22.9
1	A	248	PHE	22.9
1	D	98	TYR	22.8
1	J	341	ASN	22.9
1	M	112	THR	22.8
1	E	163	GLY	22.8
1	H	122	GLY	22.8
1	E	92	LEU	22.8
1	I	419	TYR	22.8
1	A	52	THR	22.8
1	F	315	SER	22.8
1	M	164	VAL	22.8
1	A	327	TRP	22.8

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Mol	Chain	Res	Type	RSRZ
1	B	321	ALA	22.8
1	H	344	GLY	22.8
1	L	380	ALA	22.8
1	H	95	SER	22.8
1	F	262	TYR	22.8
1	C	185	PRO	22.8
1	K	43	SER	22.8
1	F	364	THR	22.8
1	E	98	TYR	22.8
1	G	270	THR	22.8
1	K	250	THR	22.8
1	B	143	GLY	22.7
1	C	381	LYS	22.7
1	L	331	GLY	22.7
1	J	71	HIS	22.7
1	M	213	ASP	22.7
1	K	120	LEU	22.7
1	C	56	LEU	22.7
1	F	39	ARG	22.7
1	J	320	GLN	22.7
1	C	256	VAL	22.7
1	A	289	LEU	22.7
1	C	405	ARG	22.7
1	K	390	PHE	22.7
1	E	212	ASP	22.7
1	L	92	LEU	22.7
1	K	261	ILE	22.7
1	A	246	LEU	22.6
1	I	189	LEU	22.6
1	K	229	LEU	22.6
1	M	283	THR	22.6
1	F	260	THR	22.6
1	I	17	SER	22.6
1	G	325	MET	22.6
1	E	247	VAL	22.6
1	I	164	VAL	22.6
1	H	290	MET	22.6
1	L	56	LEU	22.6
1	D	338	HIS	22.6
1	K	94	ALA	22.6
1	L	257	LEU	22.6
1	D	293	ASN	22.6

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Mol	Chain	Res	Type	RSRZ
1	M	423	ARG	22.5
1	J	48	THR	22.5
1	K	41	GLU	22.5
1	F	204	ARG	22.5
1	L	330	ARG	22.5
1	D	143	GLY	22.5
1	D	181	GLY	22.5
1	E	399	LYS	22.5
1	M	382	ASN	22.5
1	L	146	SER	22.5
1	B	326	SER	22.5
1	E	343	PRO	22.5
1	C	187	ILE	22.5
1	C	357	VAL	22.5
1	C	183	PRO	22.5
1	C	182	ASP	22.5
1	B	153	ASP	22.5
1	K	30	ASP	22.4
1	I	75	GLN	22.4
1	J	250	THR	22.4
1	L	396	ASN	22.4
1	I	231	SER	22.4
1	L	214	TYR	22.4
1	L	395	MET	22.4
1	M	415	PRO	22.4
1	C	17	SER	22.4
1	I	72	TYR	22.4
1	E	409	GLY	22.4
1	F	420	THR	22.4
1	H	298	THR	22.4
1	D	382	ASN	22.4
1	L	88	THR	22.4
1	M	289	LEU	22.4
1	K	228	THR	22.3
1	L	162	GLU	22.3
1	B	221	GLN	22.3
1	L	262	TYR	22.3
1	C	432	LEU	22.3
1	B	34	GLU	22.3
1	D	81	LYS	22.3
1	M	396	ASN	22.3
1	F	317	SER	22.3

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Mol	Chain	Res	Type	RSRZ
1	C	329	ALA	22.3
1	E	360	GLY	22.3
1	J	396	ASN	22.3
1	B	186	ALA	22.3
1	H	234	ILE	22.3
1	G	172	SER	22.3
1	K	412	THR	22.3
1	D	122	GLY	22.3
1	E	77	ASN	22.3
1	G	407	ARG	22.3
1	M	141	TYR	22.3
1	I	332	SER	22.3
1	M	55	GLY	22.3
1	H	274	ARG	22.3
1	K	32	THR	22.3
1	F	267	ASP	22.3
1	F	187	ILE	22.3
1	K	163	GLY	22.3
1	G	393	GLY	22.2
1	I	120	LEU	22.2
1	I	352	VAL	22.2
1	J	164	VAL	22.2
1	H	195	ALA	22.2
1	H	226	THR	22.2
1	A	277	ALA	22.2
1	M	318	GLY	22.2
1	G	362	VAL	22.2
1	K	267	ASP	22.2
1	A	382	ASN	22.2
1	M	335	VAL	22.2
1	G	359	THR	22.2
1	M	97	ASN	22.2
1	F	197	CYS	22.2
1	J	292	PHE	22.2
1	F	91	ASN	22.2
1	I	178	VAL	22.1
1	B	192	LYS	22.1
1	J	208	ILE	22.1
1	L	430	ALA	22.1
1	L	202	ARG	22.1
1	C	230	PHE	22.1
1	C	287	ASP	22.1

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Mol	Chain	Res	Type	RSRZ
1	D	38	LEU	22.1
1	B	312	ILE	22.1
1	K	386	GLU	22.1
1	H	431	ASP	22.1
1	H	338	HIS	22.1
1	L	205	VAL	22.1
1	A	393	GLY	22.1
1	A	260	THR	22.1
1	J	299	ASN	22.1
1	K	16	ARG	22.1
1	H	84	GLN	22.1
1	H	393	GLY	22.1
1	G	216	PHE	22.1
1	J	214	TYR	22.1
1	G	343	PRO	22.1
1	F	421	ASP	22.1
1	L	64	PRO	22.1
1	B	118	TYR	22.1
1	A	221	GLN	22.0
1	I	245	GLU	22.0
1	J	49	VAL	22.0
1	E	207	THR	22.0
1	G	254	GLY	22.0
1	H	184	ILE	22.0
1	I	410	ILE	22.0
1	H	15	ILE	22.0
1	G	115	GLY	22.0
1	J	177	TYR	22.0
1	I	208	ILE	22.0
1	A	391	ASP	22.0
1	D	131	GLY	22.0
1	H	53	GLY	22.0
1	K	150	ASN	22.0
1	D	202	ARG	22.0
1	A	183	PRO	22.0
1	K	52	THR	22.0
1	G	80	TYR	22.0
1	G	322	GLY	22.0
1	J	77	ASN	22.0
1	A	36	HIS	22.0
1	M	253	HIS	22.0
1	H	209	THR	22.0

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Mol	Chain	Res	Type	RSRZ
1	A	340	GLY	22.0
1	F	400	LEU	22.0
1	H	330	ARG	22.0
1	I	148	THR	21.9
1	H	50	GLY	21.9
1	K	225	VAL	21.9
1	F	361	SER	21.9
1	B	31	ASP	21.9
1	M	353	ALA	21.9
1	H	362	VAL	21.9
1	M	381	LYS	21.9
1	M	195	ALA	21.9
1	A	339	GLY	21.9
1	J	39	ARG	21.9
1	E	208	ILE	21.9
1	L	161	GLY	21.9
1	F	186	ALA	21.9
1	I	197	CYS	21.9
1	M	192	LYS	21.9
1	L	143	GLY	21.9
1	B	404	GLU	21.8
1	M	28	ILE	21.8
1	B	212	ASP	21.8
1	G	198	ASP	21.8
1	I	347	ARG	21.8
1	C	255	LEU	21.8
1	K	416	THR	21.8
1	E	96	TYR	21.8
1	F	230	PHE	21.8
1	B	391	ASP	21.8
1	L	314	THR	21.8
1	M	199	SER	21.8
1	I	168	SER	21.8
1	K	69	GLY	21.8
1	I	338	HIS	21.8
1	G	382	ASN	21.8
1	E	346	LEU	21.8
1	L	359	THR	21.8
1	A	379	LEU	21.8
1	J	243	GLY	21.8
1	L	160	VAL	21.8
1	L	96	TYR	21.8

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Mol	Chain	Res	Type	RSRZ
1	A	239	SER	21.8
1	B	84	GLN	21.8
1	D	248	PHE	21.8
1	C	34	GLU	21.8
1	I	329	ALA	21.8
1	B	213	ASP	21.7
1	D	280	ASN	21.7
1	F	53	GLY	21.7
1	C	213	ASP	21.7
1	F	399	LYS	21.7
1	L	417	ARG	21.7
1	H	309	LYS	21.7
1	A	50	GLY	21.7
1	B	107	THR	21.7
1	D	183	PRO	21.7
1	C	307	SER	21.7
1	H	361	SER	21.7
1	E	90	GLN	21.7
1	E	427	MET	21.7
1	K	394	ALA	21.7
1	E	100	ARG	21.7
1	D	218	SER	21.7
1	E	153	ASP	21.7
1	K	271	VAL	21.7
1	G	278	ALA	21.7
1	A	303	GLN	21.7
1	K	239	SER	21.7
1	B	189	LEU	21.7
1	L	354	TYR	21.6
1	A	313	VAL	21.6
1	L	249	ARG	21.6
1	G	229	LEU	21.6
1	E	27	SER	21.6
1	J	46	ASN	21.6
1	F	248	PHE	21.6
1	G	71	HIS	21.6
1	D	229	LEU	21.6
1	J	420	THR	21.6
1	I	69	GLY	21.6
1	J	422	PHE	21.6
1	L	230	PHE	21.6
1	I	138	ASP	21.6

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Mol	Chain	Res	Type	RSRZ
1	J	316	LYS	21.6
1	I	247	VAL	21.6
1	K	374	ILE	21.6
1	L	227	ILE	21.6
1	A	154	LYS	21.6
1	G	426	PHE	21.6
1	J	240	LEU	21.6
1	F	301	ILE	21.6
1	H	231	SER	21.6
1	L	302	THR	21.6
1	F	332	SER	21.6
1	M	271	VAL	21.6
1	I	225	VAL	21.6
1	C	77	ASN	21.6
1	M	404	GLU	21.6
1	C	209	THR	21.6
1	J	333	LEU	21.6
1	D	333	LEU	21.5
1	L	364	THR	21.5
1	J	70	ALA	21.5
1	H	307	SER	21.5
1	A	425	TYR	21.5
1	E	362	VAL	21.5
1	E	440	GLY	21.5
1	D	397	TYR	21.5
1	I	285	GLY	21.5
1	L	433	ASN	21.5
1	I	412	THR	21.5
1	L	353	ALA	21.5
1	E	32	THR	21.5
1	A	109	ARG	21.5
1	B	375	PRO	21.5
1	A	358	ALA	21.5
1	B	299	ASN	21.5
1	F	309	LYS	21.5
1	B	323	ASP	21.5
1	C	115	GLY	21.5
1	H	185	PRO	21.5
1	M	17	SER	21.5
1	F	253	HIS	21.5
1	C	252	VAL	21.5
1	I	222	PRO	21.5

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Mol	Chain	Res	Type	RSRZ
1	J	106	LEU	21.5
1	E	20	MET	21.5
1	A	218	SER	21.5
1	D	186	ALA	21.5
1	M	149	ALA	21.5
1	E	158	VAL	21.5
1	B	99	CYS	21.4
1	M	278	ALA	21.4
1	A	229	LEU	21.4
1	H	243	GLY	21.4
1	K	164	VAL	21.4
1	B	333	LEU	21.4
1	B	372	GLU	21.4
1	C	261	ILE	21.4
1	J	117	VAL	21.4
1	I	262	TYR	21.4
1	C	246	LEU	21.4
1	F	403	SER	21.4
1	C	80	TYR	21.4
1	H	406	ASP	21.4
1	B	348	PRO	21.4
1	D	185	PRO	21.4
1	I	45	TYR	21.4
1	K	329	ALA	21.4
1	M	94	ALA	21.4
1	A	311	GLU	21.4
1	C	359	THR	21.4
1	F	17	SER	21.3
1	J	20	MET	21.3
1	A	273	THR	21.3
1	K	128	THR	21.3
1	J	172	SER	21.3
1	A	53	GLY	21.3
1	B	338	HIS	21.3
1	E	382	ASN	21.3
1	I	136	LEU	21.3
1	I	80	TYR	21.3
1	D	362	VAL	21.3
1	B	432	LEU	21.3
1	J	73	THR	21.3
1	M	280	ASN	21.3
1	J	42	THR	21.3

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Mol	Chain	Res	Type	RSRZ
1	G	37	THR	21.3
1	H	51	ASP	21.3
1	F	221	GLN	21.3
1	M	34	GLU	21.3
1	I	321	ALA	21.2
1	J	198	ASP	21.2
1	B	193	MET	21.2
1	F	72	TYR	21.2
1	F	292	PHE	21.2
1	G	130	GLN	21.2
1	L	30	ASP	21.2
1	D	353	ALA	21.2
1	J	206	TYR	21.2
1	A	196	THR	21.2
1	F	344	GLY	21.2
1	E	171	THR	21.2
1	C	259	VAL	21.2
1	C	384	VAL	21.2
1	L	71	HIS	21.2
1	F	357	VAL	21.2
1	E	426	PHE	21.2
1	I	411	LYS	21.2
1	K	46	ASN	21.2
1	M	92	LEU	21.2
1	M	227	ILE	21.2
1	B	42	THR	21.1
1	I	13	PRO	21.1
1	M	126	ALA	21.1
1	H	34	GLU	21.1
1	A	213	ASP	21.1
1	A	215	GLN	21.1
1	D	255	LEU	21.1
1	C	126	ALA	21.1
1	B	302	THR	21.1
1	E	150	ASN	21.1
1	B	294	LEU	21.1
1	L	157	ASN	21.1
1	B	327	TRP	21.1
1	L	147	ALA	21.1
1	D	168	SER	21.1
1	I	389	ARG	21.1
1	H	423	ARG	21.1

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Mol	Chain	Res	Type	RSRZ
1	D	319	GLY	21.1
1	E	243	GLY	21.1
1	J	173	TYR	21.1
1	E	287	ASP	21.1
1	C	310	LEU	21.1
1	G	249	ARG	21.0
1	F	319	GLY	21.0
1	C	391	ASP	21.0
1	K	221	GLN	21.0
1	L	167	LEU	21.0
1	C	109	ARG	21.0
1	A	378	GLU	21.0
1	G	136	LEU	21.0
1	H	153	ASP	21.0
1	E	81	LYS	21.0
1	F	81	LYS	21.0
1	G	347	ARG	21.0
1	B	122	GLY	21.0
1	K	359	THR	21.0
1	K	15	ILE	21.0
1	J	16	ARG	21.0
1	J	111	SER	20.9
1	M	303	GLN	20.9
1	E	327	TRP	20.9
1	C	328	SER	20.9
1	J	207	THR	20.9
1	F	90	GLN	20.9
1	J	314	THR	20.9
1	F	49	VAL	20.9
1	L	163	GLY	20.9
1	M	142	ASN	20.9
1	G	248	PHE	20.9
1	E	299	ASN	20.9
1	L	279	ASN	20.9
1	G	224	GLY	20.9
1	M	329	ALA	20.9
1	L	290	MET	20.9
1	M	364	THR	20.9
1	F	316	LYS	20.9
1	M	351	LEU	20.9
1	H	170	PRO	20.9
1	J	185	PRO	20.9

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Mol	Chain	Res	Type	RSRZ
1	J	328	SER	20.9
1	C	149	ALA	20.9
1	K	351	LEU	20.9
1	F	48	THR	20.9
1	B	165	THR	20.9
1	F	398	THR	20.9
1	D	244	GLY	20.9
1	J	367	GLY	20.9
1	L	152	ASN	20.9
1	C	70	ALA	20.9
1	G	213	ASP	20.9
1	J	124	ILE	20.9
1	H	267	ASP	20.9
1	I	273	THR	20.9
1	K	286	THR	20.8
1	J	50	GLY	20.8
1	L	291	PRO	20.8
1	F	246	LEU	20.8
1	G	89	ALA	20.8
1	E	75	GLN	20.8
1	D	121	ASN	20.8
1	H	241	SER	20.8
1	M	319	GLY	20.8
1	I	250	THR	20.8
1	E	23	THR	20.8
1	A	222	PRO	20.8
1	E	267	ASP	20.8
1	M	340	GLY	20.8
1	C	86	LEU	20.8
1	G	218	SER	20.8
1	K	245	GLU	20.8
1	A	329	ALA	20.8
1	K	159	LEU	20.8
1	E	256	VAL	20.7
1	C	13	PRO	20.7
1	M	131	GLY	20.7
1	G	323	ASP	20.7
1	L	198	ASP	20.7
1	D	411	LYS	20.7
1	F	312	ILE	20.7
1	B	51	ASP	20.7
1	G	95	SER	20.7

