



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 08:13 AM GMT

PDB ID : 3DL8
Title : Structure of the complex of aquifex aeolicus SecYEG and bacillus subtilis SecA
Authors : Nam, Y.; Zimmer, J.; Rapoport, T.A.
Deposited on : 2008-06-26
Resolution : 7.50 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<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
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

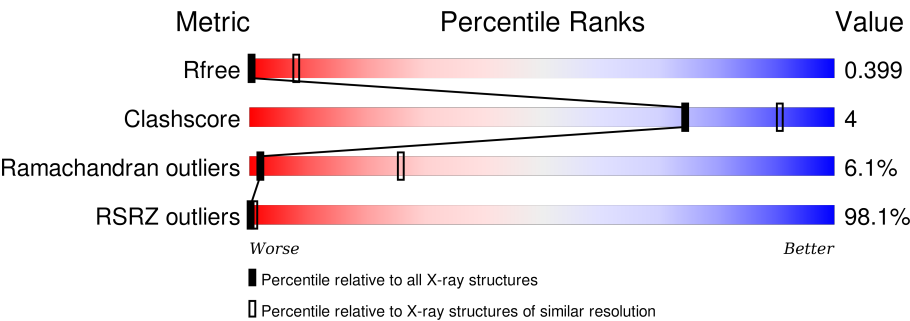
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 7.50 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R _{free}	91344	1014 (9.50-3.66)
Clashscore	102246	1063 (10.00-3.70)
Ramachandran outliers	100387	1035 (9.50-3.66)
RSRZ outliers	91569	1013 (9.50-3.66)

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	779	<div><div>96%</div><div><div></div><div>91%</div><div>8%</div><div></div></div><div></div></div>
1	B	779	<div><div>98%</div><div><div></div><div>91%</div><div>7%</div><div></div></div><div></div></div>
2	G	429	<div><div>93%</div><div><div></div><div>85%</div><div>9%</div><div>5%</div></div><div></div></div>
2	H	429	<div><div>93%</div><div><div></div><div>85%</div><div>9%</div><div>5%</div></div><div></div></div>
3	C	65	<div><div>54%</div><div><div></div><div>54%</div><div>46%</div></div><div></div></div>
3	D	65	<div><div>54%</div><div><div></div><div>54%</div><div>46%</div></div><div></div></div>
4	E	107	<div><div>61%</div><div><div></div><div>58%</div><div>39%</div></div><div></div></div>

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Mol	Chain	Length	Quality of chain
4	F	107	<div><div><div>61%</div><div>58%</div><div>39%</div></div></div>

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 10232 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 Protein translocase subunit secA.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
1	A	773	Total	C	N	O	0	0	0
			3092	1546	773	773			
1	B	773	Total	C	N	O	0	0	0
			3092	1546	773	773			

- Molecule 2 is a protein called Preprotein translocase subunit secY.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	G	406	Total	C	N	O	0	0	0
			1624	812	406	406			
2	H	406	Total	C	N	O	0	0	0
			1624	812	406	406			

- Molecule 3 is a protein called SecE.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	C	35	Total	C	N	O	0	0	0
			140	70	35	35			
3	D	35	Total	C	N	O	0	0	0
			140	70	35	35			

- Molecule 4 is a protein called Protein-export membrane protein secG.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	E	65	Total	C	N	O	0	0	0
			260	130	65	65			
4	F	65	Total	C	N	O	0	0	0
			260	130	65	65			

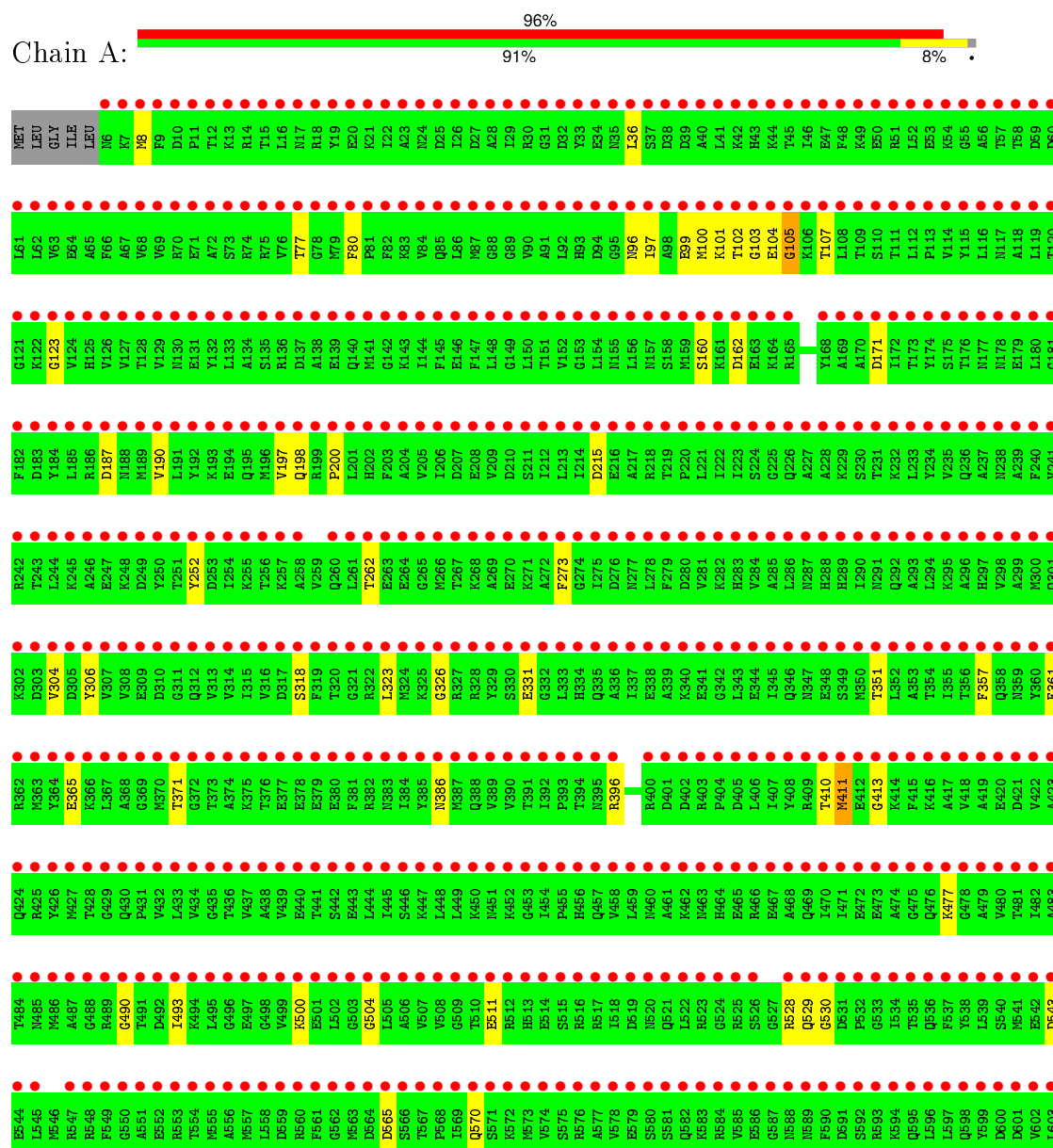
There are 14 discrepancies between the modelled and reference sequences:

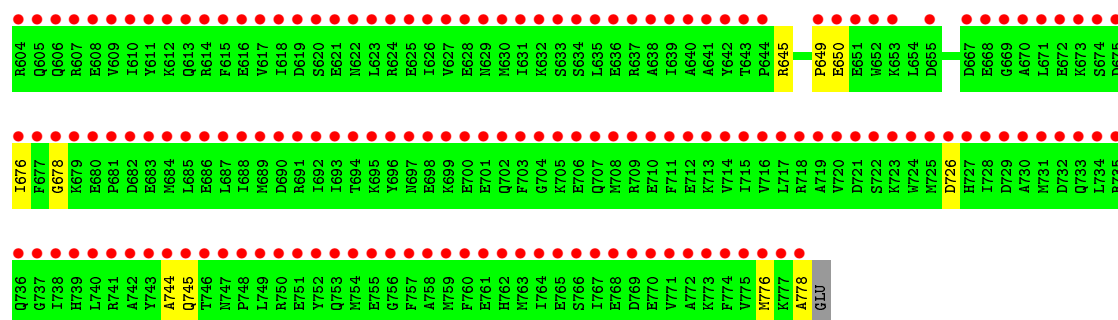
Chain	Residue	Modelled	Actual	Comment	Reference
E	101	GLY	-	EXPRESSION TAG	UNP O66505
E	102	HIS	-	EXPRESSION TAG	UNP O66505
E	103	HIS	-	INSERTION	UNP O66505
E	104	HIS	-	EXPRESSION TAG	UNP O66505
E	105	HIS	-	EXPRESSION TAG	UNP O66505
E	106	HIS	-	EXPRESSION TAG	UNP O66505
E	107	HIS	-	EXPRESSION TAG	UNP O66505
F	101	GLY	-	EXPRESSION TAG	UNP O66505
F	102	HIS	-	EXPRESSION TAG	UNP O66505
F	103	HIS	-	EXPRESSION TAG	UNP O66505
F	104	HIS	-	EXPRESSION TAG	UNP O66505
F	105	HIS	-	EXPRESSION TAG	UNP O66505
F	106	HIS	-	EXPRESSION TAG	UNP O66505
F	107	HIS	-	EXPRESSION TAG	UNP O66505

3 Residue-property plots

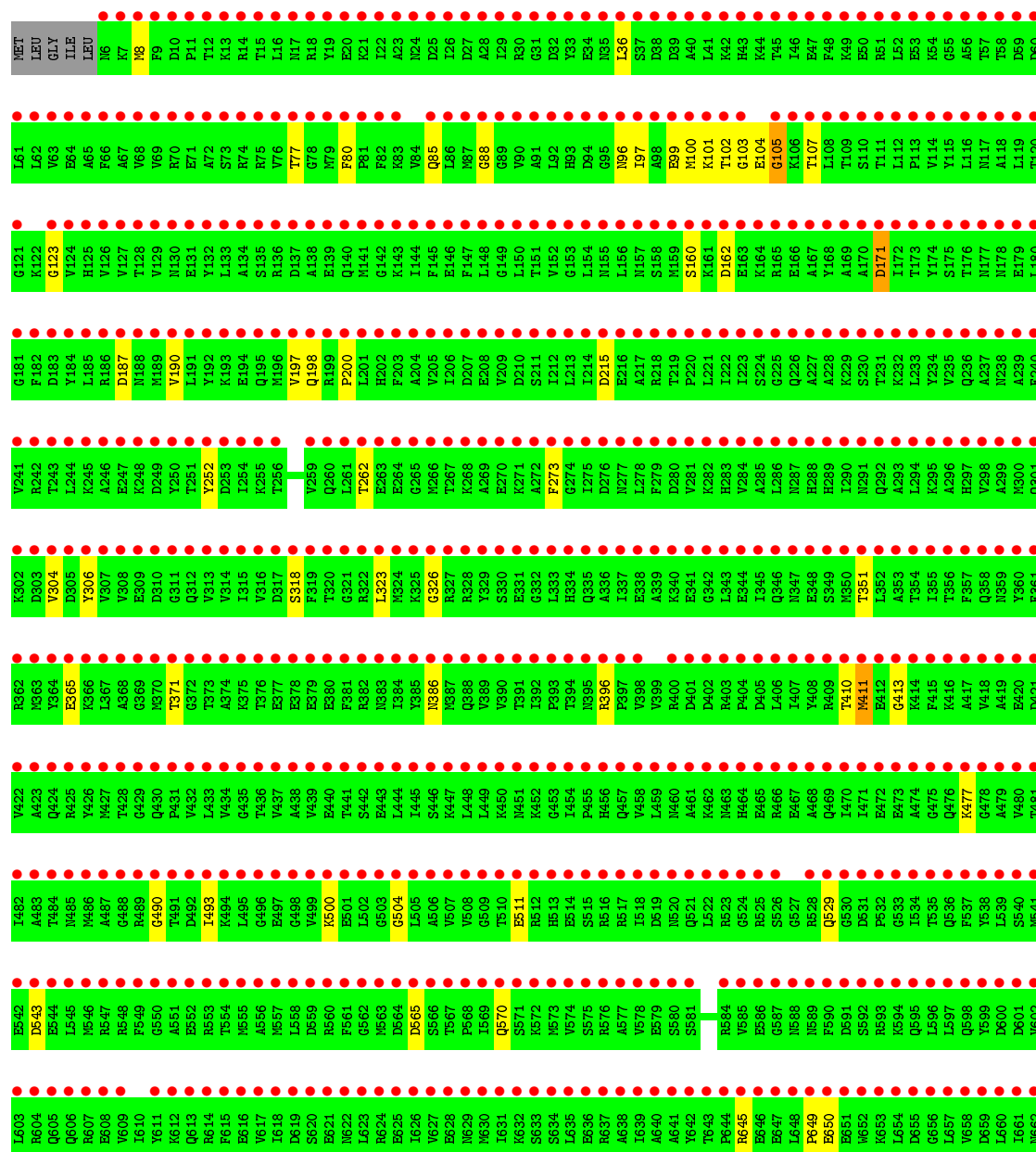
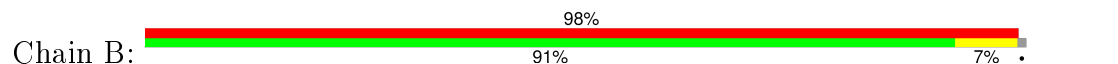
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according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