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Mol	Chain	Res	Type	RSRZ
1	M	317	SER	20.7
1	J	232	ALA	20.7
1	E	344	GLY	20.7
1	J	283	THR	20.7
1	D	345	ALA	20.7
1	K	383	LEU	20.7
1	L	309	LYS	20.7
1	G	100	ARG	20.7
1	E	229	LEU	20.7
1	L	131	GLY	20.7
1	H	245	GLU	20.7
1	F	408	LEU	20.6
1	A	33	LEU	20.6
1	C	317	SER	20.6
1	K	347	ARG	20.6
1	I	397	TYR	20.6
1	D	307	SER	20.6
1	I	110	SER	20.6
1	B	289	LEU	20.6
1	H	56	LEU	20.6
1	I	396	ASN	20.6
1	J	222	PRO	20.6
1	A	412	THR	20.6
1	C	439	ALA	20.6
1	H	203	PRO	20.6
1	J	107	THR	20.6
1	A	286	THR	20.6
1	L	437	LYS	20.6
1	C	433	ASN	20.6
1	D	140	SER	20.6
1	L	199	SER	20.6
1	L	232	ALA	20.6
1	K	19	LEU	20.5
1	L	86	LEU	20.5
1	L	124	ILE	20.5
1	G	231	SER	20.5
1	G	363	VAL	20.5
1	J	178	VAL	20.5
1	D	153	ASP	20.5
1	G	20	MET	20.5
1	H	99	CYS	20.5
1	F	290	MET	20.5

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Mol	Chain	Res	Type	RSRZ
1	G	378	GLU	20.5
1	D	304	PRO	20.5
1	J	163	GLY	20.5
1	B	196	THR	20.5
1	F	250	THR	20.5
1	I	35	LYS	20.5
1	G	318	GLY	20.5
1	K	425	TYR	20.5
1	G	230	PHE	20.5
1	D	260	THR	20.5
1	B	56	LEU	20.5
1	B	385	THR	20.5
1	E	419	TYR	20.5
1	L	399	LYS	20.5
1	B	292	PHE	20.5
1	H	341	ASN	20.5
1	A	308	ILE	20.4
1	D	55	GLY	20.4
1	H	357	VAL	20.4
1	B	208	ILE	20.4
1	M	73	THR	20.4
1	J	417	ARG	20.4
1	K	376	ASN	20.4
1	E	347	ARG	20.4
1	B	46	ASN	20.4
1	L	255	LEU	20.4
1	G	96	TYR	20.4
1	K	119	ALA	20.4
1	A	136	LEU	20.4
1	I	167	LEU	20.4
1	B	150	ASN	20.4
1	D	91	ASN	20.4
1	I	398	THR	20.4
1	E	403	SER	20.4
1	F	243	GLY	20.4
1	I	403	SER	20.4
1	C	419	TYR	20.4
1	C	389	ARG	20.4
1	C	196	THR	20.4
1	D	117	VAL	20.4
1	I	190	ASP	20.3
1	K	83	ASP	20.3

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Mol	Chain	Res	Type	RSRZ
1	M	146	SER	20.3
1	C	438	ILE	20.3
1	K	340	GLY	20.3
1	B	199	SER	20.3
1	I	406	ASP	20.3
1	D	154	LYS	20.3
1	H	251	SER	20.3
1	E	342	TYR	20.3
1	G	93	PRO	20.3
1	L	401	ILE	20.3
1	J	234	ILE	20.3
1	L	375	PRO	20.3
1	F	138	ASP	20.3
1	D	128	THR	20.3
1	H	293	ASN	20.3
1	J	157	ASN	20.3
1	K	18	LEU	20.3
1	I	125	ASN	20.3
1	G	306	THR	20.3
1	J	286	THR	20.3
1	K	241	SER	20.3
1	H	285	GLY	20.3
1	F	195	ALA	20.3
1	H	194	VAL	20.2
1	F	130	GLN	20.2
1	B	424	GLU	20.2
1	C	71	HIS	20.2
1	H	160	VAL	20.2
1	F	159	LEU	20.2
1	H	186	ALA	20.2
1	K	85	MET	20.2
1	C	418	GLU	20.2
1	I	179	ARG	20.2
1	C	100	ARG	20.2
1	B	172	SER	20.2
1	M	348	PRO	20.2
1	J	419	TYR	20.2
1	I	51	ASP	20.2
1	E	219	GLN	20.2
1	E	296	ILE	20.2
1	D	285	GLY	20.2
1	E	355	GLU	20.2

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Mol	Chain	Res	Type	RSRZ
1	B	394	ALA	20.2
1	D	54	SER	20.2
1	I	30	ASP	20.2
1	I	37	THR	20.2
1	J	313	VAL	20.2
1	J	423	ARG	20.2
1	K	357	VAL	20.2
1	F	313	VAL	20.2
1	M	152	ASN	20.2
1	H	315	SER	20.2
1	L	54	SER	20.2
1	C	107	THR	20.2
1	D	308	ILE	20.2
1	K	362	VAL	20.2
1	M	405	ARG	20.2
1	G	47	LEU	20.2
1	K	199	SER	20.1
1	D	421	ASP	20.1
1	E	191	PRO	20.1
1	G	245	GLU	20.1
1	C	260	THR	20.1
1	B	29	PRO	20.1
1	B	187	ILE	20.1
1	J	266	PHE	20.1
1	M	352	VAL	20.1
1	F	185	PRO	20.1
1	A	401	ILE	20.1
1	M	43	SER	20.1
1	M	132	SER	20.1
1	M	264	ILE	20.1
1	K	213	ASP	20.1
1	E	149	ALA	20.1
1	D	403	SER	20.1
1	D	84	GLN	20.1
1	J	242	VAL	20.1
1	M	244	GLY	20.1
1	H	207	THR	20.1
1	K	342	TYR	20.1
1	J	153	ASP	20.1
1	B	120	LEU	20.1
1	K	40	SER	20.1
1	J	269	THR	20.0

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Mol	Chain	Res	Type	RSRZ
1	B	379	LEU	20.0
1	C	218	SER	20.0
1	H	239	SER	20.0
1	H	294	LEU	20.0
1	K	124	ILE	20.0
1	D	302	THR	20.0
1	J	418	GLU	20.0
1	C	104	ARG	20.0
1	D	283	THR	20.0
1	B	371	PHE	20.0
1	C	219	GLN	20.0
1	C	277	ALA	20.0
1	F	378	GLU	20.0
1	I	255	LEU	20.0
1	C	110	SER	20.0
1	A	416	THR	20.0
1	H	100	ARG	20.0
1	M	296	ILE	20.0
1	B	209	THR	20.0
1	M	48	THR	20.0
1	C	21	PRO	20.0
1	L	18	LEU	20.0
1	L	400	LEU	20.0
1	C	304	PRO	19.9
1	I	86	LEU	19.9
1	L	243	GLY	19.9
1	A	31	ASP	19.9
1	D	286	THR	19.9
1	F	272	ILE	19.9
1	G	256	VAL	19.9
1	J	166	VAL	19.9
1	C	31	ASP	19.9
1	C	59	PHE	19.9
1	F	279	ASN	19.9
1	I	328	SER	19.9
1	J	162	GLU	19.9
1	K	137	THR	19.9
1	A	402	LEU	19.9
1	C	353	ALA	19.9
1	B	266	PHE	19.9
1	K	321	ALA	19.9
1	C	403	SER	19.9

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Mol	Chain	Res	Type	RSRZ
1	E	113	LEU	19.9
1	B	59	PHE	19.9
1	D	314	THR	19.9
1	K	198	ASP	19.9
1	I	56	LEU	19.9
1	D	359	THR	19.9
1	H	219	GLN	19.8
1	G	360	GLY	19.8
1	A	124	ILE	19.8
1	F	59	PHE	19.8
1	G	52	THR	19.8
1	H	400	LEU	19.8
1	D	74	LEU	19.8
1	I	264	ILE	19.8
1	F	280	ASN	19.8
1	C	55	GLY	19.8
1	J	332	SER	19.8
1	C	253	HIS	19.8
1	M	354	TYR	19.8
1	F	382	ASN	19.8
1	H	356	ARG	19.8
1	I	337	ILE	19.8
1	D	251	SER	19.8
1	B	287	ASP	19.8
1	B	279	ASN	19.8
1	H	74	LEU	19.8
1	K	311	GLU	19.8
1	A	129	PHE	19.7
1	J	64	PRO	19.7
1	F	61	PRO	19.7
1	E	17	SER	19.7
1	E	183	PRO	19.7
1	F	305	ILE	19.7
1	E	248	PHE	19.7
1	M	287	ASP	19.7
1	A	280	ASN	19.7
1	J	170	PRO	19.7
1	L	329	ALA	19.7
1	H	190	ASP	19.7
1	J	51	ASP	19.7
1	G	42	THR	19.7
1	C	197	CYS	19.7

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Mol	Chain	Res	Type	RSRZ
1	K	148	THR	19.7
1	A	413	VAL	19.7
1	A	47	LEU	19.7
1	J	120	LEU	19.7
1	A	152	ASN	19.7
1	E	303	GLN	19.7
1	I	351	LEU	19.7
1	D	150	ASN	19.7
1	D	120	LEU	19.7
1	J	413	VAL	19.7
1	H	295	VAL	19.7
1	B	75	GLN	19.7
1	L	113	LEU	19.7
1	E	394	ALA	19.7
1	I	191	PRO	19.6
1	A	293	ASN	19.6
1	I	260	THR	19.6
1	M	137	THR	19.6
1	I	246	LEU	19.6
1	G	392	PRO	19.6
1	H	107	THR	19.6
1	L	296	ILE	19.6
1	L	347	ARG	19.6
1	J	412	THR	19.6
1	L	153	ASP	19.6
1	E	336	THR	19.6
1	C	191	PRO	19.6
1	I	121	ASN	19.6
1	A	323	ASP	19.6
1	D	309	LYS	19.6
1	C	168	SER	19.6
1	A	244	GLY	19.6
1	B	178	VAL	19.6
1	F	379	LEU	19.6
1	E	335	VAL	19.6
1	J	365	VAL	19.6
1	E	128	THR	19.6
1	L	183	PRO	19.6
1	A	385	THR	19.6
1	B	173	TYR	19.6
1	K	174	ASP	19.6
1	F	188	GLY	19.6

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Mol	Chain	Res	Type	RSRZ
1	D	375	PRO	19.5
1	E	272	ILE	19.5
1	A	138	ASP	19.5
1	D	372	GLU	19.5
1	B	225	VAL	19.5
1	C	53	GLY	19.5
1	G	120	LEU	19.5
1	C	296	ILE	19.5
1	F	121	ASN	19.5
1	J	241	SER	19.5
1	D	149	ALA	19.5
1	M	343	PRO	19.5
1	D	406	ASP	19.5
1	C	395	MET	19.5
1	B	403	SER	19.5
1	G	221	GLN	19.5
1	A	29	PRO	19.5
1	F	100	ARG	19.5
1	D	77	ASN	19.5
1	E	31	ASP	19.5
1	G	123	THR	19.5
1	J	160	VAL	19.5
1	L	213	ASP	19.5
1	E	179	ARG	19.5
1	I	184	ILE	19.5
1	I	350	THR	19.5
1	M	32	THR	19.5
1	L	114	PRO	19.5
1	L	37	THR	19.5
1	J	260	THR	19.5
1	M	230	PHE	19.5
1	E	85	MET	19.4
1	I	59	PHE	19.4
1	E	411	LYS	19.4
1	E	34	GLU	19.4
1	G	41	GLU	19.4
1	J	397	TYR	19.4
1	E	312	ILE	19.4
1	H	395	MET	19.4
1	K	17	SER	19.4
1	F	286	THR	19.4
1	F	75	GLN	19.4

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Mol	Chain	Res	Type	RSRZ
1	I	221	GLN	19.4
1	H	72	TYR	19.4
1	H	96	TYR	19.4
1	H	340	GLY	19.4
1	F	302	THR	19.4
1	G	193	MET	19.4
1	G	333	LEU	19.4
1	J	403	SER	19.4
1	B	179	ARG	19.4
1	K	298	THR	19.4
1	A	283	THR	19.4
1	A	332	SER	19.4
1	C	241	SER	19.4
1	H	79	ASN	19.4
1	M	215	GLN	19.4
1	L	370	ASN	19.4
1	L	91	ASN	19.3
1	E	386	GLU	19.3
1	L	99	CYS	19.3
1	I	310	LEU	19.3
1	D	435	PRO	19.3
1	L	432	LEU	19.3
1	M	431	ASP	19.3
1	G	419	TYR	19.3
1	L	201	ASP	19.3
1	G	132	SER	19.3
1	I	175	LEU	19.3
1	C	428	GLU	19.3
1	K	157	ASN	19.3
1	D	130	GLN	19.3
1	I	123	THR	19.3
1	C	75	GLN	19.3
1	L	222	PRO	19.3
1	A	187	ILE	19.3
1	B	17	SER	19.3
1	C	179	ARG	19.3
1	C	327	TRP	19.3
1	B	421	ASP	19.3
1	H	380	ALA	19.3
1	B	252	VAL	19.3
1	A	212	ASP	19.3
1	B	30	ASP	19.3

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Mol	Chain	Res	Type	RSRZ
1	C	96	TYR	19.3
1	K	403	SER	19.3
1	K	299	ASN	19.3
1	E	213	ASP	19.3
1	M	255	LEU	19.3
1	H	183	PRO	19.2
1	C	351	LEU	19.2
1	H	215	GLN	19.2
1	J	135	GLU	19.2
1	D	217	SER	19.2
1	A	261	ILE	19.2
1	G	112	THR	19.2
1	D	23	THR	19.2
1	I	340	GLY	19.2
1	D	72	TYR	19.2
1	L	338	HIS	19.2
1	F	122	GLY	19.2
1	I	241	SER	19.2
1	L	194	VAL	19.2
1	L	365	VAL	19.2
1	M	398	THR	19.2
1	B	382	ASN	19.2
1	F	308	ILE	19.2
1	D	60	PHE	19.2
1	A	330	ARG	19.2
1	A	88	THR	19.2
1	G	350	THR	19.2
1	A	424	GLU	19.2
1	H	49	VAL	19.2
1	B	331	GLY	19.1
1	E	170	PRO	19.1
1	I	270	THR	19.1
1	K	170	PRO	19.1
1	I	52	THR	19.1
1	B	32	THR	19.1
1	B	259	VAL	19.1
1	E	110	SER	19.1
1	C	95	SER	19.1
1	C	161	GLY	19.1
1	G	39	ARG	19.1
1	I	172	SER	19.1
1	D	377	PRO	19.1

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Mol	Chain	Res	Type	RSRZ
1	K	264	ILE	19.1
1	F	88	THR	19.1
1	C	234	ILE	19.1
1	F	324	GLN	19.1
1	G	54	SER	19.1
1	A	315	SER	19.1
1	A	390	PHE	19.1
1	G	286	THR	19.1
1	I	219	GLN	19.1
1	E	72	TYR	19.1
1	C	275	ALA	19.1
1	H	402	LEU	19.1
1	H	339	GLY	19.1
1	B	286	THR	19.1
1	D	225	VAL	19.1
1	L	95	SER	19.1
1	C	204	ARG	19.1
1	H	376	ASN	19.1
1	B	129	PHE	19.1
1	D	269	THR	19.0
1	L	382	ASN	19.0
1	L	358	ALA	19.0
1	A	295	VAL	19.0
1	H	201	ASP	19.0
1	H	286	THR	19.0
1	F	84	GLN	19.0
1	H	192	LYS	19.0
1	E	313	VAL	19.0
1	E	199	SER	19.0
1	I	202	ARG	19.0
1	F	345	ALA	19.0
1	E	42	THR	19.0
1	J	104	ARG	19.0
1	B	130	GLN	19.0
1	H	281	GLY	19.0
1	A	157	ASN	19.0
1	H	343	PRO	19.0
1	J	430	ALA	19.0
1	D	252	VAL	19.0
1	G	234	ILE	19.0
1	C	29	PRO	19.0
1	A	56	LEU	19.0

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Mol	Chain	Res	Type	RSRZ
1	G	422	PHE	19.0
1	E	62	GLY	19.0
1	L	105	SER	19.0
1	I	393	GLY	19.0
1	E	269	THR	19.0
1	K	80	TYR	19.0
1	K	138	ASP	19.0
1	K	290	MET	19.0
1	C	267	ASP	18.9
1	J	119	ALA	18.9
1	K	413	VAL	18.9
1	I	42	THR	18.9
1	J	399	LYS	18.9
1	A	54	SER	18.9
1	C	229	LEU	18.9
1	G	38	LEU	18.9
1	L	285	GLY	18.9
1	M	300	GLU	18.9
1	E	441	ALA	18.9
1	F	183	PRO	18.9
1	E	356	ARG	18.9
1	G	370	ASN	18.9
1	J	284	THR	18.9
1	I	261	ILE	18.9
1	B	15	ILE	18.9
1	M	76	GLY	18.9
1	K	197	CYS	18.9
1	A	191	PRO	18.9
1	J	231	SER	18.9
1	L	136	LEU	18.9
1	A	49	VAL	18.9
1	B	319	GLY	18.9
1	M	298	THR	18.9
1	M	412	THR	18.9
1	I	384	VAL	18.9
1	K	200	SER	18.9
1	I	137	THR	18.9
1	J	425	TYR	18.9
1	B	335	VAL	18.8
1	I	305	ILE	18.8
1	A	144	LEU	18.8
1	D	294	LEU	18.8

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Mol	Chain	Res	Type	RSRZ
1	D	191	PRO	18.8
1	A	427	MET	18.8
1	B	220	TYR	18.8
1	G	327	TRP	18.8
1	G	46	ASN	18.8
1	B	200	SER	18.8
1	K	308	ILE	18.8
1	A	381	LYS	18.8
1	J	344	GLY	18.8
1	M	136	LEU	18.8
1	H	317	SER	18.8
1	H	308	ILE	18.8
1	D	51	ASP	18.8
1	G	293	ASN	18.8
1	D	88	THR	18.8
1	D	342	TYR	18.8
1	H	85	MET	18.8
1	J	68	VAL	18.8
1	C	360	GLY	18.8
1	F	259	VAL	18.7
1	E	239	SER	18.7
1	F	252	VAL	18.7
1	I	409	GLY	18.7
1	L	98	TYR	18.7
1	I	364	THR	18.7
1	A	387	TYR	18.7
1	H	58	VAL	18.7
1	A	383	LEU	18.7
1	G	326	SER	18.7
1	B	345	ALA	18.7
1	C	63	PHE	18.7
1	J	30	ASP	18.7
1	I	355	GLU	18.7
1	B	88	THR	18.7
1	A	90	GLN	18.7
1	A	377	PRO	18.7
1	F	310	LEU	18.7
1	L	78	GLY	18.7
1	H	27	SER	18.7
1	G	425	TYR	18.7
1	J	59	PHE	18.7
1	I	218	SER	18.7

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Mol	Chain	Res	Type	RSRZ
1	C	162	GLU	18.7
1	G	74	LEU	18.7
1	E	200	SER	18.6
1	H	14	PHE	18.6
1	K	100	ARG	18.6
1	E	439	ALA	18.6
1	I	313	VAL	18.6
1	H	324	GLN	18.6
1	L	177	TYR	18.6
1	K	392	PRO	18.6
1	D	56	LEU	18.6
1	K	343	PRO	18.6
1	E	135	GLU	18.6
1	C	240	LEU	18.6
1	G	264	ILE	18.6
1	A	16	ARG	18.6
1	A	81	LYS	18.6
1	D	272	ILE	18.6
1	E	348	PRO	18.6
1	I	112	THR	18.6
1	I	238	THR	18.6
1	E	393	GLY	18.6
1	I	232	ALA	18.6
1	C	421	ASP	18.6
1	J	356	ARG	18.6
1	G	368	VAL	18.6
1	M	259	VAL	18.6
1	C	299	ASN	18.6
1	E	49	VAL	18.6
1	J	262	TYR	18.6
1	L	170	PRO	18.6
1	D	58	VAL	18.5
1	K	319	GLY	18.5
1	K	411	LYS	18.5
1	E	284	THR	18.5
1	F	115	GLY	18.5
1	G	312	ILE	18.5
1	J	128	THR	18.5
1	A	182	ASP	18.5
1	B	240	LEU	18.5
1	C	342	TYR	18.5
1	I	36	HIS	18.5

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Mol	Chain	Res	Type	RSRZ
1	M	202	ARG	18.5
1	B	24	GLY	18.5
1	G	30	ASP	18.5
1	M	263	LEU	18.5
1	E	95	SER	18.5
1	A	436	LEU	18.5
1	M	190	ASP	18.5
1	A	230	PHE	18.5
1	C	216	PHE	18.5
1	J	254	GLY	18.5
1	D	162	GLU	18.5
1	F	269	THR	18.5
1	K	188	GLY	18.5
1	E	357	VAL	18.5
1	C	294	LEU	18.5
1	G	195	ALA	18.5
1	C	324	GLN	18.5
1	F	265	GLY	18.4
1	M	325	MET	18.4
1	C	30	ASP	18.4
1	F	242	VAL	18.4
1	G	376	ASN	18.4
1	E	190	ASP	18.4
1	E	151	ILE	18.4
1	E	323	ASP	18.4
1	K	272	ILE	18.4
1	J	424	GLU	18.4
1	D	64	PRO	18.4
1	H	20	MET	18.4
1	M	328	SER	18.4
1	B	138	ASP	18.4
1	D	305	ILE	18.4
1	L	391	ASP	18.4
1	M	229	LEU	18.4
1	E	370	ASN	18.4
1	G	411	LYS	18.4
1	B	325	MET	18.3
1	C	221	GLN	18.3
1	A	342	TYR	18.3
1	C	206	TYR	18.3
1	M	86	LEU	18.3
1	L	169	LEU	18.3

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Mol	Chain	Res	Type	RSRZ
1	F	412	THR	18.3
1	I	62	GLY	18.3
1	A	125	ASN	18.3
1	K	82	PHE	18.3
1	H	152	ASN	18.3
1	M	110	SER	18.3
1	H	61	PRO	18.3
1	C	155	ILE	18.3
1	A	328	SER	18.3
1	L	239	SER	18.3
1	M	266	PHE	18.3
1	F	97	ASN	18.3
1	B	363	VAL	18.3
1	D	100	ARG	18.3
1	M	89	ALA	18.3
1	E	141	TYR	18.2
1	I	177	TYR	18.2
1	M	400	LEU	18.2
1	I	278	ALA	18.2
1	A	370	ASN	18.2
1	D	220	TYR	18.2
1	H	161	GLY	18.2
1	J	273	THR	18.2
1	F	328	SER	18.2
1	A	403	SER	18.2
1	L	185	PRO	18.2
1	M	342	TYR	18.2
1	H	235	ASP	18.2
1	A	435	PRO	18.2
1	F	342	TYR	18.2
1	M	321	ALA	18.2
1	D	370	ASN	18.2
1	B	278	ALA	18.2
1	I	217	SER	18.2
1	J	361	SER	18.2
1	B	249	ARG	18.2
1	I	100	ARG	18.2
1	K	389	ARG	18.2
1	M	83	ASP	18.2
1	M	46	ASN	18.2
1	H	179	ARG	18.2
1	L	321	ALA	18.2

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Mol	Chain	Res	Type	RSRZ
1	C	121	ASN	18.2
1	J	279	ASN	18.2
1	E	39	ARG	18.2
1	B	324	GLN	18.2
1	M	130	GLN	18.2
1	C	368	VAL	18.2
1	A	175	LEU	18.1
1	M	58	VAL	18.1
1	H	360	GLY	18.1
1	L	438	ILE	18.1
1	J	355	GLU	18.1
1	F	178	VAL	18.1
1	M	226	THR	18.1
1	K	50	GLY	18.1
1	L	283	THR	18.1
1	K	111	SER	18.1
1	J	315	SER	18.1
1	G	135	GLU	18.1
1	B	291	PRO	18.1
1	C	302	THR	18.1
1	E	311	GLU	18.1
1	A	170	PRO	18.1
1	B	281	GLY	18.1
1	E	28	ILE	18.1
1	D	230	PHE	18.1
1	C	108	VAL	18.1
1	B	197	CYS	18.1
1	L	59	PHE	18.1
1	I	295	VAL	18.1
1	H	325	MET	18.1
1	H	292	PHE	18.1
1	G	13	PRO	18.0
1	A	298	THR	18.0
1	F	228	THR	18.0
1	B	207	THR	18.0
1	F	193	MET	18.0
1	B	387	TYR	18.0
1	G	261	ILE	18.0
1	B	318	GLY	18.0
1	B	332	SER	18.0
1	D	152	ASN	18.0
1	G	381	LYS	18.0

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Mol	Chain	Res	Type	RSRZ
1	E	119	ALA	18.0
1	C	91	ASN	18.0
1	J	312	ILE	18.0
1	M	35	LYS	18.0
1	M	390	PHE	18.0
1	H	257	LEU	18.0
1	H	282	LEU	18.0
1	G	437	LYS	18.0
1	D	364	THR	18.0
1	G	157	ASN	18.0
1	K	122	GLY	17.9
1	D	204	ARG	17.9
1	C	280	ASN	17.9
1	M	181	GLY	17.9
1	M	197	CYS	17.9
1	M	394	ALA	17.9
1	E	320	GLN	17.9
1	L	377	PRO	17.9
1	G	187	ILE	17.9
1	H	211	ALA	17.9
1	D	182	ASP	17.9
1	K	420	THR	17.9
1	E	144	LEU	17.9
1	H	77	ASN	17.9
1	G	59	PHE	17.9
1	E	363	VAL	17.9
1	I	395	MET	17.9
1	L	352	VAL	17.9
1	A	123	THR	17.9
1	G	50	GLY	17.9
1	L	97	ASN	17.9
1	I	381	LYS	17.8
1	F	256	VAL	17.8
1	G	384	VAL	17.8
1	J	215	GLN	17.8
1	K	113	LEU	17.8
1	M	233	ASN	17.8
1	B	423	ARG	17.8
1	L	129	PHE	17.8
1	M	363	VAL	17.8
1	G	56	LEU	17.8
1	K	364	THR	17.8

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Mol	Chain	Res	Type	RSRZ
1	F	154	LYS	17.8
1	D	384	VAL	17.8
1	G	358	ALA	17.8
1	D	160	VAL	17.8
1	A	338	HIS	17.8
1	A	122	GLY	17.8
1	G	409	GLY	17.8
1	E	142	ASN	17.8
1	H	276	VAL	17.8
1	C	35	LYS	17.8
1	D	259	VAL	17.8
1	D	282	LEU	17.8
1	I	163	GLY	17.8
1	I	173	TYR	17.8
1	H	76	GLY	17.8
1	B	144	LEU	17.8
1	A	55	GLY	17.8
1	M	433	ASN	17.8
1	C	120	LEU	17.8
1	C	339	GLY	17.8
1	E	263	LEU	17.7
1	J	152	ASN	17.7
1	K	126	ALA	17.7
1	L	89	ALA	17.7
1	F	431	ASP	17.7
1	K	387	TYR	17.7
1	M	188	GLY	17.7
1	F	249	ARG	17.7
1	J	204	ARG	17.7
1	B	232	ALA	17.7
1	B	102	VAL	17.7
1	J	380	ALA	17.7
1	G	43	SER	17.7
1	K	335	VAL	17.7
1	C	414	TRP	17.7
1	J	389	ARG	17.7
1	D	301	ILE	17.7
1	G	51	ASP	17.7
1	D	211	ALA	17.7
1	D	303	GLN	17.7
1	E	99	CYS	17.7
1	J	95	SER	17.7

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Mol	Chain	Res	Type	RSRZ
1	K	344	GLY	17.7
1	I	39	ARG	17.7
1	K	29	PRO	17.7
1	F	107	THR	17.7
1	K	177	TYR	17.7
1	J	247	VAL	17.7
1	I	426	PHE	17.7
1	F	7	GLN	17.6
1	I	111	SER	17.6
1	B	296	ILE	17.6
1	M	165	THR	17.6
1	B	97	ASN	17.6
1	H	302	THR	17.6
1	A	434	SER	17.6
1	D	134	SER	17.6
1	C	249	ARG	17.6
1	B	194	VAL	17.6
1	L	271	VAL	17.6
1	D	240	LEU	17.6
1	G	238	THR	17.6
1	L	187	ILE	17.6
1	H	288	ASN	17.6
1	D	27	SER	17.6
1	E	19	LEU	17.6
1	I	428	GLU	17.6
1	F	393	GLY	17.6
1	L	188	GLY	17.6
1	A	225	VAL	17.6
1	B	36	HIS	17.6
1	E	307	SER	17.6
1	D	206	TYR	17.6
1	G	298	THR	17.6
1	L	140	SER	17.6
1	M	261	ILE	17.6
1	G	182	ASP	17.6
1	E	88	THR	17.6
1	G	400	LEU	17.6
1	B	384	VAL	17.5
1	D	161	GLY	17.5
1	L	313	VAL	17.5
1	B	182	ASP	17.5
1	C	264	ILE	17.5

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Mol	Chain	Res	Type	RSRZ
1	F	422	PHE	17.5
1	M	80	TYR	17.5
1	G	436	LEU	17.5
1	J	190	ASP	17.5
1	D	138	ASP	17.5
1	L	339	GLY	17.5
1	C	150	ASN	17.5
1	C	303	GLN	17.5
1	J	354	TYR	17.5
1	I	198	ASP	17.5
1	I	38	LEU	17.5
1	B	418	GLU	17.5
1	G	184	ILE	17.5
1	M	248	PHE	17.5
1	H	69	GLY	17.5
1	K	368	VAL	17.5
1	L	186	ALA	17.5
1	A	115	GLY	17.5
1	J	57	ILE	17.5
1	C	50	GLY	17.5
1	L	402	LEU	17.5
1	L	175	LEU	17.5
1	B	224	GLY	17.4
1	F	205	VAL	17.4
1	J	205	VAL	17.4
1	G	87	LEU	17.4
1	K	214	TYR	17.4
1	B	92	LEU	17.4
1	M	206	TYR	17.4
1	E	334	ALA	17.4
1	A	35	LYS	17.4
1	D	405	ARG	17.4
1	M	327	TRP	17.4
1	M	45	TYR	17.4
1	A	139	VAL	17.4
1	H	224	GLY	17.4
1	C	51	ASP	17.4
1	M	72	TYR	17.4
1	B	82	PHE	17.4
1	K	154	LYS	17.4
1	B	343	PRO	17.4
1	I	333	LEU	17.4

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Mol	Chain	Res	Type	RSRZ
1	E	358	ALA	17.4
1	F	363	VAL	17.4
1	F	60	PHE	17.4
1	H	103	SER	17.3
1	L	79	ASN	17.3
1	D	193	MET	17.3
1	K	140	SER	17.3
1	B	80	TYR	17.3
1	I	304	PRO	17.3
1	B	388	GLY	17.3
1	E	262	TYR	17.3
1	I	356	ARG	17.3
1	E	397	TYR	17.3
1	C	312	ILE	17.3
1	E	174	ASP	17.3
1	F	137	THR	17.3
1	B	360	GLY	17.3
1	K	384	VAL	17.3
1	D	424	GLU	17.3
1	E	232	ALA	17.3
1	K	330	ARG	17.3
1	C	90	GLN	17.3
1	E	319	GLY	17.3
1	I	367	GLY	17.3
1	E	261	ILE	17.3
1	E	134	SER	17.3
1	L	72	TYR	17.3
1	D	30	ASP	17.3
1	H	370	ASN	17.3
1	J	72	TYR	17.3
1	J	368	VAL	17.2
1	M	347	ARG	17.2
1	A	27	SER	17.2
1	L	245	GLU	17.2
1	M	90	GLN	17.2
1	E	188	GLY	17.2
1	K	222	PRO	17.2
1	K	294	LEU	17.2
1	F	6	ASP	17.2
1	K	243	GLY	17.2
1	L	137	THR	17.2
1	M	260	THR	17.2

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Mol	Chain	Res	Type	RSRZ
1	J	347	ARG	17.2
1	C	436	LEU	17.2
1	A	281	GLY	17.2
1	F	387	TYR	17.2
1	H	150	ASN	17.2
1	A	345	ALA	17.2
1	E	285	GLY	17.2
1	J	125	ASN	17.2
1	K	361	SER	17.2
1	D	157	ASN	17.2
1	M	84	GLN	17.2
1	A	166	VAL	17.2
1	I	240	LEU	17.2
1	G	342	TYR	17.2
1	E	279	ASN	17.2
1	E	169	LEU	17.2
1	J	300	GLU	17.2
1	A	108	VAL	17.2
1	B	261	ILE	17.2
1	G	148	THR	17.2
1	G	369	SER	17.2
1	L	288	ASN	17.2
1	J	369	SER	17.2
1	D	148	THR	17.2
1	K	151	ILE	17.2
1	L	51	ASP	17.2
1	A	57	ILE	17.1
1	H	204	ARG	17.1
1	A	61	PRO	17.1
1	A	275	ALA	17.1
1	K	167	LEU	17.1
1	F	8	THR	17.1
1	H	18	LEU	17.1
1	B	399	LYS	17.1
1	F	225	VAL	17.1
1	J	404	GLU	17.1
1	A	179	ARG	17.1
1	K	363	VAL	17.1
1	D	410	ILE	17.1
1	I	82	PHE	17.1
1	C	200	SER	17.1
1	I	54	SER	17.1