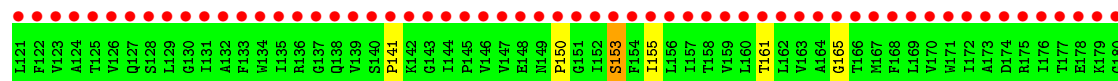
● Molecule 1: Protein translocase subunit secA

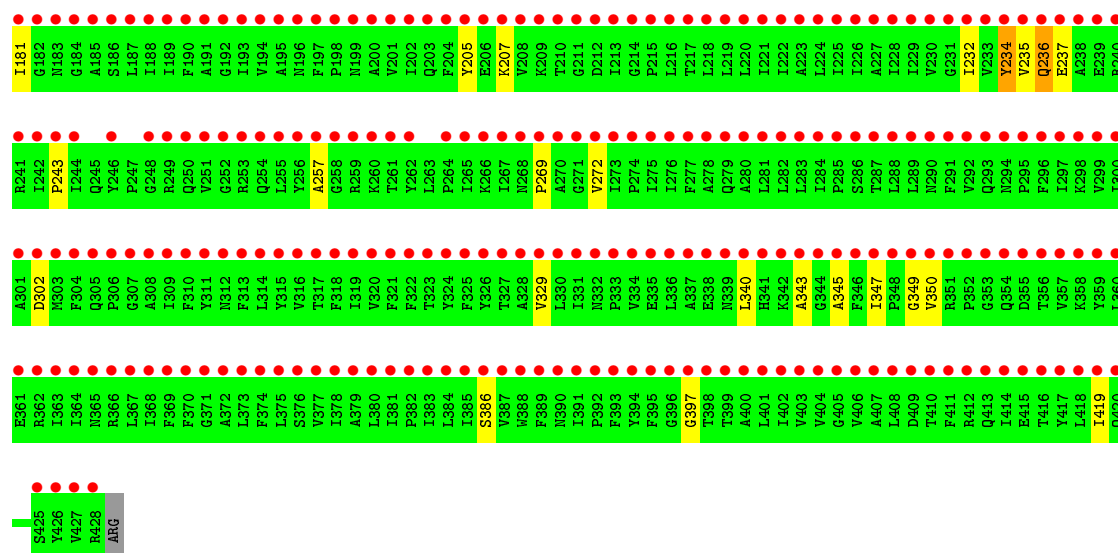




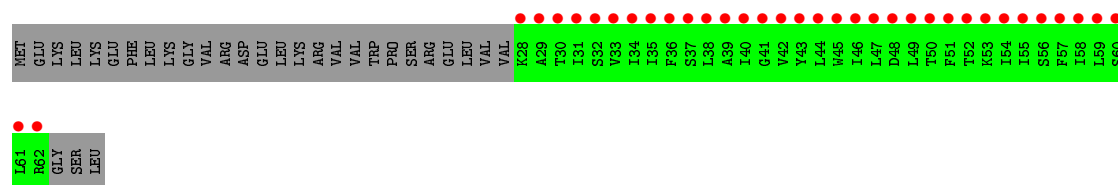
• Molecule 1: Protein translocase subunit secA