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Mol	Chain	Res	Type	RSRZ
1	J	43	SER	17.1
1	K	20	MET	17.1
1	G	99	CYS	17.1
1	F	284	THR	17.1
1	C	62	GLY	17.1
1	A	169	LEU	17.1
1	F	348	PRO	17.1
1	J	236	ALA	17.1
1	A	227	ILE	17.1
1	J	41	GLU	17.1
1	J	151	ILE	17.1
1	G	186	ALA	17.1
1	L	171	THR	17.1
1	M	100	ARG	17.1
1	F	294	LEU	17.0
1	C	262	TYR	17.0
1	C	295	VAL	17.0
1	H	83	ASP	17.0
1	G	232	ALA	17.0
1	G	266	PHE	17.0
1	G	223	GLY	17.0
1	F	287	ASP	17.0
1	G	299	ASN	17.0
1	A	114	PRO	17.0
1	G	106	LEU	17.0
1	M	53	GLY	17.0
1	B	174	ASP	17.0
1	B	350	THR	17.0
1	J	348	PRO	17.0
1	I	204	ARG	17.0
1	L	23	THR	17.0
1	H	174	ASP	17.0
1	K	297	PRO	16.9
1	H	146	SER	16.9
1	A	394	ALA	16.9
1	I	188	GLY	16.9
1	D	118	TYR	16.9
1	H	371	PHE	16.9
1	K	70	ALA	16.9
1	L	115	GLY	16.9
1	B	422	PHE	16.9
1	M	77	ASN	16.9

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Mol	Chain	Res	Type	RSRZ
1	D	313	VAL	16.9
1	C	257	LEU	16.9
1	D	163	GLY	16.9
1	E	254	GLY	16.9
1	E	337	ILE	16.9
1	M	207	THR	16.9
1	A	190	ASP	16.9
1	B	117	VAL	16.9
1	B	105	SER	16.9
1	D	125	ASN	16.9
1	A	165	THR	16.8
1	D	295	VAL	16.8
1	D	336	THR	16.8
1	B	135	GLU	16.8
1	H	346	LEU	16.8
1	I	149	ALA	16.8
1	M	70	ALA	16.8
1	H	13	PRO	16.8
1	M	332	SER	16.8
1	J	201	ASP	16.8
1	E	56	LEU	16.8
1	G	152	ASN	16.8
1	G	162	GLU	16.8
1	I	382	ASN	16.8
1	F	356	ARG	16.8
1	I	106	LEU	16.8
1	H	321	ALA	16.8
1	B	222	PRO	16.8
1	J	108	VAL	16.8
1	K	47	LEU	16.8
1	H	225	VAL	16.8
1	H	176	GLY	16.8
1	C	159	LEU	16.8
1	I	349	VAL	16.8
1	F	99	CYS	16.8
1	L	154	LYS	16.8
1	L	90	GLN	16.8
1	I	365	VAL	16.8
1	E	198	ASP	16.8
1	A	419	TYR	16.7
1	A	91	ASN	16.7
1	A	219	GLN	16.7

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Mol	Chain	Res	Type	RSRZ
1	D	243	GLY	16.7
1	K	345	ALA	16.7
1	E	91	ASN	16.7
1	M	198	ASP	16.7
1	H	359	THR	16.7
1	F	95	SER	16.7
1	I	303	GLN	16.7
1	M	154	LYS	16.7
1	G	225	VAL	16.7
1	I	312	ILE	16.7
1	K	86	LEU	16.7
1	I	227	ILE	16.7
1	J	358	ALA	16.7
1	M	79	ASN	16.7
1	B	305	ILE	16.7
1	K	305	ILE	16.7
1	A	306	THR	16.7
1	F	142	ASN	16.7
1	C	222	PRO	16.7
1	J	411	LYS	16.7
1	C	67	ILE	16.7
1	E	242	VAL	16.7
1	F	149	ALA	16.7
1	H	278	ALA	16.7
1	D	97	ASN	16.7
1	E	259	VAL	16.7
1	M	373	LEU	16.7
1	A	188	GLY	16.7
1	F	275	ALA	16.6
1	D	82	PHE	16.6
1	M	374	ILE	16.6
1	L	439	ALA	16.6
1	J	110	SER	16.6
1	D	164	VAL	16.6
1	G	154	LYS	16.6
1	F	416	THR	16.6
1	H	424	GLU	16.6
1	E	173	TYR	16.6
1	F	285	GLY	16.6
1	C	283	THR	16.6
1	J	98	TYR	16.6
1	C	125	ASN	16.6

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Mol	Chain	Res	Type	RSRZ
1	H	373	LEU	16.6
1	G	317	SER	16.6
1	J	370	ASN	16.6
1	K	44	THR	16.6
1	B	154	LYS	16.6
1	C	81	LYS	16.6
1	H	92	LEU	16.6
1	H	86	LEU	16.6
1	M	221	GLN	16.6
1	H	38	LEU	16.6
1	F	281	GLY	16.6
1	G	242	VAL	16.6
1	J	426	PHE	16.6
1	F	219	GLN	16.6
1	J	325	MET	16.6
1	A	359	THR	16.6
1	C	263	LEU	16.6
1	J	148	THR	16.6
1	B	293	ASN	16.6
1	I	324	GLN	16.6
1	M	297	PRO	16.6
1	C	330	ARG	16.6
1	L	349	VAL	16.6
1	B	111	SER	16.6
1	G	367	GLY	16.5
1	M	75	GLN	16.5
1	E	392	PRO	16.5
1	B	74	LEU	16.5
1	D	297	PRO	16.5
1	D	171	THR	16.5
1	C	199	SER	16.5
1	L	44	THR	16.5
1	L	389	ARG	16.5
1	B	37	THR	16.5
1	E	41	GLU	16.5
1	J	359	THR	16.5
1	I	199	SER	16.5
1	E	412	THR	16.5
1	H	350	THR	16.5
1	C	98	TYR	16.5
1	I	334	ALA	16.5
1	F	135	GLU	16.5

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Mol	Chain	Res	Type	RSRZ
1	G	194	VAL	16.5
1	L	278	ALA	16.5
1	G	189	LEU	16.5
1	K	234	ILE	16.5
1	D	189	LEU	16.5
1	C	347	ARG	16.5
1	F	34	GLU	16.5
1	D	431	ASP	16.5
1	G	105	SER	16.4
1	E	214	TYR	16.4
1	G	124	ILE	16.4
1	M	223	GLY	16.4
1	B	113	LEU	16.4
1	L	41	GLU	16.4
1	H	256	VAL	16.4
1	D	233	ASN	16.4
1	G	403	SER	16.4
1	K	98	TYR	16.4
1	D	192	LYS	16.4
1	K	36	HIS	16.4
1	A	142	ASN	16.4
1	E	82	PHE	16.4
1	F	189	LEU	16.4
1	L	287	ASP	16.4
1	M	346	LEU	16.4
1	E	138	ASP	16.4
1	L	341	ASN	16.4
1	F	304	PRO	16.4
1	M	277	ALA	16.4
1	M	238	THR	16.4
1	H	279	ASN	16.4
1	I	153	ASP	16.4
1	A	243	GLY	16.4
1	C	169	LEU	16.4
1	A	214	TYR	16.4
1	H	98	TYR	16.4
1	A	156	GLY	16.3
1	H	304	PRO	16.3
1	I	161	GLY	16.3
1	L	102	VAL	16.3
1	G	118	TYR	16.3
1	B	309	LYS	16.3

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Mol	Chain	Res	Type	RSRZ
1	C	88	THR	16.3
1	J	136	LEU	16.3
1	K	34	GLU	16.3
1	K	208	ILE	16.3
1	M	309	LYS	16.3
1	M	60	PHE	16.3
1	K	377	PRO	16.3
1	D	39	ARG	16.3
1	D	298	THR	16.3
1	E	258	GLY	16.3
1	E	89	ALA	16.3
1	I	380	ALA	16.3
1	M	196	THR	16.3
1	L	372	GLU	16.3
1	E	146	SER	16.2
1	E	124	ILE	16.2
1	M	384	VAL	16.2
1	D	409	GLY	16.2
1	B	288	ASN	16.2
1	C	37	THR	16.2
1	M	161	GLY	16.2
1	B	139	VAL	16.2
1	E	377	PRO	16.2
1	A	199	SER	16.2
1	L	355	GLU	16.2
1	M	212	ASP	16.2
1	C	57	ILE	16.2
1	A	193	MET	16.2
1	K	254	GLY	16.2
1	L	252	VAL	16.2
1	A	210	ALA	16.2
1	J	357	VAL	16.2
1	C	38	LEU	16.2
1	H	111	SER	16.2
1	I	31	ASP	16.2
1	I	67	ILE	16.2
1	I	18	LEU	16.2
1	M	78	GLY	16.2
1	H	328	SER	16.1
1	I	335	VAL	16.1
1	B	295	VAL	16.1
1	C	170	PRO	16.1

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Mol	Chain	Res	Type	RSRZ
1	J	54	SER	16.1
1	D	28	ILE	16.1
1	E	391	ASP	16.1
1	D	374	ILE	16.1
1	C	64	PRO	16.1
1	J	287	ASP	16.1
1	M	51	ASP	16.1
1	E	137	THR	16.1
1	L	351	LEU	16.1
1	F	339	GLY	16.1
1	H	329	ALA	16.1
1	A	197	CYS	16.1
1	F	162	GLU	16.1
1	G	412	THR	16.1
1	K	95	SER	16.1
1	F	62	GLY	16.1
1	G	173	TYR	16.1
1	J	123	THR	16.1
1	I	140	SER	16.1
1	L	315	SER	16.1
1	J	186	ALA	16.1
1	B	297	PRO	16.1
1	D	271	VAL	16.1
1	M	421	ASP	16.1
1	B	78	GLY	16.1
1	F	211	ALA	16.1
1	G	429	VAL	16.1
1	L	423	ARG	16.1
1	M	389	ARG	16.1
1	C	233	ASN	16.1
1	D	275	ALA	16.1
1	C	124	ILE	16.0
1	G	297	PRO	16.1
1	C	215	GLN	16.0
1	L	422	PHE	16.0
1	H	89	ALA	16.0
1	B	18	LEU	16.0
1	B	262	TYR	16.0
1	I	229	LEU	16.0
1	J	272	ILE	16.0
1	I	49	VAL	16.0
1	K	353	ALA	16.0

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Mol	Chain	Res	Type	RSRZ
1	K	292	PHE	16.0
1	G	31	ASP	16.0
1	D	227	ILE	16.0
1	E	136	LEU	16.0
1	C	54	SER	16.0
1	E	301	ILE	16.0
1	G	55	GLY	16.0
1	G	389	ARG	16.0
1	F	409	GLY	16.0
1	G	181	GLY	16.0
1	B	389	ARG	16.0
1	J	225	VAL	16.0
1	H	372	GLU	16.0
1	D	21	PRO	16.0
1	K	57	ILE	16.0
1	A	326	SER	16.0
1	F	411	LYS	16.0
1	I	68	VAL	15.9
1	B	370	ASN	15.9
1	H	232	ALA	15.9
1	M	144	LEU	15.9
1	L	345	ALA	15.9
1	J	382	ASN	15.9
1	J	301	ILE	15.9
1	D	426	PHE	15.9
1	J	52	THR	15.9
1	L	373	LEU	15.9
1	C	184	ILE	15.9
1	F	198	ASP	15.9
1	M	411	LYS	15.9
1	J	76	GLY	15.9
1	L	112	THR	15.9
1	A	201	ASP	15.9
1	E	196	THR	15.9
1	C	79	ASN	15.9
1	K	279	ASN	15.9
1	L	50	GLY	15.9
1	F	150	ASN	15.8
1	I	94	ALA	15.8
1	I	63	PHE	15.8
1	G	277	ALA	15.8
1	K	107	THR	15.8

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Mol	Chain	Res	Type	RSRZ
1	J	129	PHE	15.8
1	B	201	ASP	15.8
1	I	201	ASP	15.8
1	B	39	ARG	15.8
1	G	414	TRP	15.8
1	J	131	GLY	15.8
1	L	38	LEU	15.8
1	D	127	VAL	15.8
1	M	44	THR	15.8
1	F	229	LEU	15.8
1	B	243	GLY	15.8
1	D	188	GLY	15.8
1	G	61	PRO	15.8
1	I	344	GLY	15.8
1	I	104	ARG	15.8
1	M	358	ALA	15.8
1	A	17	SER	15.8
1	L	149	ALA	15.8
1	K	31	ASP	15.8
1	A	374	ILE	15.8
1	K	354	TYR	15.8
1	B	373	LEU	15.8
1	H	242	VAL	15.8
1	B	303	GLN	15.8
1	H	210	ALA	15.8
1	C	361	SER	15.8
1	D	423	ARG	15.8
1	M	16	ARG	15.8
1	D	350	THR	15.7
1	I	325	MET	15.7
1	H	162	GLU	15.7
1	K	109	ARG	15.7
1	K	76	GLY	15.7
1	H	132	SER	15.7
1	L	303	GLN	15.7
1	M	210	ALA	15.7
1	M	413	VAL	15.7
1	G	161	GLY	15.7
1	J	276	VAL	15.7
1	M	285	GLY	15.7
1	D	47	LEU	15.7
1	D	289	LEU	15.7

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Mol	Chain	Res	Type	RSRZ
1	M	162	GLU	15.7
1	M	185	PRO	15.7
1	I	266	PHE	15.7
1	A	428	GLU	15.7
1	B	416	THR	15.7
1	F	266	PHE	15.7
1	G	281	GLY	15.7
1	K	246	LEU	15.6
1	H	348	PRO	15.6
1	B	96	TYR	15.6
1	L	142	ASN	15.6
1	G	345	ALA	15.6
1	B	156	GLY	15.6
1	E	339	GLY	15.6
1	G	163	GLY	15.6
1	B	246	LEU	15.6
1	D	96	TYR	15.6
1	I	144	LEU	15.6
1	E	22	THR	15.6
1	L	211	ALA	15.6
1	E	35	LYS	15.6
1	B	227	ILE	15.6
1	A	314	THR	15.6
1	L	281	GLY	15.6
1	E	401	ILE	15.6
1	F	247	VAL	15.6
1	L	335	VAL	15.6
1	A	167	LEU	15.6
1	D	214	TYR	15.6
1	H	258	GLY	15.6
1	C	89	ALA	15.6
1	A	194	VAL	15.6
1	C	33	LEU	15.6
1	C	135	GLU	15.6
1	K	165	THR	15.6
1	A	75	GLN	15.6
1	A	137	THR	15.6
1	A	348	PRO	15.6
1	A	312	ILE	15.6
1	L	332	SER	15.6
1	H	390	PHE	15.6
1	A	174	ASP	15.6

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Mol	Chain	Res	Type	RSRZ
1	D	133	LEU	15.6
1	G	313	VAL	15.6
1	D	16	ARG	15.6
1	A	168	SER	15.6
1	K	249	ARG	15.5
1	L	388	GLY	15.5
1	A	159	LEU	15.5
1	F	184	ILE	15.5
1	K	186	ALA	15.5
1	C	146	SER	15.5
1	J	116	GLY	15.5
1	H	403	SER	15.5
1	A	347	ARG	15.5
1	I	154	LYS	15.5
1	C	352	VAL	15.5
1	F	12	VAL	15.5
1	L	206	TYR	15.5
1	A	437	LYS	15.5
1	K	219	GLN	15.5
1	M	385	THR	15.5
1	A	297	PRO	15.5
1	A	242	VAL	15.5
1	J	360	GLY	15.5
1	E	324	GLN	15.5
1	A	72	TYR	15.5
1	F	153	ASP	15.5
1	J	87	LEU	15.5
1	M	139	VAL	15.5
1	F	214	TYR	15.5
1	B	435	PRO	15.5
1	H	358	ALA	15.5
1	C	411	LYS	15.5
1	J	81	LYS	15.5
1	D	166	VAL	15.5
1	I	139	VAL	15.5
1	L	126	ALA	15.4
1	K	75	GLN	15.4
1	L	392	PRO	15.4
1	A	135	GLU	15.4
1	C	340	GLY	15.4
1	K	193	MET	15.4
1	G	387	TYR	15.4

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Mol	Chain	Res	Type	RSRZ
1	C	412	THR	15.4
1	A	423	ARG	15.4
1	M	386	GLU	15.4
1	H	198	ASP	15.4
1	J	121	ASN	15.4
1	C	58	VAL	15.4
1	H	205	VAL	15.4
1	G	14	PHE	15.4
1	I	73	THR	15.4
1	L	156	GLY	15.4
1	G	185	PRO	15.4
1	J	45	TYR	15.4
1	M	387	TYR	15.4
1	K	202	ARG	15.4
1	G	131	GLY	15.4
1	H	109	ARG	15.4
1	A	96	TYR	15.4
1	I	322	GLY	15.3
1	E	131	GLY	15.3
1	G	303	GLN	15.3
1	J	168	SER	15.3
1	K	144	LEU	15.3
1	H	62	GLY	15.3
1	K	346	LEU	15.3
1	J	304	PRO	15.3
1	B	41	GLU	15.3
1	F	194	VAL	15.3
1	I	66	SER	15.3
1	B	204	ARG	15.3
1	B	430	ALA	15.3
1	E	204	ARG	15.3
1	M	249	ARG	15.3
1	G	408	LEU	15.3
1	B	69	GLY	15.3
1	G	108	VAL	15.3
1	I	383	LEU	15.3
1	K	209	THR	15.3
1	B	124	ILE	15.3
1	E	63	PHE	15.3
1	A	309	LYS	15.3
1	B	390	PHE	15.3
1	F	223	GLY	15.3