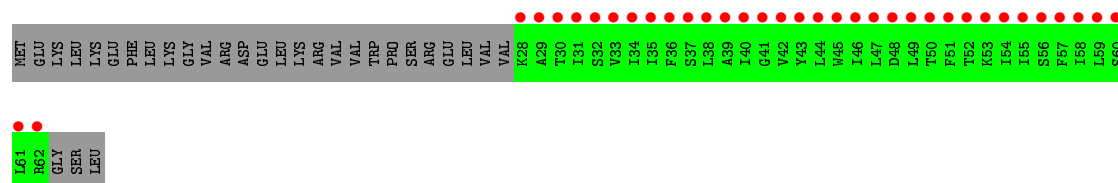




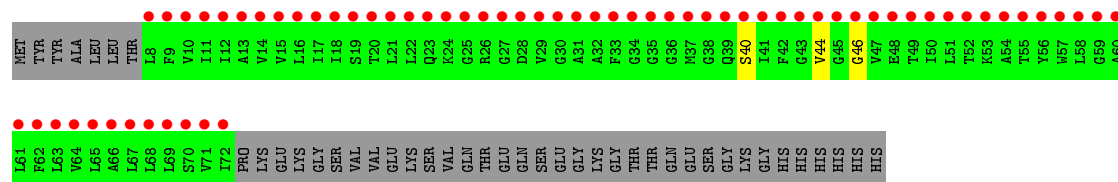
- Molecule 3: SecE



- Molecule 3: SecE

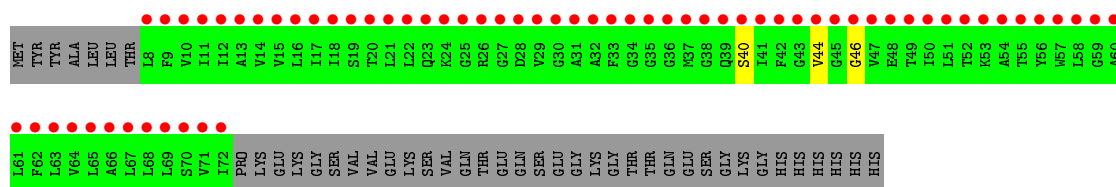


- Molecule 4: Protein-export membrane protein secG



- Molecule 4: Protein-export membrane protein secG





4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	146.36Å 167.97Å 187.72Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	14.99 – 7.50 48.09 – 7.49	Depositor EDS
% Data completeness (in resolution range)	99.5 (14.99-7.50) 99.0 (48.09-7.49)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.28 (at 7.37Å)	Xtriage
Refinement program	CNS 1.2	Depositor
R, R_{free}	0.365 , 0.390 0.397 , 0.399	Depositor DCC
R_{free} test set	No test flags present.	DCC
Wilson B-factor (Å ²)	530.1	Xtriage
Anisotropy	0.140	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.59 , -10.0	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.43$, $\langle L^2 \rangle = 0.26$	Xtriage
Outliers	1 of 6217 reflections (0.016%)	Xtriage
F_o, F_c correlation	0.60	EDS
Total number of atoms	10232	wwPDB-VP
Average B, all atoms (Å ²)	452.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.91% 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, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.88	0/3091	0.90	2/3862 (0.1%)
1	B	0.88	0/3091	0.90	2/3862 (0.1%)
2	G	0.98	0/1622	0.96	2/2024 (0.1%)
2	H	0.97	0/1622	0.96	2/2024 (0.1%)
3	C	0.94	0/139	0.75	0/172
3	D	0.94	0/139	0.75	0/172
4	E	1.02	0/259	0.93	0/322
4	F	1.02	0/259	0.93	0/322
All	All	0.92	0/10222	0.92	8/12760 (0.1%)

There are no bond length outliers.

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	160	SER	N-CA-C	-7.19	91.59	111.00
1	B	160	SER	N-CA-C	-7.17	91.63	111.00
1	A	304	VAL	C-N-CA	6.29	137.41	121.70
1	B	304	VAL	C-N-CA	6.25	137.31	121.70
2	H	302	ASP	C-N-CA	-5.36	108.31	121.70
2	G	235	VAL	C-N-CA	5.31	134.97	121.70
2	G	302	ASP	C-N-CA	-5.29	108.49	121.70
2	H	235	VAL	C-N-CA	5.26	134.85	121.70

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	3092	0	856	18	0
1	B	3092	0	856	12	0
2	G	1624	0	446	17	0
2	H	1624	0	446	13	0
3	C	140	0	36	0	0
3	D	140	0	36	0	0
4	E	260	0	86	1	0
4	F	260	0	86	1	0
All	All	10232	0	2848	52	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 4.

All (52) 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:A:776:MET:O	1:B:778:ALA:O	1.54	1.25
1:A:776:MET:O	1:B:778:ALA:C	1.98	1.02
1:A:778:ALA:C	1:B:776:MET:O	1.99	1.00
1:A:778:ALA:O	1:B:776:MET:O	1.83	0.95
2:H:103:GLU:H	2:H:108:GLY:HA3	1.39	0.86
2:G:103:GLU:H	2:G:108:GLY:HA3	1.39	0.85
1:A:726:ASP:O	2:G:258:GLY:CA	2.29	0.80
1:A:726:ASP:O	2:G:258:GLY:HA2	1.84	0.77
2:H:103:GLU:H	2:H:108:GLY:CA	2.03	0.72
2:G:103:GLU:H	2:G:108:GLY:CA	2.03	0.71
1:A:726:ASP:C	2:G:258:GLY:HA2	2.16	0.64
1:A:726:ASP:O	2:G:258:GLY:HA3	2.00	0.62
2:H:57:ALA:O	2:H:59:TYR:N	2.33	0.62
2:G:57:ALA:O	2:G:59:TYR:N	2.33	0.61
1:B:103:GLY:H	1:B:529:GLN:H	1.47	0.61
2:H:56:PHE:O	2:H:63:SER:CA	2.48	0.61
2:G:56:PHE:O	2:G:63:SER:CA	2.48	0.60
1:A:103:GLY:H	1:A:529:GLN:H	1.47	0.59
2:G:56:PHE:O	2:G:63:SER:C	2.42	0.58
2:G:343:ALA:O	2:G:349:GLY:HA3	2.03	0.58
2:H:343:ALA:O	2:H:349:GLY:HA3	2.03	0.58
2:H:56:PHE:O	2:H:63:SER:C	2.42	0.57
1:A:500:LYS:CA	1:A:504:GLY:HA2	2.35	0.57
1:B:500:LYS:CA	1:B:504:GLY:HA2	2.35	0.56
2:H:57:ALA:O	2:H:58:LEU:C	2.46	0.53
2:G:57:ALA:O	2:G:58:LEU:C	2.46	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:103:GLY:N	1:B:529:GLN:H	2.09	0.51
1:A:778:ALA:CA	1:B:776:MET:O	2.59	0.50
1:A:103:GLY:N	1:A:529:GLN:H	2.09	0.50
1:A:331:GLU:N	2:G:253:ARG:O	2.35	0.49
2:H:103:GLU:N	2:H:108:GLY:HA3	2.20	0.47
1:B:123:GLY:HA2	1:B:171:ASP:O	2.14	0.47
1:A:123:GLY:HA2	1:A:171:ASP:O	2.14	0.47
2:G:103:GLU:N	2:G:108:GLY:HA3	2.20	0.47
4:E:44:VAL:C	4:E:46:GLY:H	2.20	0.45
1:A:411:MET:C	1:A:413:GLY:H	2.21	0.45
4:F:44:VAL:C	4:F:46:GLY:H	2.20	0.44
2:H:62:PHE:O	2:H:63:SER:O	2.35	0.44
2:G:62:PHE:O	2:G:63:SER:O	2.35	0.44
1:B:411:MET:C	1:B:413:GLY:H	2.21	0.44
2:H:161:THR:O	2:H:165:GLY:HA3	2.19	0.43
2:G:161:THR:O	2:G:165:GLY:HA3	2.19	0.43
1:A:105:GLY:O	1:A:107:THR:N	2.50	0.42
2:G:234:TYR:C	2:G:236:GLN:H	2.23	0.42
2:H:153:SER:C	2:H:155:ILE:N	2.72	0.42
1:A:528:ARG:C	1:A:530:GLY:H	2.24	0.41
1:B:105:GLY:O	1:B:107:THR:N	2.50	0.41
1:B:85:GLN:C	1:B:88:GLY:H	2.25	0.41
2:H:234:TYR:C	2:H:236:GLN:H	2.23	0.40
2:G:234:TYR:C	2:G:236:GLN:N	2.74	0.40
1:A:357:PHE:O	1:A:361:PHE:N	2.54	0.40
2:H:232:ILE:C	2:H:234:TYR:N	2.74	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	771/779 (99%)	638 (83%)	86 (11%)	47 (6%)	2	26
1	B	771/779 (99%)	638 (83%)	85 (11%)	48 (6%)	2	26
2	G	402/429 (94%)	321 (80%)	52 (13%)	29 (7%)	1	22
2	H	402/429 (94%)	319 (79%)	54 (13%)	29 (7%)	1	22
3	C	33/65 (51%)	33 (100%)	0	0	100	100
3	D	33/65 (51%)	33 (100%)	0	0	100	100
4	E	63/107 (59%)	57 (90%)	5 (8%)	1 (2%)	12	56
4	F	63/107 (59%)	57 (90%)	5 (8%)	1 (2%)	12	56
All	All	2538/2760 (92%)	2096 (83%)	287 (11%)	155 (6%)	2	26