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Mol	Chain	Res	Type	RSRZ
1	F	163	GLY	15.3
1	B	210	ALA	15.2
1	G	291	PRO	15.2
1	E	109	ARG	15.2
1	E	361	SER	15.2
1	C	292	PHE	15.2
1	A	113	LEU	15.2
1	E	405	ARG	15.2
1	H	106	LEU	15.2
1	E	132	SER	15.2
1	C	288	ASN	15.2
1	E	180	LEU	15.2
1	K	73	THR	15.2
1	B	241	SER	15.2
1	K	93	PRO	15.2
1	I	224	GLY	15.2
1	H	419	TYR	15.2
1	G	199	SER	15.2
1	I	369	SER	15.2
1	J	140	SER	15.2
1	E	233	ASN	15.2
1	F	136	LEU	15.2
1	E	130	GLN	15.2
1	M	201	ASP	15.2
1	C	136	LEU	15.2
1	J	427	MET	15.2
1	A	354	TYR	15.2
1	E	156	GLY	15.2
1	K	352	VAL	15.2
1	A	216	PHE	15.2
1	F	233	ASN	15.1
1	H	135	GLU	15.1
1	H	316	LYS	15.1
1	M	18	LEU	15.1
1	G	28	ILE	15.1
1	B	63	PHE	15.1
1	L	155	ILE	15.1
1	E	250	THR	15.1
1	J	167	LEU	15.1
1	M	182	ASP	15.1
1	E	350	THR	15.1
1	F	69	GLY	15.1

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Mol	Chain	Res	Type	RSRZ
1	B	106	LEU	15.1
1	L	203	PRO	15.1
1	F	288	ASN	15.1
1	A	118	TYR	15.1
1	B	263	LEU	15.1
1	E	387	TYR	15.1
1	G	284	THR	15.1
1	F	355	GLU	15.1
1	J	363	VAL	15.1
1	M	193	MET	15.1
1	A	155	ILE	15.1
1	J	378	GLU	15.1
1	A	107	THR	15.0
1	J	383	LEU	15.0
1	F	353	ALA	15.0
1	C	338	HIS	15.0
1	D	234	ILE	15.0
1	B	362	VAL	15.0
1	A	74	LEU	15.0
1	M	216	PHE	15.0
1	H	411	LYS	15.0
1	K	242	VAL	15.0
1	K	176	GLY	15.0
1	L	101	LEU	15.0
1	H	128	THR	15.0
1	L	263	LEU	15.0
1	L	148	THR	15.0
1	B	147	ALA	15.0
1	L	306	THR	15.0
1	C	354	TYR	15.0
1	E	353	ALA	15.0
1	A	266	PHE	15.0
1	B	380	ALA	15.0
1	E	74	LEU	15.0
1	A	375	PRO	15.0
1	C	355	GLU	15.0
1	M	365	VAL	15.0
1	L	159	LEU	15.0
1	D	165	THR	14.9
1	L	378	GLU	14.9
1	G	366	ALA	14.9
1	A	421	ASP	14.9

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Mol	Chain	Res	Type	RSRZ
1	E	437	LYS	14.9
1	C	337	ILE	14.9
1	E	172	SER	14.9
1	H	430	ALA	14.9
1	E	341	ASN	14.9
1	A	20	MET	14.9
1	F	140	SER	14.9
1	H	175	LEU	14.9
1	I	105	SER	14.9
1	K	134	SER	14.9
1	M	242	VAL	14.9
1	D	180	LEU	14.9
1	A	282	LEU	14.9
1	C	370	ASN	14.9
1	I	265	GLY	14.9
1	L	411	LYS	14.9
1	E	164	VAL	14.9
1	M	306	THR	14.9
1	M	388	GLY	14.9
1	M	20	MET	14.9
1	H	21	PRO	14.9
1	E	414	TRP	14.9
1	I	157	ASN	14.9
1	D	156	GLY	14.9
1	L	238	THR	14.9
1	K	106	LEU	14.9
1	F	300	GLU	14.9
1	I	55	GLY	14.9
1	M	74	LEU	14.9
1	A	119	ALA	14.8
1	B	114	PRO	14.8
1	H	193	MET	14.8
1	D	334	ALA	14.8
1	G	44	THR	14.8
1	A	276	VAL	14.8
1	D	277	ALA	14.8
1	F	82	PHE	14.8
1	K	356	ARG	14.8
1	I	65	GLY	14.8
1	F	168	SER	14.8
1	I	422	PHE	14.8
1	H	220	TYR	14.8

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Mol	Chain	Res	Type	RSRZ
1	J	303	GLN	14.8
1	F	14	PHE	14.8
1	I	277	ALA	14.8
1	I	386	GLU	14.8
1	G	114	PRO	14.8
1	B	158	VAL	14.8
1	B	365	VAL	14.8
1	G	273	THR	14.8
1	B	77	ASN	14.8
1	F	268	GLY	14.8
1	I	193	MET	14.8
1	F	179	ARG	14.8
1	L	84	GLN	14.8
1	F	282	LEU	14.8
1	D	132	SER	14.8
1	F	27	SER	14.8
1	G	421	ASP	14.8
1	F	68	VAL	14.8
1	F	3	ASN	14.8
1	I	158	VAL	14.8
1	I	346	LEU	14.8
1	M	232	ALA	14.8
1	L	371	PHE	14.7
1	C	188	GLY	14.7
1	M	344	GLY	14.7
1	C	374	ILE	14.7
1	G	34	GLU	14.7
1	J	327	TRP	14.7
1	L	292	PHE	14.7
1	E	189	LEU	14.7
1	B	218	SER	14.7
1	J	274	ARG	14.7
1	B	411	LYS	14.7
1	M	129	PHE	14.7
1	A	146	SER	14.7
1	G	101	LEU	14.7
1	K	66	SER	14.7
1	K	92	LEU	14.7
1	I	385	THR	14.7
1	F	258	GLY	14.7
1	J	62	GLY	14.7
1	L	16	ARG	14.7

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Mol	Chain	Res	Type	RSRZ
1	F	171	THR	14.7
1	J	127	VAL	14.7
1	D	380	ALA	14.7
1	G	19	LEU	14.7
1	I	44	THR	14.7
1	L	277	ALA	14.7
1	M	430	ALA	14.7
1	I	256	VAL	14.7
1	D	258	GLY	14.7
1	B	191	PRO	14.6
1	G	413	VAL	14.6
1	K	309	LYS	14.6
1	L	75	GLN	14.6
1	A	26	ALA	14.6
1	H	71	HIS	14.6
1	C	394	ALA	14.6
1	K	300	GLU	14.6
1	F	31	ASP	14.6
1	K	67	ILE	14.6
1	B	271	VAL	14.6
1	H	105	SER	14.6
1	C	371	PHE	14.6
1	I	301	ILE	14.6
1	H	171	THR	14.6
1	M	231	SER	14.6
1	C	198	ASP	14.6
1	E	127	VAL	14.6
1	F	424	GLU	14.6
1	C	122	GLY	14.6
1	L	109	ARG	14.6
1	A	22	THR	14.6
1	B	13	PRO	14.5
1	B	95	SER	14.5
1	I	357	VAL	14.5
1	L	413	VAL	14.5
1	D	151	ILE	14.5
1	I	40	SER	14.5
1	J	239	SER	14.5
1	L	390	PHE	14.5
1	A	200	SER	14.5
1	B	128	THR	14.5
1	J	142	ASN	14.5

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Mol	Chain	Res	Type	RSRZ
1	F	426	PHE	14.5
1	E	421	ASP	14.5
1	C	271	VAL	14.5
1	K	127	VAL	14.5
1	L	394	ALA	14.5
1	A	296	ILE	14.5
1	B	159	LEU	14.5
1	C	217	SER	14.5
1	D	17	SER	14.5
1	J	28	ILE	14.5
1	E	187	ILE	14.5
1	L	132	SER	14.5
1	L	158	VAL	14.5
1	D	49	VAL	14.5
1	E	402	LEU	14.5
1	C	16	ARG	14.5
1	L	344	GLY	14.5
1	M	145	MET	14.5
1	K	161	GLY	14.5
1	B	149	ALA	14.5
1	E	298	THR	14.5
1	F	283	THR	14.5
1	F	370	ASN	14.4
1	K	293	ASN	14.4
1	K	304	PRO	14.4
1	K	146	SER	14.4
1	F	160	VAL	14.4
1	J	159	LEU	14.4
1	J	351	LEU	14.4
1	D	92	LEU	14.4
1	M	403	SER	14.4
1	E	376	ASN	14.4
1	B	417	ARG	14.4
1	E	364	THR	14.4
1	E	372	GLU	14.4
1	K	175	LEU	14.4
1	L	139	VAL	14.4
1	A	60	PHE	14.4
1	K	49	VAL	14.4
1	I	41	GLU	14.4
1	E	60	PHE	14.4
1	D	428	GLU	14.4

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Mol	Chain	Res	Type	RSRZ
1	E	206	TYR	14.4
1	F	271	VAL	14.4
1	I	408	LEU	14.4
1	K	53	GLY	14.4
1	C	48	THR	14.4
1	C	214	TYR	14.4
1	D	432	LEU	14.4
1	H	173	TYR	14.4
1	M	56	LEU	14.4
1	E	182	ASP	14.4
1	G	72	TYR	14.4
1	D	379	LEU	14.4
1	F	170	PRO	14.4
1	F	435	PRO	14.4
1	A	406	ASP	14.3
1	E	271	VAL	14.3
1	C	20	MET	14.3
1	K	79	ASN	14.3
1	J	319	GLY	14.3
1	G	138	ASP	14.3
1	G	178	VAL	14.3
1	B	283	THR	14.3
1	G	176	GLY	14.3
1	L	363	VAL	14.3
1	L	272	ILE	14.3
1	B	132	SER	14.3
1	G	113	LEU	14.3
1	D	76	GLY	14.3
1	H	262	TYR	14.3
1	K	13	PRO	14.3
1	E	398	THR	14.3
1	L	82	PHE	14.3
1	F	23	THR	14.3
1	F	58	VAL	14.3
1	J	275	ALA	14.3
1	G	305	ILE	14.3
1	F	369	SER	14.3
1	I	242	VAL	14.3
1	B	62	GLY	14.3
1	M	211	ALA	14.3
1	L	412	THR	14.3
1	J	248	PHE	14.3

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Mol	Chain	Res	Type	RSRZ
1	C	92	LEU	14.3
1	B	401	ILE	14.3
1	G	169	LEU	14.3
1	H	310	LEU	14.2
1	L	150	ASN	14.2
1	B	54	SER	14.2
1	M	395	MET	14.2
1	I	233	ASN	14.2
1	F	327	TRP	14.2
1	G	373	LEU	14.2
1	H	199	SER	14.2
1	K	156	GLY	14.2
1	F	132	SER	14.2
1	G	239	SER	14.2
1	M	370	ASN	14.2
1	A	30	ASP	14.2
1	K	81	LYS	14.2
1	J	384	VAL	14.2
1	K	61	PRO	14.2
1	F	419	TYR	14.2
1	G	351	LEU	14.2
1	H	142	ASN	14.2
1	E	71	HIS	14.2
1	G	295	VAL	14.2
1	E	87	LEU	14.2
1	C	425	TYR	14.2
1	G	217	SER	14.2
1	K	147	ALA	14.2
1	C	181	GLY	14.2
1	K	414	TRP	14.2
1	B	119	ALA	14.2
1	J	34	GLU	14.2
1	D	346	LEU	14.2
1	F	28	ILE	14.2
1	M	105	SER	14.2
1	J	345	ALA	14.2
1	G	128	THR	14.2
1	K	365	VAL	14.2
1	J	305	ILE	14.2
1	B	409	GLY	14.1
1	G	133	LEU	14.1
1	F	44	THR	14.1

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Mol	Chain	Res	Type	RSRZ
1	K	37	THR	14.1
1	D	376	ASN	14.1
1	H	57	ILE	14.1
1	I	368	VAL	14.1
1	H	265	GLY	14.1
1	E	379	LEU	14.1
1	G	338	HIS	14.1
1	H	272	ILE	14.1
1	L	70	ALA	14.1
1	E	152	ASN	14.1
1	B	43	SER	14.1
1	K	358	ALA	14.1
1	B	211	ALA	14.1
1	B	276	VAL	14.1
1	I	402	LEU	14.1
1	H	33	LEU	14.1
1	H	23	THR	14.1
1	B	308	ILE	14.1
1	D	276	VAL	14.1
1	M	194	VAL	14.1
1	J	146	SER	14.0
1	F	433	ASN	14.0
1	I	345	ALA	14.0
1	A	292	PHE	14.0
1	F	172	SER	14.0
1	C	27	SER	14.0
1	I	354	TYR	14.0
1	M	305	ILE	14.0
1	D	300	GLU	14.0
1	F	199	SER	14.0
1	C	94	ALA	14.0
1	G	58	VAL	14.0
1	J	47	LEU	14.0
1	B	19	LEU	14.0
1	G	276	VAL	14.0
1	J	282	LEU	14.0
1	L	289	LEU	14.0
1	G	377	PRO	14.0
1	M	435	PRO	14.0
1	D	358	ALA	14.0
1	A	220	TYR	14.0
1	D	158	VAL	14.0

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Mol	Chain	Res	Type	RSRZ
1	B	151	ILE	14.0
1	C	23	THR	14.0
1	K	256	VAL	14.0
1	M	15	ILE	14.0
1	G	235	ASP	14.0
1	B	58	VAL	14.0
1	B	425	TYR	14.0
1	K	348	PRO	14.0
1	L	100	ARG	14.0
1	F	144	LEU	14.0
1	L	120	LEU	13.9
1	A	40	SER	13.9
1	L	207	THR	13.9
1	F	143	GLY	13.9
1	J	238	THR	13.9
1	B	374	ILE	13.9
1	B	383	LEU	13.9
1	E	168	SER	13.9
1	E	438	ILE	13.9
1	G	64	PRO	13.9
1	L	425	TYR	13.9
1	F	157	ASN	13.9
1	L	397	TYR	13.9
1	C	114	PRO	13.9
1	M	183	PRO	13.9
1	G	36	HIS	13.9
1	C	47	LEU	13.9
1	J	257	LEU	13.9
1	J	343	PRO	13.9
1	A	67	ILE	13.9
1	L	235	ASP	13.9
1	H	213	ASP	13.9
1	C	73	THR	13.9
1	D	107	THR	13.9
1	L	125	ASN	13.9
1	I	195	ALA	13.9
1	D	389	ARG	13.9
1	M	107	THR	13.9
1	F	220	TYR	13.9
1	F	381	LYS	13.8
1	E	375	PRO	13.8
1	H	354	TYR	13.8

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Mol	Chain	Res	Type	RSRZ
1	L	65	GLY	13.8
1	G	174	ASP	13.8
1	G	97	ASN	13.8
1	L	204	ARG	13.8
1	J	321	ALA	13.8
1	L	220	TYR	13.8
1	M	312	ILE	13.8
1	L	58	VAL	13.8
1	G	76	GLY	13.8
1	M	85	MET	13.8
1	K	212	ASP	13.8
1	G	17	SER	13.8
1	F	261	ILE	13.8
1	J	109	ARG	13.8
1	K	189	LEU	13.8
1	J	295	VAL	13.8
1	C	72	TYR	13.8
1	K	260	THR	13.8
1	A	58	VAL	13.8
1	J	401	ILE	13.8
1	C	138	ASP	13.8
1	D	14	PHE	13.8
1	L	414	TRP	13.8
1	A	233	ASN	13.8
1	F	436	LEU	13.8
1	L	45	TYR	13.8
1	G	18	LEU	13.8
1	B	169	LEU	13.7
1	A	234	ILE	13.7
1	C	74	LEU	13.7
1	J	122	GLY	13.7
1	E	37	THR	13.7
1	A	285	GLY	13.7
1	F	429	VAL	13.7
1	H	97	ASN	13.7
1	K	194	VAL	13.7
1	L	334	ALA	13.7
1	K	45	TYR	13.7
1	H	384	VAL	13.7
1	D	360	GLY	13.7
1	M	308	ILE	13.7
1	A	384	VAL	13.7