All (155) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	36	LEU
1	A	80	PHE
1	A	99	GLU
1	A	100	MET
1	A	101	LYS
1	A	197	VAL
1	A	306	TYR
1	A	326	GLY
1	A	371	THR
1	A	543	ASP
1	A	570	GLN
1	A	645	ARG
1	A	649	PRO
1	A	650	GLU
1	A	744	ALA
1	B	36	LEU
1	B	80	PHE
1	B	99	GLU
1	B	100	MET
1	B	101	LYS
1	B	197	VAL
1	B	306	TYR
1	B	326	GLY
1	B	371	THR
1	B	543	ASP
1	B	570	GLN
1	B	645	ARG

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Mol	Chain	Res	Type
1	B	649	PRO
1	B	650	GLU
1	B	744	ALA
2	G	36	ILE
2	G	37	PRO
2	G	58	LEU
2	G	63	SER
2	G	236	GLN
2	G	347	ILE
2	G	350	VAL
2	H	36	ILE
2	H	37	PRO
2	H	58	LEU
2	H	63	SER
2	H	236	GLN
2	H	347	ILE
2	H	350	VAL
1	A	8	MET
1	A	102	THR
1	A	104	GLU
1	A	198	GLN
1	A	252	TYR
1	A	351	THR
1	A	410	THR
1	A	477	LYS
1	A	490	GLY
1	A	676	ILE
1	B	8	MET
1	B	102	THR
1	B	104	GLU
1	B	198	GLN
1	B	252	TYR
1	B	351	THR
1	B	410	THR
1	B	477	LYS
1	B	490	GLY
1	B	676	ILE
2	G	181	ILE
2	G	237	GLU
2	G	257	ALA
2	G	340	LEU
2	G	419	ILE

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Mol	Chain	Res	Type
2	H	181	ILE
2	H	237	GLU
2	H	257	ALA
2	H	340	LEU
2	H	419	ILE
4	E	40	SER
4	F	40	SER
1	A	187	ASP
1	A	262	THR
1	A	323	LEU
1	A	493	ILE
1	A	511	GLU
1	A	565	ASP
1	A	678	GLY
1	B	187	ASP
1	B	262	THR
1	B	323	LEU
1	B	493	ILE
1	B	511	GLU
1	B	565	ASP
1	B	678	GLY
2	G	13	GLU
2	G	207	LYS
2	G	234	TYR
2	G	329	VAL
2	G	345	ALA
2	H	13	GLU
2	H	207	LYS
2	H	234	TYR
2	H	329	VAL
2	H	345	ALA
1	A	77	THR
1	A	96	ASN
1	A	162	ASP
1	A	273	PHE
1	A	365	GLU
1	A	386	ASN
1	A	745	GLN
1	B	77	THR
1	B	96	ASN
1	B	162	ASP
1	B	200	PRO

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Mol	Chain	Res	Type
1	B	273	PHE
1	B	365	GLU
1	B	386	ASN
1	B	745	GLN
2	G	150	PRO
2	G	153	SER
2	G	205	TYR
2	G	269	PRO
2	G	272	VAL
2	H	150	PRO
2	H	153	SER
2	H	205	TYR
2	H	269	PRO
2	H	272	VAL
1	A	200	PRO
1	A	318	SER
1	A	411	MET
1	B	318	SER
1	B	411	MET
2	G	76	GLY
2	G	141	PRO
2	G	243	PRO
2	G	386	SER
2	G	397	GLY
2	H	76	GLY
2	H	141	PRO
2	H	243	PRO
2	H	386	SER
2	H	397	GLY
1	A	105	GLY
1	A	215	ASP
1	B	105	GLY
1	B	171	ASP
1	B	215	ASP
2	G	68	GLY
2	H	68	GLY
1	A	97	ILE
1	A	396	ARG
1	B	97	ILE
1	B	396	ARG
1	A	190	VAL
1	B	190	VAL

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Mol	Chain	Res	Type
2	G	34	ILE
2	H	34	ILE

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	773/779 (99%)	11.54	749 (96%) 0 1	321, 444, 550, 648	0
1	B	773/779 (99%)	12.42	762 (98%) 0 0	340, 470, 540, 612	0
2	G	406/429 (94%)	13.16	400 (98%) 0 0	321, 409, 488, 512	0
2	H	406/429 (94%)	13.15	398 (98%) 0 1	372, 466, 536, 558	0
3	C	35/65 (53%)	19.86	35 (100%) 0 0	328, 363, 402, 405	0
3	D	35/65 (53%)	27.20	35 (100%) 0 0	383, 396, 463, 466	0
4	E	65/107 (60%)	15.91	65 (100%) 0 0	386, 446, 468, 473	0
4	F	65/107 (60%)	8.92	65 (100%) 0 0	477, 523, 550, 551	0
All	All	2558/2760 (92%)	12.69	2509 (98%) 0 1	321, 450, 541, 648	0