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Mol	Chain	Res	Type	RSRZ
1	L	74	LEU	13.7
1	F	362	VAL	13.7
1	G	111	SER	13.7
1	H	182	ASP	13.7
1	K	110	SER	13.7
1	F	430	ALA	13.7
1	I	88	THR	13.7
1	G	166	VAL	13.7
1	H	368	VAL	13.7
1	B	298	THR	13.7
1	K	238	THR	13.7
1	M	175	LEU	13.7
1	B	229	LEU	13.6
1	I	400	LEU	13.6
1	F	425	TYR	13.6
1	J	180	LEU	13.6
1	L	208	ILE	13.6
1	K	355	GLU	13.6
1	L	174	ASP	13.6
1	B	357	VAL	13.6
1	C	306	THR	13.6
1	M	345	ALA	13.6
1	B	282	LEU	13.6
1	D	146	SER	13.6
1	G	335	VAL	13.6
1	G	145	MET	13.6
1	E	16	ARG	13.6
1	J	353	ALA	13.6
1	H	31	ASP	13.6
1	L	25	PRO	13.6
1	E	275	ALA	13.6
1	K	108	VAL	13.6
1	L	122	GLY	13.6
1	G	388	GLY	13.6
1	E	433	ASN	13.6
1	H	134	SER	13.6
1	M	95	SER	13.6
1	I	319	GLY	13.6
1	J	53	GLY	13.6
1	B	79	ASN	13.6
1	D	20	MET	13.6
1	A	241	SER	13.6

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Mol	Chain	Res	Type	RSRZ
1	D	381	LYS	13.6
1	B	168	SER	13.6
1	B	60	PHE	13.5
1	G	180	LEU	13.5
1	F	371	PHE	13.5
1	G	179	ARG	13.5
1	B	28	ILE	13.5
1	K	302	THR	13.5
1	M	33	LEU	13.5
1	D	31	ASP	13.5
1	D	416	THR	13.5
1	D	417	ARG	13.5
1	I	53	GLY	13.5
1	M	274	ARG	13.5
1	F	182	ASP	13.5
1	G	208	ILE	13.5
1	C	388	GLY	13.5
1	K	117	VAL	13.5
1	E	283	THR	13.5
1	G	205	VAL	13.5
1	M	214	TYR	13.5
1	L	61	PRO	13.5
1	F	270	THR	13.5
1	E	306	THR	13.5
1	H	68	VAL	13.5
1	M	49	VAL	13.5
1	K	54	SER	13.5
1	K	28	ILE	13.5
1	H	428	GLU	13.5
1	H	165	THR	13.5
1	F	158	VAL	13.4
1	J	270	THR	13.4
1	I	296	ILE	13.4
1	A	162	GLU	13.4
1	M	36	HIS	13.4
1	D	24	GLY	13.4
1	D	129	PHE	13.4
1	I	281	GLY	13.4
1	M	168	SER	13.4
1	F	264	ILE	13.4
1	J	161	GLY	13.4
1	E	86	LEU	13.4

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Mol	Chain	Res	Type	RSRZ
1	B	166	VAL	13.4
1	L	242	VAL	13.4
1	E	322	GLY	13.4
1	E	351	LEU	13.4
1	B	234	ILE	13.4
1	G	24	GLY	13.4
1	C	404	GLU	13.4
1	C	358	ALA	13.4
1	C	173	TYR	13.4
1	H	17	SER	13.4
1	F	9	GLN	13.4
1	L	247	VAL	13.4
1	A	367	GLY	13.4
1	D	42	THR	13.4
1	D	296	ILE	13.4
1	L	52	THR	13.4
1	H	28	ILE	13.4
1	A	204	ARG	13.4
1	G	160	VAL	13.4
1	M	301	ILE	13.4
1	H	40	SER	13.4
1	H	277	ALA	13.4
1	L	66	SER	13.4
1	K	262	TYR	13.4
1	B	398	THR	13.3
1	E	29	PRO	13.3
1	K	274	ARG	13.3
1	D	179	ARG	13.3
1	D	73	THR	13.3
1	K	33	LEU	13.3
1	E	238	THR	13.3
1	J	145	MET	13.3
1	M	104	ARG	13.3
1	E	38	LEU	13.3
1	H	178	VAL	13.3
1	H	433	ASN	13.3
1	F	373	LEU	13.3
1	E	154	LYS	13.3
1	B	101	LEU	13.3
1	I	60	PHE	13.3
1	A	238	THR	13.3
1	L	340	GLY	13.3

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Mol	Chain	Res	Type	RSRZ
1	L	189	LEU	13.3
1	B	93	PRO	13.3
1	E	181	GLY	13.3
1	H	375	PRO	13.3
1	K	99	CYS	13.3
1	A	346	LEU	13.3
1	J	349	VAL	13.3
1	C	434	SER	13.3
1	F	152	ASN	13.3
1	M	432	LEU	13.3
1	H	145	MET	13.3
1	I	58	VAL	13.3
1	B	134	SER	13.3
1	C	103	SER	13.2
1	J	150	ASN	13.2
1	G	310	LEU	13.2
1	I	99	CYS	13.2
1	I	415	PRO	13.2
1	A	426	PHE	13.2
1	F	74	LEU	13.2
1	B	214	TYR	13.2
1	F	155	ILE	13.2
1	M	180	LEU	13.2
1	E	297	PRO	13.2
1	I	387	TYR	13.2
1	G	380	ALA	13.2
1	D	429	VAL	13.2
1	I	257	LEU	13.2
1	L	305	ILE	13.2
1	A	28	ILE	13.2
1	C	19	LEU	13.2
1	A	258	GLY	13.2
1	A	43	SER	13.2
1	G	129	PHE	13.2
1	A	301	ILE	13.2
1	J	294	LEU	13.2
1	L	248	PHE	13.2
1	H	379	LEU	13.2
1	A	414	TRP	13.2
1	J	66	SER	13.2
1	B	20	MET	13.2
1	H	115	GLY	13.2

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Mol	Chain	Res	Type	RSRZ
1	I	171	THR	13.2
1	I	388	GLY	13.2
1	G	23	THR	13.2
1	K	125	ASN	13.1
1	H	303	GLN	13.1
1	C	242	VAL	13.1
1	M	133	LEU	13.1
1	I	361	SER	13.1
1	G	29	PRO	13.1
1	C	365	VAL	13.1
1	D	335	VAL	13.1
1	L	294	LEU	13.1
1	B	167	LEU	13.1
1	L	312	ILE	13.1
1	G	110	SER	13.1
1	J	271	VAL	13.1
1	K	325	MET	13.1
1	B	223	GLY	13.1
1	G	60	PHE	13.1
1	K	74	LEU	13.1
1	H	301	ILE	13.1
1	F	43	SER	13.1
1	H	236	ALA	13.1
1	M	424	GLU	13.0
1	D	167	LEU	13.0
1	E	255	LEU	13.0
1	C	160	VAL	13.0
1	D	124	ILE	13.0
1	C	266	PHE	13.0
1	F	124	ILE	13.0
1	H	296	ILE	13.0
1	D	235	ASP	13.0
1	G	25	PRO	13.0
1	E	120	LEU	13.0
1	K	23	THR	13.0
1	C	326	SER	13.0
1	E	309	LYS	13.0
1	M	101	LEU	13.0
1	L	282	LEU	13.0
1	M	235	ASP	13.0
1	J	67	ILE	13.0
1	E	308	ILE	13.0

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Mol	Chain	Res	Type	RSRZ
1	F	108	VAL	13.0
1	F	239	SER	13.0
1	E	221	GLN	13.0
1	E	304	PRO	13.0
1	J	255	LEU	13.0
1	A	263	LEU	13.0
1	M	37	THR	12.9
1	B	91	ASN	12.9
1	F	94	ALA	12.9
1	E	281	GLY	12.9
1	J	154	LYS	12.9
1	D	41	GLU	12.9
1	F	134	SER	12.9
1	K	371	PHE	12.9
1	C	113	LEU	12.9
1	F	32	THR	12.9
1	F	232	ALA	12.9
1	L	134	SER	12.9
1	H	148	THR	12.9
1	D	434	SER	12.9
1	A	181	GLY	12.9
1	A	15	ILE	12.9
1	H	222	PRO	12.9
1	E	167	LEU	12.9
1	D	388	GLY	12.9
1	J	297	PRO	12.9
1	M	256	VAL	12.9
1	C	194	VAL	12.9
1	G	116	GLY	12.9
1	M	42	THR	12.9
1	E	315	SER	12.9
1	B	64	PRO	12.8
1	D	425	TYR	12.8
1	B	412	THR	12.8
1	M	47	LEU	12.8
1	M	128	THR	12.8
1	E	194	VAL	12.8
1	A	254	GLY	12.8
1	K	72	TYR	12.8
1	L	275	ALA	12.8
1	E	435	PRO	12.8
1	J	101	LEU	12.8

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Mol	Chain	Res	Type	RSRZ
1	I	143	GLY	12.8
1	L	144	LEU	12.8
1	B	198	ASP	12.8
1	B	420	THR	12.8
1	C	85	MET	12.8
1	I	237	ILE	12.8
1	J	23	THR	12.8
1	C	316	LYS	12.8
1	C	238	THR	12.8
1	L	123	THR	12.8
1	G	391	ASP	12.8
1	D	415	PRO	12.8
1	H	147	ALA	12.8
1	L	410	ILE	12.8
1	F	56	LEU	12.8
1	M	377	PRO	12.8
1	D	349	VAL	12.8
1	K	331	GLY	12.8
1	L	19	LEU	12.8
1	D	199	SER	12.7
1	L	24	GLY	12.7
1	G	207	THR	12.7
1	I	370	ASN	12.7
1	J	44	THR	12.7
1	B	361	SER	12.7
1	H	367	GLY	12.7
1	A	259	VAL	12.7
1	C	66	SER	12.7
1	M	200	SER	12.7
1	M	383	LEU	12.7
1	J	134	SER	12.7
1	D	85	MET	12.7
1	I	142	ASN	12.7
1	K	423	ARG	12.7
1	C	402	LEU	12.7
1	H	168	SER	12.7
1	L	368	VAL	12.7
1	F	104	ARG	12.7
1	F	350	THR	12.7
1	B	175	LEU	12.7
1	A	120	LEU	12.7
1	J	263	LEU	12.7

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Mol	Chain	Res	Type	RSRZ
1	A	66	SER	12.7
1	F	87	LEU	12.7
1	G	158	VAL	12.7
1	A	93	PRO	12.7
1	F	434	SER	12.6
1	E	371	PHE	12.6
1	H	157	ASN	12.6
1	F	45	TYR	12.6
1	C	28	ILE	12.6
1	E	195	ALA	12.6
1	C	39	ARG	12.6
1	H	383	LEU	12.6
1	C	178	VAL	12.6
1	A	18	LEU	12.6
1	C	129	PHE	12.6
1	C	408	LEU	12.6
1	B	61	PRO	12.6
1	C	18	LEU	12.6
1	B	427	MET	12.6
1	D	112	THR	12.6
1	L	138	ASP	12.6
1	L	182	ASP	12.6
1	L	273	THR	12.6
1	A	202	ARG	12.6
1	E	126	ALA	12.6
1	G	365	VAL	12.6
1	H	167	LEU	12.5
1	B	49	VAL	12.5
1	E	413	VAL	12.5
1	M	108	VAL	12.5
1	A	189	LEU	12.5
1	G	334	ALA	12.5
1	M	61	PRO	12.5
1	I	258	GLY	12.5
1	H	414	TRP	12.5
1	C	117	VAL	12.5
1	J	409	GLY	12.5
1	D	198	ASP	12.5
1	F	30	ASP	12.5
1	D	239	SER	12.5
1	M	434	SER	12.5
1	C	212	ASP	12.5

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Mol	Chain	Res	Type	RSRZ
1	I	259	VAL	12.5
1	G	283	THR	12.5
1	F	297	PRO	12.5
1	E	310	LEU	12.5
1	G	220	TYR	12.5
1	J	133	LEU	12.5
1	M	410	ILE	12.5
1	L	181	GLY	12.5
1	C	243	GLY	12.5
1	M	87	LEU	12.5
1	C	193	MET	12.4
1	A	46	ASN	12.4
1	B	301	ILE	12.4
1	J	58	VAL	12.4
1	J	175	LEU	12.4
1	K	91	ASN	12.4
1	C	127	VAL	12.4
1	M	275	ALA	12.4
1	J	14	PHE	12.4
1	C	24	GLY	12.4
1	K	289	LEU	12.4
1	A	417	ARG	12.4
1	D	139	VAL	12.4
1	I	134	SER	12.4
1	C	148	THR	12.4
1	J	103	SER	12.4
1	C	211	ALA	12.4
1	J	38	LEU	12.4
1	J	126	ALA	12.4
1	K	68	VAL	12.4
1	K	332	SER	12.4
1	G	127	VAL	12.4
1	F	289	LEU	12.4
1	D	62	GLY	12.4
1	H	63	PHE	12.4
1	L	17	SER	12.4
1	K	182	ASP	12.3
1	B	48	THR	12.3
1	M	371	PHE	12.3
1	C	345	ALA	12.3
1	J	91	ASN	12.3
1	G	374	ILE	12.3

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Mol	Chain	Res	Type	RSRZ
1	L	60	PHE	12.3
1	B	155	ILE	12.3
1	B	38	LEU	12.3
1	I	81	LYS	12.3
1	C	348	PRO	12.3
1	E	67	ILE	12.3
1	G	137	THR	12.3
1	D	422	PHE	12.3
1	D	414	TRP	12.3
1	A	23	THR	12.3
1	G	75	GLN	12.3
1	H	177	TYR	12.3
1	E	186	ALA	12.3
1	F	201	ASP	12.3
1	C	145	MET	12.3
1	K	195	ALA	12.3
1	H	252	VAL	12.3
1	K	207	THR	12.2
1	F	432	LEU	12.2
1	J	265	GLY	12.2
1	A	100	ARG	12.2
1	C	101	LEU	12.2
1	K	103	SER	12.2
1	F	64	PRO	12.2
1	B	23	THR	12.2
1	K	349	VAL	12.2
1	D	257	LEU	12.2
1	E	373	LEU	12.2
1	G	21	PRO	12.2
1	E	116	GLY	12.2
1	G	294	LEU	12.2
1	A	151	ILE	12.2
1	A	13	PRO	12.2
1	H	389	ARG	12.2
1	B	238	THR	12.2
1	E	114	PRO	12.2
1	L	387	TYR	12.2
1	E	383	LEU	12.2
1	I	210	ALA	12.1
1	G	45	TYR	12.1
1	A	324	GLN	12.1
1	I	174	ASP	12.1

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Mol	Chain	Res	Type	RSRZ
1	K	303	GLN	12.1
1	L	426	PHE	12.1
1	M	170	PRO	12.1
1	M	68	VAL	12.1
1	B	76	GLY	12.1
1	J	88	THR	12.1
1	J	93	PRO	12.1
1	I	127	VAL	12.1
1	G	168	SER	12.1
1	A	134	SER	12.1
1	A	87	LEU	12.1
1	D	292	PHE	12.1
1	M	234	ILE	12.1
1	M	160	VAL	12.1
1	H	155	ILE	12.1
1	F	391	ASP	12.1
1	K	360	GLY	12.1
1	H	104	ARG	12.1
1	J	100	ARG	12.1
1	K	132	SER	12.1
1	E	115	GLY	12.1
1	H	172	SER	12.1
1	D	367	GLY	12.1
1	J	211	ALA	12.0
1	I	87	LEU	12.0
1	M	272	ILE	12.0
1	H	306	THR	12.0
1	B	369	SER	12.0
1	B	277	ALA	12.0
1	I	348	PRO	12.0
1	M	31	ASP	12.0
1	K	139	VAL	12.0
1	E	57	ILE	12.0
1	K	104	ARG	12.0
1	K	155	ILE	12.0
1	E	148	THR	12.0
1	D	105	SER	12.0
1	C	427	MET	12.0
1	D	390	PHE	12.0
1	D	408	LEU	12.0
1	F	349	VAL	12.0
1	B	141	TYR	12.0

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Mol	Chain	Res	Type	RSRZ
1	H	369	SER	12.0
1	H	425	TYR	12.0
1	A	325	MET	12.0
1	K	158	VAL	12.0
1	M	220	TYR	12.0
1	E	33	LEU	12.0
1	B	257	LEU	12.0
1	L	108	VAL	12.0
1	C	97	ASN	12.0
1	C	235	ASP	11.9
1	H	159	LEU	11.9
1	I	91	ASN	11.9
1	M	428	GLU	11.9
1	F	105	SER	11.9
1	D	401	ILE	11.9
1	C	440	GLY	11.9
1	J	138	ASP	11.9
1	K	118	TYR	11.9
1	E	165	THR	11.9
1	E	105	SER	11.9
1	I	235	ASP	11.9
1	F	174	ASP	11.9
1	K	310	LEU	11.9
1	M	27	SER	11.8
1	M	103	SER	11.8
1	D	236	ALA	11.8
1	E	321	ALA	11.8
1	J	158	VAL	11.8
1	I	74	LEU	11.8
1	B	413	VAL	11.8
1	H	30	ASP	11.8
1	D	104	ARG	11.8
1	I	131	GLY	11.8
1	A	32	THR	11.8
1	G	331	GLY	11.8
1	L	31	ASP	11.8
1	A	65	GLY	11.8
1	F	177	TYR	11.8
1	K	56	LEU	11.8
1	J	431	ASP	11.8
1	A	321	ALA	11.8
1	G	175	LEU	11.8

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Mol	Chain	Res	Type	RSRZ
1	L	293	ASN	11.8
1	C	426	PHE	11.8
1	I	363	VAL	11.8
1	M	148	THR	11.8
1	D	315	SER	11.8
1	F	388	GLY	11.8
1	D	63	PHE	11.8
1	G	410	ILE	11.8
1	L	361	SER	11.8
1	J	99	CYS	11.8
1	F	180	LEU	11.8
1	A	180	LEU	11.8
1	M	71	HIS	11.8
1	H	212	ASP	11.8
1	K	301	ILE	11.8
1	A	195	ALA	11.8
1	I	109	ARG	11.8
1	H	164	VAL	11.8
1	K	180	LEU	11.8
1	E	352	VAL	11.7
1	H	166	VAL	11.7
1	D	61	PRO	11.7
1	E	432	LEU	11.7
1	C	83	ASP	11.7
1	H	413	VAL	11.7
1	C	119	ALA	11.7
1	D	18	LEU	11.7
1	D	407	ARG	11.7
1	K	58	VAL	11.7
1	A	62	GLY	11.7
1	M	24	GLY	11.7
1	M	219	GLN	11.7
1	C	60	PHE	11.7
1	F	375	PRO	11.7
1	F	10	GLN	11.7
1	G	150	ASN	11.7
1	M	310	LEU	11.7
1	H	64	PRO	11.7
1	D	363	VAL	11.7
1	H	163	GLY	11.7
1	D	144	LEU	11.7
1	H	102	VAL	11.7

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Mol	Chain	Res	Type	RSRZ
1	E	257	LEU	11.7
1	G	62	GLY	11.7
1	B	57	ILE	11.7
1	J	280	ASN	11.7
1	J	210	ALA	11.7
1	H	412	THR	11.7
1	J	21	PRO	11.7
1	K	259	VAL	11.7
1	L	76	GLY	11.7
1	D	147	ALA	11.7
1	J	296	ILE	11.7
1	K	258	GLY	11.7
1	D	242	VAL	11.6
1	D	57	ILE	11.6
1	J	331	GLY	11.6
1	K	62	GLY	11.6
1	M	429	VAL	11.6
1	C	281	GLY	11.6
1	M	369	SER	11.6
1	B	346	LEU	11.6
1	D	113	LEU	11.6
1	M	307	SER	11.6
1	A	149	ALA	11.6
1	M	111	SER	11.6
1	K	187	ILE	11.6
1	L	81	LYS	11.6
1	M	166	VAL	11.6
1	D	430	ALA	11.6
1	A	82	PHE	11.6
1	E	18	LEU	11.6
1	K	105	SER	11.6
1	I	366	ALA	11.6
1	H	137	THR	11.6
1	J	281	GLY	11.5
1	E	111	SER	11.5
1	H	25	PRO	11.5
1	H	45	TYR	11.5
1	F	428	GLU	11.5
1	A	361	SER	11.5
1	A	368	VAL	11.5
1	E	434	SER	11.5
1	B	125	ASN	11.5

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Mol	Chain	Res	Type	RSRZ
1	A	103	SER	11.5
1	H	200	SER	11.5
1	J	144	LEU	11.5
1	B	310	LEU	11.5
1	G	346	LEU	11.5
1	G	271	VAL	11.5
1	K	181	GLY	11.5
1	L	80	TYR	11.5
1	I	108	VAL	11.5
1	J	114	PRO	11.5
1	L	34	GLU	11.5
1	E	305	ILE	11.5
1	A	389	ARG	11.5
1	M	30	ASP	11.4
1	J	97	ASN	11.4
1	G	371	PHE	11.4
1	E	249	ARG	11.4
1	D	387	TYR	11.4
1	F	346	LEU	11.4
1	B	53	GLY	11.4
1	A	333	LEU	11.4
1	H	75	GLN	11.4
1	G	144	LEU	11.4
1	J	169	LEU	11.4
1	A	205	VAL	11.4
1	J	143	GLY	11.4
1	M	127	VAL	11.4
1	A	386	GLU	11.4
1	D	369	SER	11.4
1	D	288	ASN	11.4
1	D	75	GLN	11.4
1	J	65	GLY	11.4
1	J	182	ASP	11.4
1	E	211	ALA	11.4
1	J	306	THR	11.4
1	K	60	PHE	11.4
1	M	189	LEU	11.4
1	E	46	ASN	11.4
1	F	102	VAL	11.3
1	B	90	GLN	11.3
1	G	146	SER	11.3
1	F	13	PRO	11.3

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Mol	Chain	Res	Type	RSRZ
1	I	150	ASN	11.3
1	L	251	SER	11.3
1	M	134	SER	11.3
1	C	423	ARG	11.3
1	C	429	VAL	11.3
1	B	27	SER	11.3
1	J	102	VAL	11.3
1	I	97	ASN	11.3
1	D	89	ALA	11.3
1	K	312	ILE	11.3
1	C	12	VAL	11.3
1	E	202	ARG	11.3
1	B	426	PHE	11.3
1	E	36	HIS	11.3
1	H	113	LEU	11.3
1	K	101	LEU	11.3
1	D	155	ILE	11.3
1	L	424	GLU	11.3
1	L	85	MET	11.3
1	B	429	VAL	11.3
1	E	349	VAL	11.3
1	D	86	LEU	11.2
1	A	274	ARG	11.2
1	F	146	SER	11.2
1	L	21	PRO	11.2
1	J	174	ASP	11.2
1	J	352	VAL	11.2
1	A	94	ALA	11.2
1	J	388	GLY	11.2
1	H	392	PRO	11.2
1	I	248	PHE	11.2
1	L	48	THR	11.2
1	E	388	GLY	11.2
1	G	211	ALA	11.2
1	I	220	TYR	11.2
1	E	58	VAL	11.2
1	A	371	PHE	11.1
1	K	116	GLY	11.1
1	K	388	GLY	11.1
1	I	147	ALA	11.1
1	H	154	LYS	11.1
1	C	174	ASP	11.1

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Mol	Chain	Res	Type	RSRZ
1	C	32	THR	11.1
1	D	43	SER	11.1
1	D	142	ASN	11.1
1	G	103	SER	11.1
1	F	278	ALA	11.1
1	J	400	LEU	11.1
1	L	36	HIS	11.1
1	B	127	VAL	11.1
1	F	33	LEU	11.1
1	A	42	THR	11.1
1	L	104	ARG	11.1
1	E	178	VAL	11.1
1	H	351	LEU	11.1
1	B	40	SER	11.1
1	M	81	LYS	11.1
1	A	410	ILE	11.0
1	F	24	GLY	11.0
1	I	401	ILE	11.0
1	J	29	PRO	11.0
1	L	28	ILE	11.0
1	A	95	SER	11.0
1	F	173	TYR	11.0
1	H	223	GLY	11.0
1	M	177	TYR	11.0
1	B	104	ARG	11.0
1	K	143	GLY	11.0
1	G	32	THR	11.0
1	A	360	GLY	11.0
1	C	369	SER	11.0
1	D	418	GLU	11.0
1	F	109	ARG	11.0
1	C	42	THR	11.0
1	F	103	SER	11.0
1	I	162	GLU	11.0
1	A	310	LEU	11.0
1	F	89	ALA	11.0
1	D	135	GLU	11.0
1	B	87	LEU	11.0
1	K	278	ALA	10.9
1	M	147	ALA	10.9
1	E	193	MET	10.9
1	I	394	ALA	10.9

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Mol	Chain	Res	Type	RSRZ
1	H	180	LEU	10.9
1	M	174	ASP	10.9
1	M	118	TYR	10.9
1	B	103	SER	10.9
1	L	176	GLY	10.9
1	E	117	VAL	10.9
1	E	59	PHE	10.9
1	M	372	GLU	10.9
1	D	205	VAL	10.9
1	G	26	ALA	10.9
1	M	25	PRO	10.9
1	E	280	ASN	10.9
1	F	402	LEU	10.9
1	E	369	SER	10.9
1	I	122	GLY	10.8
1	D	22	THR	10.8
1	M	106	LEU	10.8
1	I	275	ALA	10.8
1	A	86	LEU	10.8
1	G	147	ALA	10.8
1	H	66	SER	10.8
1	K	114	PRO	10.8
1	A	63	PHE	10.8
1	H	130	GLN	10.8
1	L	27	SER	10.8
1	F	21	PRO	10.8
1	B	44	THR	10.8
1	E	197	CYS	10.8
1	L	67	ILE	10.8
1	D	106	LEU	10.8
1	F	374	ILE	10.8
1	H	26	ALA	10.8
1	A	41	GLU	10.8
1	E	184	ILE	10.8
1	G	159	LEU	10.8
1	M	167	LEU	10.8
1	M	39	ARG	10.8
1	L	180	LEU	10.8
1	G	354	TYR	10.8
1	I	156	GLY	10.7
1	G	40	SER	10.7
1	K	65	GLY	10.7

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Mol	Chain	Res	Type	RSRZ
1	H	434	SER	10.7
1	B	242	VAL	10.7
1	M	173	TYR	10.7
1	J	94	ALA	10.7
1	G	143	GLY	10.7
1	H	144	LEU	10.7
1	D	241	SER	10.7
1	J	89	ALA	10.7
1	K	84	GLN	10.7
1	A	105	SER	10.7
1	J	288	ASN	10.7
1	A	59	PHE	10.7
1	E	143	GLY	10.7
1	A	71	HIS	10.7
1	J	132	SER	10.6
1	G	197	CYS	10.6
1	A	104	ARG	10.6
1	E	43	SER	10.6
1	L	427	MET	10.6
1	C	43	SER	10.6
1	J	220	TYR	10.6
1	A	198	ASP	10.6
1	F	413	VAL	10.6
1	G	349	VAL	10.6
1	G	301	ILE	10.6
1	H	143	GLY	10.6
1	A	272	ILE	10.6
1	F	351	LEU	10.6
1	L	103	SER	10.6
1	J	24	GLY	10.5
1	E	314	THR	10.5
1	H	22	THR	10.5
1	D	178	VAL	10.5
1	B	349	VAL	10.5
1	I	103	SER	10.5
1	J	31	ASP	10.5
1	J	37	THR	10.5
1	K	145	MET	10.5
1	A	365	VAL	10.5
1	K	201	ASP	10.5
1	M	367	GLY	10.5
1	M	349	VAL	10.5

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Mol	Chain	Res	Type	RSRZ
1	D	69	GLY	10.5
1	H	432	LEU	10.5
1	M	62	GLY	10.5
1	E	384	VAL	10.4
1	L	244	GLY	10.4
1	C	293	ASN	10.4
1	G	372	GLU	10.4
1	C	147	ALA	10.4
1	F	86	LEU	10.4
1	D	174	ASP	10.4
1	L	383	LEU	10.4
1	M	82	PHE	10.4
1	F	67	ILE	10.4
1	F	234	ILE	10.4
1	K	408	LEU	10.4
1	E	68	VAL	10.4
1	I	276	VAL	10.4
1	M	116	GLY	10.4
1	F	85	MET	10.4
1	E	103	SER	10.4
1	G	177	TYR	10.4
1	A	223	GLY	10.4
1	B	137	THR	10.4
1	L	256	VAL	10.4
1	K	90	GLN	10.4
1	C	151	ILE	10.3
1	F	11	ILE	10.3
1	H	435	PRO	10.3
1	H	366	ALA	10.3
1	B	71	HIS	10.3
1	B	161	GLY	10.3
1	K	141	TYR	10.3
1	C	14	PHE	10.3
1	J	181	GLY	10.3
1	E	107	THR	10.3
1	E	133	LEU	10.3
1	F	169	LEU	10.3
1	A	161	GLY	10.3
1	L	374	ILE	10.3
1	E	404	GLU	10.3
1	J	433	ASN	10.3
1	K	22	THR	10.3

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Mol	Chain	Res	Type	RSRZ
1	D	310	LEU	10.3
1	I	130	GLN	10.2
1	M	57	ILE	10.2
1	K	282	LEU	10.2
1	M	172	SER	10.2
1	H	133	LEU	10.2
1	D	170	PRO	10.2
1	K	55	GLY	10.2
1	M	237	ILE	10.2
1	E	155	ILE	10.2
1	J	377	PRO	10.2
1	K	78	GLY	10.2
1	C	26	ALA	10.2
1	B	126	ALA	10.2
1	E	436	LEU	10.2
1	B	162	GLU	10.2
1	H	32	THR	10.2
1	K	281	GLY	10.2
1	H	114	PRO	10.2
1	L	22	THR	10.2
1	F	303	GLN	10.2
1	F	63	PHE	10.2
1	I	236	ALA	10.2
1	I	12	VAL	10.2
1	F	181	GLY	10.2
1	K	38	LEU	10.2
1	I	211	ALA	10.1
1	C	102	VAL	10.1
1	F	22	THR	10.1
1	M	427	MET	10.1
1	A	14	PHE	10.1
1	F	57	ILE	10.1
1	H	19	LEU	10.1
1	G	352	VAL	10.1
1	J	264	ILE	10.1
1	J	32	THR	10.1
1	H	24	GLY	10.1
1	G	126	ALA	10.1
1	H	365	VAL	10.1
1	G	63	PHE	10.1
1	A	372	GLU	10.1
1	K	334	ALA	10.0

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Mol	Chain	Res	Type	RSRZ
1	F	389	ARG	10.0
1	J	346	LEU	10.0
1	E	104	ARG	10.0
1	B	110	SER	10.0
1	B	136	LEU	10.0
1	J	414	TRP	10.0
1	C	410	ILE	10.0
1	M	64	PRO	10.0
1	C	134	SER	10.0
1	C	22	THR	10.0
1	B	180	LEU	10.0
1	J	256	VAL	10.0
1	G	263	LEU	10.0
1	G	209	THR	10.0
1	F	145	MET	10.0
1	E	282	LEU	10.0
1	E	40	SER	9.9
1	I	93	PRO	9.9
1	A	39	ARG	9.9
1	I	414	TRP	9.9
1	G	142	ASN	9.9
1	C	305	ILE	9.9
1	F	40	SER	9.9
1	A	369	SER	9.9
1	K	372	GLU	9.9
1	B	351	LEU	9.9
1	J	147	ALA	9.9
1	D	371	PHE	9.9
1	I	128	THR	9.9
1	B	47	LEU	9.9
1	G	292	PHE	9.9
1	I	282	LEU	9.9
1	D	126	ALA	9.9
1	E	389	ARG	9.9
1	C	220	TYR	9.9
1	K	89	ALA	9.9
1	G	156	GLY	9.8
1	H	227	ILE	9.8
1	H	131	GLY	9.8
1	A	433	ASN	9.8
1	E	139	VAL	9.8
1	H	407	ARG	9.8

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Mol	Chain	Res	Type	RSRZ
1	C	132	SER	9.8
1	E	61	PRO	9.8
1	A	45	TYR	9.8
1	M	163	GLY	9.8
1	I	102	VAL	9.8
1	J	374	ILE	9.8
1	J	92	LEU	9.8
1	L	193	MET	9.8
1	B	89	ALA	9.8
1	D	420	THR	9.8
1	A	64	PRO	9.8
1	D	95	SER	9.8
1	G	125	ASN	9.8
1	H	181	GLY	9.7
1	K	88	THR	9.7
1	M	19	LEU	9.7
1	I	25	PRO	9.7
1	A	235	ASP	9.7
1	K	115	GLY	9.7
1	K	235	ASP	9.7
1	C	44	THR	9.7
1	K	14	PHE	9.7
1	E	14	PHE	9.7
1	K	27	SER	9.7
1	J	60	PHE	9.7
1	M	281	GLY	9.7
1	B	68	VAL	9.6
1	H	156	GLY	9.6
1	K	21	PRO	9.6
1	A	294	LEU	9.6
1	H	118	TYR	9.6
1	H	158	VAL	9.6
1	H	271	VAL	9.6
1	M	257	LEU	9.6
1	J	176	GLY	9.6
1	H	44	THR	9.6
1	H	263	LEU	9.6
1	G	236	ALA	9.6
1	G	140	SER	9.5
1	C	45	TYR	9.5
1	M	65	GLY	9.5
1	M	153	ASP	9.5