All (2509) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	H	153	SER	61.1
1	B	472	GLU	56.9
1	A	694	THR	56.8
2	G	356	THR	54.8
2	H	158	THR	52.8
2	H	125	THR	52.7
2	H	154	PHE	52.5
2	G	153	SER	51.9
1	B	471	ILE	51.1
2	G	149	ASN	50.7
3	D	50	THR	49.5
1	B	470	ILE	49.4
3	D	54	ILE	48.0
1	B	469	GLN	47.3
1	B	768	GLU	47.1
1	A	690	ASP	46.6

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Mol	Chain	Res	Type	RSRZ
4	E	23	GLN	46.0
1	B	60	ASP	45.8
2	H	156	LEU	45.0
1	B	267	THR	43.9
1	B	441	THR	43.7
1	B	467	GLU	42.5
1	A	679	LYS	42.3
2	G	361	GLU	42.1
2	H	155	ILE	41.9
3	D	55	ILE	41.9
1	A	695	LYS	41.8
4	E	57	TRP	41.7
2	G	215	PRO	41.3
2	G	221	ILE	41.2
2	G	360	LEU	41.1
2	H	124	ALA	40.6
1	B	65	ALA	40.6
3	D	56	SER	40.4
1	A	697	ASN	40.4
4	E	20	THR	40.3
1	A	280	ASP	40.3
2	H	34	ILE	40.3
2	H	365	ASN	40.0
1	A	696	TYR	39.6
2	H	128	SER	39.4
2	H	159	VAL	39.2
1	A	718	ARG	39.2
1	A	693	ILE	38.9
2	G	357	VAL	38.9
2	G	152	ILE	38.5
2	H	33	HIS	38.4
1	A	536	GLN	38.4
2	G	220	LEU	38.3
2	H	368	ILE	37.9
2	G	359	TYR	37.8
1	B	473	GLU	37.6
1	B	769	ASP	37.6
2	G	351	ARG	37.4
3	D	51	PHE	37.1
2	G	195	ALA	36.6
1	B	770	GLU	36.6
1	A	691	ARG	36.6

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Mol	Chain	Res	Type	RSRZ
2	G	222	ILE	36.5
1	B	771	VAL	36.5
2	G	352	PRO	36.2
1	A	283	HIS	36.1
1	B	468	ALA	36.0
2	H	372	ALA	36.0
3	C	32	SER	36.0
2	G	196	ASN	35.8
2	H	366	ARG	35.7
3	D	41	GLY	35.7
1	A	628	GLU	35.6
4	E	26	ARG	35.5
2	G	355	ASP	35.5
1	B	675	ASP	35.4
1	A	560	ARG	35.3
1	B	266	MET	35.3
4	E	19	SER	35.0
3	D	37	SER	35.0
3	C	45	TRP	34.7
2	G	365	ASN	34.7
3	D	38	LEU	34.5
1	B	264	GLU	34.3
1	B	64	GLU	34.1
1	A	520	ASN	34.1
2	H	219	LEU	34.0
1	B	63	VAL	34.0
1	B	37	SER	34.0
2	H	59	TYR	33.9
1	B	672	GLU	33.8
1	A	689	MET	33.7
2	H	369	PHE	33.6
1	A	701	GLU	33.6
3	D	42	VAL	33.5
2	H	301	ALA	33.4
2	H	210	THR	33.3
3	D	48	ASP	33.3
2	G	151	GLY	33.3
2	G	219	LEU	33.2
1	A	430	GLN	33.1
2	G	364	ILE	32.8
3	D	52	THR	32.8
2	H	152	ILE	32.7

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Mol	Chain	Res	Type	RSRZ
4	E	58	LEU	32.7
3	D	36	PHE	32.7
2	H	161	THR	32.6
1	B	629	ASN	32.6
2	H	367	LEU	32.5
2	H	327	THR	32.5
1	B	756	GLY	32.5
1	A	535	THR	32.4
2	H	217	THR	32.3
1	A	627	VAL	32.3
2	H	289	LEU	32.2
2	G	197	PHE	32.2
1	A	722	SER	32.2
2	G	363	ILE	32.1
2	H	362	ARG	32.1
2	G	124	ALA	32.0
3	C	48	ASP	31.8
3	C	50	THR	31.8
3	C	49	LEU	31.7
1	B	466	ARG	31.7
2	G	150	PRO	31.7
2	G	223	ALA	31.6
1	A	682	ASP	31.5
1	A	232	LYS	31.5
2	G	224	LEU	31.4
2	H	32	SER	31.3
4	E	55	THR	31.3
2	H	290	ASN	31.1
3	D	39	ALA	31.1
2	G	362	ARG	31.0
2	H	38	GLY	31.0
1	B	715	ILE	31.0
2	G	198	PRO	30.9
4	E	54	ALA	30.8
1	B	664	THR	30.8
1	B	773	LYS	30.8
1	B	146	GLU	30.8
1	B	502	LEU	30.7
2	H	302	ASP	30.7
1	B	772	ALA	30.6
2	G	199	ASN	30.3
1	B	753	GLN	30.2

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Mol	Chain	Res	Type	RSRZ
3	C	44	LEU	30.1
2	H	127	GLN	30.1
2	H	298	LYS	30.0
1	A	684	MET	29.9
2	H	162	LEU	29.7
1	B	456	HIS	29.7
1	A	431	PRO	29.6
3	D	57	PHE	29.4
1	A	685	LEU	29.3
1	B	128	THR	29.3
1	A	264	GLU	29.3
3	D	60	SER	29.3
1	A	509	GLY	29.2
3	D	44	LEU	29.0
2	H	226	ILE	29.0
3	D	53	LYS	29.0
1	A	630	MET	29.0
1	B	535	THR	28.9
4	E	24	LYS	28.9
1	B	674	SER	28.8
1	B	292	GLN	28.8
2	G	218	LEU	28.7
1	B	68	VAL	28.7
3	C	37	SER	28.7
3	C	41	GLY	28.7
2	H	223	ALA	28.6
2	G	358	LYS	28.5
2	G	123	VAL	28.4
1	A	559	ASP	28.4
1	B	67	ALA	28.3
1	B	204	ALA	28.3
2	G	154	PHE	28.3
1	B	428	THR	28.3
2	H	149	ASN	28.2
1	A	681	PRO	28.1
1	A	426	TYR	28.0
1	B	663	THR	28.0
2	G	148	GLU	28.0
2	H	370	PHE	28.0
1	B	718	ARG	27.9
1	B	38	ASP	27.9
1	A	435	GLY	27.9

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Mol	Chain	Res	Type	RSRZ
1	A	719	ALA	27.8
1	A	479	ALA	27.5
2	H	315	TYR	27.3
2	G	217	THR	27.3
1	B	41	LEU	27.2
2	H	287	THR	27.1
1	B	655	ASP	27.0
3	C	43	TYR	27.0
3	D	40	ILE	27.0
1	B	660	LEU	26.9
2	H	319	ILE	26.9
1	A	236	GLN	26.8
2	H	325	PHE	26.8
1	A	698	GLU	26.7
3	D	35	ILE	26.7
1	A	534	ILE	26.7
1	B	291	ASN	26.6
1	A	678	GLY	26.6
3	C	33	VAL	26.5
2	H	225	ILE	26.5
3	D	33	VAL	26.5
1	B	26	ILE	26.4
2	G	147	VAL	26.4
1	B	625	GLU	26.4
1	B	442	SER	26.4
1	A	60	ASP	26.4
2	H	364	ILE	26.3
1	B	262	THR	26.3
1	B	440	GLU	26.3
1	B	288	HIS	26.2
2	H	317	THR	26.1
4	E	53	LYS	26.1
2	G	157	ILE	26.1
1	B	40	ALA	26.1
1	A	700	GLU	26.0
2	H	307	GLY	25.9
2	G	350	VAL	25.8
4	E	62	PHE	25.8
2	H	60	ASP	25.7
1	A	537	PHE	25.7
2	H	35	PRO	25.6
1	B	59	ASP	25.6

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Mol	Chain	Res	Type	RSRZ
1	B	630	MET	25.5
2	H	157	ILE	25.5
1	B	507	VAL	25.4
1	A	441	THR	25.4
1	B	677	PHE	25.3
1	B	757	PHE	25.3
2	H	30	LEU	25.3
2	H	324	TYR	25.2
1	A	629	ASN	25.1
1	A	279	PHE	25.1
1	A	631	ILE	25.1
1	A	692	ILE	25.0
1	B	24	ASN	25.0
3	D	45	TRP	25.0
1	A	680	GLU	24.9
1	A	562	GLY	24.9
1	B	265	GLY	24.8
1	B	626	ILE	24.8
4	F	23	GLN	24.7
3	C	30	THR	24.7
2	G	200	ALA	24.7
1	B	455	PRO	24.6
1	B	44	LYS	24.6
1	A	634	SER	24.5
1	B	506	ALA	24.5
1	A	561	PHE	24.5
2	G	354	GLN	24.5
1	B	676	ILE	24.5
3	C	38	LEU	24.4
4	E	25	GLY	24.4
2	G	214	GLY	24.4
1	B	45	THR	24.4
2	G	203	GLN	24.4
1	B	127	VAL	24.3
1	B	62	LEU	24.3
4	F	18	ILE	24.2
2	H	95	PRO	24.2
2	G	283	LEU	24.1
2	G	119	LEU	24.0
2	G	118	TYR	24.0
2	H	222	ILE	24.0
2	H	211	GLY	23.9

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Mol	Chain	Res	Type	RSRZ
2	H	216	LEU	23.9
3	D	49	LEU	23.9
2	G	145	PRO	23.9
2	H	320	VAL	23.9
1	B	656	GLY	23.9
1	A	721	ASP	23.9
2	G	117	LYS	23.8
2	H	74	ALA	23.8
3	C	35	ILE	23.8
1	B	501	GLU	23.7
4	F	22	LEU	23.7
1	A	715	ILE	23.7
1	A	686	GLU	23.6
3	C	34	ILE	23.5
1	A	64	GLU	23.5
1	B	765	GLU	23.5
1	A	483	ALA	23.5
2	H	209	LYS	23.5
4	E	66	ALA	23.4
4	E	52	THR	23.4
1	B	705	LYS	23.3
2	G	333	PRO	23.3
1	A	436	THR	23.2
1	B	263	GLU	23.2
1	B	429	GLY	23.2
3	D	46	ILE	23.1
2	H	31	GLY	23.1
2	H	151	GLY	23.1
1	B	313	VAL	23.1
3	D	34	ILE	23.0
1	A	111	THR	23.0
1	A	708	MET	23.0
2	H	37	PRO	23.0
3	D	47	LEU	22.9
2	G	227	ALA	22.9
3	D	58	ILE	22.9
2	H	212	ASP	22.9
1	A	519	ASP	22.9
1	B	27	ASP	22.9
2	H	208	VAL	22.9
2	G	228	ILE	22.9
1	A	563	MET	22.9

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Mol	Chain	Res	Type	RSRZ
1	A	204	ALA	22.8
1	B	28	ALA	22.8
1	B	682	ASP	22.8
1	B	508	VAL	22.8
1	B	25	ASP	22.7
2	H	221	ILE	22.7
3	D	43	TYR	22.6
4	E	22	LEU	22.6
1	B	732	ASP	22.6
1	B	534	ILE	22.5
1	B	126	VAL	22.5
1	B	631	ILE	22.5
4	F	21	LEU	22.5
2	H	96	SER	22.4
2	G	132	ALA	22.4
1	B	566	SER	22.4
2	H	311	TYR	22.3
1	B	32	ASP	22.3
2	H	371	GLY	22.2
1	A	285	ALA	22.2
1	B	652	TRP	22.1
1	A	367	LEU	22.1
2	H	150	PRO	22.0
1	A	704	GLY	22.0
2	H	288	LEU	22.0
1	B	90	VAL	21.9
1	B	268	LYS	21.9
1	B	33	TYR	21.9
1	A	432	VAL	21.9
2	G	35	PRO	21.8
1	A	485	ASN	21.7
3	C	39	ALA	21.7
2	H	373	LEU	21.7
4	E	27	GLY	21.7
1	B	43	HIS	21.6
1	B	31	GLY	21.6
1	B	659	ASP	21.6
2	H	75	LEU	21.6
1	A	338	GLU	21.6
1	A	688	ILE	21.5
1	B	61	LEU	21.5
1	A	707	GLN	21.5