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Mol	Chain	Res	Type	RSRZ
1	E	101	LEU	9.5
1	F	128	THR	9.5
1	D	136	LEU	9.5
1	C	25	PRO	9.5
1	A	373	LEU	9.5
1	B	22	THR	9.5
1	C	82	PHE	9.5
1	J	289	LEU	9.4
1	E	76	GLY	9.4
1	I	132	SER	9.4
1	C	301	ILE	9.4
1	K	333	LEU	9.4
1	K	220	TYR	9.4
1	A	102	VAL	9.4
1	B	86	LEU	9.4
1	C	76	GLY	9.4
1	C	142	ASN	9.4
1	D	34	GLU	9.4
1	D	65	GLY	9.4
1	J	36	HIS	9.4
1	B	12	VAL	9.4
1	E	210	ALA	9.4
1	F	166	VAL	9.4
1	A	84	GLN	9.4
1	H	136	LEU	9.4
1	J	25	PRO	9.3
1	H	388	GLY	9.3
1	K	77	ASN	9.3
1	B	353	ALA	9.3
1	M	109	ARG	9.3
1	H	129	PHE	9.3
1	I	272	ILE	9.3
1	I	155	ILE	9.3
1	H	78	GLY	9.3
1	F	210	ALA	9.3
1	A	145	MET	9.3
1	C	140	SER	9.2
1	G	383	LEU	9.2
1	M	169	LEU	9.2
1	M	176	GLY	9.2
1	C	177	TYR	9.2
1	L	77	ASN	9.2

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Mol	Chain	Res	Type	RSRZ
1	A	68	VAL	9.2
1	M	143	GLY	9.2
1	I	133	LEU	9.2
1	C	205	VAL	9.2
1	M	66	SER	9.2
1	F	257	LEU	9.2
1	A	44	THR	9.2
1	H	266	PHE	9.2
1	M	368	VAL	9.2
1	C	118	TYR	9.2
1	F	2	THR	9.2
1	L	360	GLY	9.2
1	A	349	VAL	9.2
1	E	410	ILE	9.1
1	G	33	LEU	9.1
1	A	160	VAL	9.1
1	G	390	PHE	9.1
1	A	132	SER	9.1
1	G	155	ILE	9.1
1	C	40	SER	9.1
1	C	93	PRO	9.1
1	A	37	THR	9.1
1	A	271	VAL	9.1
1	A	429	VAL	9.1
1	M	414	TRP	9.1
1	C	195	ALA	9.1
1	I	151	ILE	9.1
1	J	371	PHE	9.1
1	C	276	VAL	9.1
1	E	175	LEU	9.0
1	M	282	LEU	9.0
1	F	71	HIS	9.0
1	H	169	LEU	9.0
1	I	116	GLY	9.0
1	M	23	THR	9.0
1	J	385	THR	9.0
1	M	425	TYR	9.0
1	J	139	VAL	9.0
1	M	14	PHE	9.0
1	I	288	ASN	9.0
1	I	373	LEU	9.0
1	B	108	VAL	8.9

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Mol	Chain	Res	Type	RSRZ
1	B	145	MET	8.9
1	H	238	THR	8.9
1	I	32	THR	8.9
1	E	69	GLY	8.9
1	F	365	VAL	8.9
1	H	116	GLY	8.9
1	I	101	LEU	8.9
1	D	111	SER	8.9
1	I	274	ARG	8.9
1	K	280	ASN	8.9
1	A	388	GLY	8.9
1	G	12	VAL	8.9
1	F	151	ILE	8.9
1	M	115	GLY	8.9
1	B	21	PRO	8.9
1	E	145	MET	8.9
1	H	261	ILE	8.9
1	L	237	ILE	8.9
1	H	305	ILE	8.9
1	C	46	ASN	8.9
1	F	368	VAL	8.9
1	L	274	ARG	8.9
1	M	102	VAL	8.8
1	M	205	VAL	8.8
1	E	147	ALA	8.8
1	G	353	ALA	8.8
1	G	117	VAL	8.8
1	K	275	ALA	8.8
1	C	366	ALA	8.8
1	D	287	ASP	8.8
1	E	177	TYR	8.8
1	G	282	LEU	8.8
1	J	249	ARG	8.8
1	E	97	ASN	8.8
1	J	115	GLY	8.7
1	E	220	TYR	8.7
1	J	141	TYR	8.7
1	B	16	ARG	8.7
1	G	22	THR	8.7
1	K	223	GLY	8.7
1	D	172	SER	8.7
1	K	63	PHE	8.7

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Mol	Chain	Res	Type	RSRZ
1	I	113	LEU	8.7
1	C	325	MET	8.7
1	A	147	ALA	8.7
1	H	138	ASP	8.7
1	F	18	LEU	8.6
1	F	415	PRO	8.6
1	I	89	ALA	8.6
1	J	237	ILE	8.6
1	F	164	VAL	8.6
1	L	301	ILE	8.6
1	I	20	MET	8.6
1	K	373	LEU	8.6
1	D	419	TYR	8.6
1	F	147	ALA	8.6
1	L	32	THR	8.6
1	K	210	ALA	8.6
1	L	29	PRO	8.6
1	F	4	LEU	8.5
1	I	223	GLY	8.5
1	D	141	TYR	8.5
1	I	271	VAL	8.5
1	I	372	GLU	8.5
1	D	201	ASP	8.5
1	B	410	ILE	8.5
1	H	410	ILE	8.5
1	G	332	SER	8.5
1	F	167	LEU	8.5
1	A	85	MET	8.5
1	F	106	LEU	8.5
1	L	118	TYR	8.4
1	I	117	VAL	8.4
1	L	151	ILE	8.4
1	E	66	SER	8.4
1	L	141	TYR	8.4
1	M	50	GLY	8.4
1	H	151	ILE	8.4
1	I	358	ALA	8.4
1	G	272	ILE	8.4
1	B	148	THR	8.4
1	D	169	LEU	8.4
1	I	170	PRO	8.4
1	D	200	SER	8.4

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Mol	Chain	Res	Type	RSRZ
1	M	236	ALA	8.3
1	L	408	LEU	8.3
1	D	175	LEU	8.3
1	F	133	LEU	8.3
1	L	346	LEU	8.3
1	H	124	ILE	8.3
1	B	356	ARG	8.3
1	J	372	GLU	8.3
1	B	163	GLY	8.3
1	C	84	GLN	8.3
1	D	71	HIS	8.3
1	I	34	GLU	8.3
1	M	41	GLU	8.3
1	M	330	ARG	8.3
1	M	21	PRO	8.3
1	H	429	VAL	8.3
1	K	64	PRO	8.3
1	B	367	GLY	8.3
1	E	102	VAL	8.2
1	F	176	GLY	8.2
1	C	41	GLU	8.2
1	I	27	SER	8.2
1	F	352	VAL	8.2
1	B	181	GLY	8.2
1	G	206	TYR	8.2
1	L	26	ALA	8.2
1	G	109	ARG	8.2
1	H	141	TYR	8.2
1	J	22	THR	8.2
1	I	19	LEU	8.2
1	F	5	GLN	8.2
1	L	342	TYR	8.2
1	F	367	GLY	8.2
1	F	394	ALA	8.1
1	C	349	VAL	8.1
1	C	175	LEU	8.1
1	B	45	TYR	8.1
1	E	166	VAL	8.1
1	F	276	VAL	8.1
1	C	282	LEU	8.1
1	K	211	ALA	8.1
1	E	129	PHE	8.1

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Mol	Chain	Res	Type	RSRZ
1	J	90	GLN	8.1
1	G	167	LEU	8.1
1	D	137	THR	8.1
1	F	427	MET	8.1
1	I	181	GLY	8.1
1	L	343	PRO	8.1
1	I	180	LEU	8.1
1	I	371	PHE	8.1
1	F	139	VAL	8.1
1	D	15	ILE	8.0
1	F	165	THR	8.0
1	J	63	PHE	8.0
1	L	63	PHE	8.0
1	B	368	VAL	8.0
1	F	410	ILE	8.0
1	L	333	LEU	8.0
1	F	383	LEU	8.0
1	H	60	PHE	8.0
1	M	13	PRO	7.9
1	F	366	ALA	7.9
1	D	109	ARG	7.9
1	D	110	SER	7.9
1	F	42	THR	7.9
1	G	66	SER	7.9
1	L	276	VAL	7.9
1	H	67	ILE	7.9
1	B	352	VAL	7.9
1	E	374	ILE	7.9
1	M	22	THR	7.9
1	I	182	ASP	7.9
1	I	21	PRO	7.9
1	B	70	ALA	7.9
1	H	65	GLY	7.9
1	H	353	ALA	7.9
1	B	436	LEU	7.8
1	H	408	LEU	7.8
1	J	33	LEU	7.8
1	E	185	PRO	7.8
1	A	184	ILE	7.8
1	H	140	SER	7.8
1	K	102	VAL	7.8
1	B	176	GLY	7.8

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Mol	Chain	Res	Type	RSRZ
1	B	439	ALA	7.8
1	D	19	LEU	7.8
1	K	257	LEU	7.8
1	G	237	ILE	7.8
1	D	108	VAL	7.8
1	M	436	LEU	7.8
1	M	26	ALA	7.8
1	J	235	ASP	7.8
1	L	62	GLY	7.8
1	J	373	LEU	7.8
1	D	32	THR	7.8
1	F	227	ILE	7.7
1	A	148	THR	7.7
1	F	235	ASP	7.7
1	B	85	MET	7.7
1	C	143	GLY	7.7
1	D	45	TYR	7.7
1	H	237	ILE	7.7
1	B	437	LYS	7.7
1	M	276	VAL	7.7
1	D	238	THR	7.7
1	E	325	MET	7.6
1	F	156	GLY	7.6
1	B	355	GLU	7.6
1	A	106	LEU	7.6
1	M	40	SER	7.6
1	A	21	PRO	7.6
1	C	144	LEU	7.6
1	M	402	LEU	7.6
1	G	67	ILE	7.5
1	F	41	GLU	7.5
1	E	234	ILE	7.5
1	D	67	ILE	7.5
1	B	414	TRP	7.5
1	J	27	SER	7.5
1	D	87	LEU	7.5
1	J	432	LEU	7.5
1	K	26	ALA	7.5
1	M	117	VAL	7.5
1	L	133	LEU	7.5
1	B	358	ALA	7.4
1	E	125	ASN	7.4

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Mol	Chain	Res	Type	RSRZ
1	M	67	ILE	7.4
1	J	26	ALA	7.4
1	D	103	SER	7.4
1	D	366	ALA	7.4
1	A	25	PRO	7.4
1	I	249	ARG	7.4
1	F	148	THR	7.4
1	C	346	LEU	7.4
1	B	25	PRO	7.3
1	B	14	PHE	7.3
1	B	419	TYR	7.3
1	D	70	ALA	7.3
1	E	15	ILE	7.3
1	H	214	TYR	7.3
1	B	133	LEU	7.3
1	D	368	VAL	7.3
1	F	120	LEU	7.3
1	I	115	GLY	7.3
1	F	127	VAL	7.3
1	C	236	ALA	7.2
1	C	180	LEU	7.2
1	E	70	ALA	7.2
1	H	70	ALA	7.2
1	H	427	MET	7.2
1	I	114	PRO	7.2
1	D	383	LEU	7.2
1	A	92	LEU	7.2
1	H	127	VAL	7.2
1	I	129	PHE	7.2
1	H	101	LEU	7.1
1	J	394	ALA	7.1
1	D	237	ILE	7.1
1	D	145	MET	7.1
1	I	90	GLN	7.1
1	F	25	PRO	7.1
1	L	49	VAL	7.1
1	A	69	GLY	7.1
1	A	304	PRO	7.0
1	D	66	SER	7.0
1	M	401	ILE	7.0
1	F	238	THR	7.0
1	I	29	PRO	7.0

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Mol	Chain	Res	Type	RSRZ
1	B	438	ILE	7.0
1	I	118	TYR	6.9
1	H	352	VAL	6.9
1	D	68	VAL	6.9
1	M	366	ALA	6.9
1	C	176	GLY	6.9
1	F	200	SER	6.9
1	M	38	LEU	6.8
1	E	26	ALA	6.8
1	F	29	PRO	6.8
1	M	63	PHE	6.8
1	F	1	MET	6.8
1	F	119	ALA	6.8
1	K	133	LEU	6.8
1	E	24	GLY	6.8
1	F	390	PHE	6.8
1	K	25	PRO	6.8
1	J	12	VAL	6.7
1	M	113	LEU	6.7
1	C	139	VAL	6.7
1	E	21	PRO	6.7
1	F	141	TYR	6.7
1	A	366	ALA	6.7
1	D	25	PRO	6.7
1	F	19	LEU	6.7
1	E	235	ASP	6.7
1	F	175	LEU	6.7
1	A	38	LEU	6.7
1	A	101	LEU	6.6
1	K	236	ALA	6.6
1	A	24	GLY	6.6
1	J	13	PRO	6.6
1	I	141	TYR	6.6
1	D	173	TYR	6.6
1	E	64	PRO	6.6
1	G	139	VAL	6.6
1	A	70	ALA	6.5
1	A	133	LEU	6.5
1	H	374	ILE	6.5
1	L	116	GLY	6.5
1	E	205	VAL	6.4
1	C	133	LEU	6.4

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Mol	Chain	Res	Type	RSRZ
1	B	235	ASP	6.3
1	G	151	ILE	6.3
1	F	129	PHE	6.3
1	E	276	VAL	6.3
1	A	432	LEU	6.3
1	M	331	GLY	6.3
1	B	440	GLY	6.3
1	K	276	VAL	6.2
1	F	395	MET	6.2
1	D	176	GLY	6.2
1	F	101	LEU	6.2
1	H	426	PHE	6.2
1	C	65	GLY	6.2
1	F	384	VAL	6.2
1	B	402	LEU	6.2
1	B	237	ILE	6.2
1	F	65	GLY	6.2
1	E	278	ALA	6.1
1	C	237	ILE	6.1
1	B	94	ALA	6.1
1	K	24	GLY	6.0
1	E	118	TYR	6.0
1	F	414	TRP	6.0
1	B	366	ALA	6.0
1	E	65	GLY	6.0
1	D	101	LEU	6.0
1	F	26	ALA	6.0
1	D	351	LEU	5.9
1	H	125	ASN	5.9
1	K	87	LEU	5.9
1	B	160	VAL	5.9
1	A	431	ASP	5.8
1	L	33	LEU	5.8
1	A	305	ILE	5.8
1	B	177	TYR	5.8
1	E	365	VAL	5.8
1	G	65	GLY	5.7
1	I	26	ALA	5.7
1	D	177	TYR	5.7
1	I	33	LEU	5.7
1	D	29	PRO	5.7
1	A	19	LEU	5.7

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Mol	Chain	Res	Type	RSRZ
1	B	66	SER	5.7
1	E	13	PRO	5.6
1	F	70	ALA	5.6
1	F	236	ALA	5.6
1	H	117	VAL	5.6
1	E	25	PRO	5.5
1	I	28	ILE	5.5
1	F	117	VAL	5.5
1	A	236	ALA	5.5
1	A	430	ALA	5.4
1	H	349	VAL	5.4
1	D	365	VAL	5.4
1	D	44	THR	5.4
1	G	210	ALA	5.3
1	E	108	VAL	5.3
1	E	201	ASP	5.3
1	D	102	VAL	5.3
1	E	277	ALA	5.3
1	D	33	LEU	5.3
1	I	23	THR	5.3
1	B	236	ALA	5.3
1	D	26	ALA	5.3
1	E	176	GLY	5.2
1	B	67	ILE	5.2
1	E	45	TYR	5.2
1	F	66	SER	5.0
1	D	352	VAL	5.0
1	G	141	TYR	5.0
1	K	277	ALA	5.0
1	B	441	ALA	5.0
1	G	102	VAL	5.0
1	E	390	PHE	4.9
1	M	426	PHE	4.9
1	H	29	PRO	4.9
1	C	141	TYR	4.9
1	H	126	ALA	4.8
1	B	65	GLY	4.8
1	M	114	PRO	4.8
1	J	408	LEU	4.7
1	B	109	ARG	4.7
1	F	125	ASN	4.7
1	E	367	GLY	4.7

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Mol	Chain	Res	Type	RSRZ
1	M	441	ALA	4.6
1	H	139	VAL	4.5
1	B	26	ALA	4.5
1	E	106	LEU	4.4
1	C	441	ALA	4.3
1	E	44	THR	4.3
1	I	169	LEU	4.2
1	F	126	ALA	4.2
1	J	410	ILE	4.2
1	K	237	ILE	4.0
1	E	368	VAL	4.0
1	F	237	ILE	4.0
1	I	24	GLY	4.0
1	A	237	ILE	3.9
1	I	22	THR	3.8
1	L	117	VAL	3.7
1	F	277	ALA	3.7
1	E	366	ALA	3.6
1	E	236	ALA	3.2
1	E	237	ILE	3.0
1	J	434	SER	2.8

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.