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Mol	Chain	Res	Type	RSRZ
1	B	30	ARG	21.4
4	E	16	LEU	21.4
2	H	164	ALA	21.3
1	B	438	ALA	21.3
2	H	36	ILE	21.3
2	G	158	THR	21.3
2	G	281	LEU	21.2
1	B	500	LYS	21.2
1	B	716	VAL	21.1
1	B	238	ASN	21.1
2	H	91	THR	21.1
4	F	19	SER	21.1
2	G	225	ILE	21.0
1	A	505	LEU	21.0
2	H	163	VAL	20.9
2	G	31	GLY	20.9
1	B	654	LEU	20.9
2	H	303	MET	20.9
4	E	9	PHE	20.9
1	B	239	ALA	20.8
1	B	29	ILE	20.8
2	H	297	ILE	20.8
1	B	463	ASN	20.8
1	B	284	VAL	20.7
2	H	126	VAL	20.7
3	C	46	ILE	20.7
1	B	653	LYS	20.6
1	B	89	GLY	20.6
1	B	42	LYS	20.6
2	G	345	ALA	20.6
2	G	212	ASP	20.5
1	B	661	ILE	20.5
2	H	220	LEU	20.5
2	H	160	LEU	20.5
2	G	128	SER	20.4
1	B	755	GLU	20.4
1	B	411	MET	20.4
1	B	338	GLU	20.4
2	G	366	ARG	20.3
1	B	558	LEU	20.3
1	A	68	VAL	20.3
2	H	123	VAL	20.2

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Mol	Chain	Res	Type	RSRZ
1	B	678	GLY	20.2
1	A	284	VAL	20.2
2	H	328	ALA	20.2
1	B	673	LYS	20.2
2	H	312	ASN	20.2
2	G	194	VAL	20.1
1	A	540	SER	20.1
1	B	758	ALA	20.1
1	A	480	VAL	20.1
1	A	312	GLN	20.1
1	A	533	GLY	20.1
2	G	170	VAL	20.0
2	H	299	VAL	20.0
1	A	402	ASP	20.0
4	E	56	TYR	20.0
1	B	559	ASP	20.0
3	C	47	LEU	20.0
2	H	215	PRO	20.0
1	B	554	THR	20.0
2	H	316	VAL	19.9
1	A	59	ASP	19.9
1	A	720	VAL	19.9
2	G	367	LEU	19.9
2	H	213	ILE	19.9
2	G	156	LEU	19.8
2	G	122	PHE	19.8
2	H	323	THR	19.8
1	A	199	ARG	19.8
1	A	626	ILE	19.8
1	A	557	MET	19.7
3	C	53	LYS	19.7
1	B	542	GLU	19.7
2	H	321	PHE	19.7
1	A	484	THR	19.7
2	G	229	ILE	19.7
4	F	20	THR	19.7
1	A	558	LEU	19.6
1	A	510	THR	19.6
2	H	115	TYR	19.6
2	G	34	ILE	19.6
2	G	379	ALA	19.5
2	H	286	SER	19.5

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Mol	Chain	Res	Type	RSRZ
2	G	97	LEU	19.5
2	G	378	ILE	19.5
1	B	35	ASN	19.5
1	A	425	ARG	19.5
2	G	343	ALA	19.5
1	A	481	THR	19.4
1	A	310	ASP	19.4
2	G	135	ILE	19.4
1	A	608	GLU	19.4
2	G	206	GLU	19.4
2	G	120	THR	19.4
2	G	334	VAL	19.3
1	B	143	LYS	19.3
1	B	499	VAL	19.3
4	E	15	VAL	19.3
2	G	282	LEU	19.3
1	A	403	ARG	19.3
1	A	429	GLY	19.2
1	B	680	GLU	19.2
2	G	36	ILE	19.2
4	E	11	ILE	19.2
1	A	380	GLU	19.2
1	B	719	ALA	19.2
1	B	296	ALA	19.2
2	G	226	ILE	19.2
1	A	44	LYS	19.2
1	B	510	THR	19.1
2	G	216	LEU	19.1
1	B	308	VAL	19.1
1	A	521	GLN	19.1
2	H	314	LEU	19.1
1	B	280	ASP	19.1
1	B	177	ASN	19.1
1	B	627	VAL	19.1
1	A	683	GLU	19.0
1	B	572	LYS	19.0
1	B	270	GLU	19.0
1	A	633	SER	19.0
1	B	712	GLU	19.0
1	B	766	SER	19.0
1	B	628	GLU	18.9
1	B	125	HIS	18.9

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Mol	Chain	Res	Type	RSRZ
1	B	314	VAL	18.9
2	H	363	ILE	18.9
1	A	428	THR	18.9
1	A	233	LEU	18.8
3	C	52	THR	18.8
4	E	8	LEU	18.8
2	G	390	ASN	18.8
1	B	249	ASP	18.8
2	H	169	LEU	18.8
1	B	66	PHE	18.8
1	B	704	GLY	18.8
4	E	13	ALA	18.7
1	A	754	MET	18.7
1	B	180	LEU	18.6
1	A	282	LYS	18.6
1	A	281	VAL	18.6
1	B	752	TYR	18.6
1	A	125	HIS	18.5
1	B	112	LEU	18.5
1	A	457	GLN	18.5
2	H	279	GLN	18.5
2	H	218	LEU	18.5
2	G	428	ARG	18.4
2	H	165	GLY	18.4
1	A	518	ILE	18.4
1	B	113	PRO	18.4
1	A	478	GLY	18.3
1	B	437	VAL	18.3
2	H	313	PHE	18.3
1	B	454	ILE	18.2
1	A	267	THR	18.2
1	A	482	ILE	18.2
2	H	40	ASN	18.2
1	B	39	ASP	18.2
1	A	699	LYS	18.2
1	A	61	LEU	18.2
2	G	205	TYR	18.2
2	H	12	LYS	18.2
2	G	323	THR	18.2
1	B	657	LEU	18.1
3	C	51	PHE	18.1
2	G	284	ILE	18.1

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Mol	Chain	Res	Type	RSRZ
2	H	205	TYR	18.1
1	A	139	GLU	18.1
3	C	40	ILE	18.1
2	G	310	PHE	18.1
1	B	708	MET	18.1
1	A	42	LYS	18.1
1	B	250	TYR	18.1
1	B	557	MET	18.1
1	A	15	THR	18.0
1	A	45	THR	18.0
1	B	293	ALA	18.0
1	B	624	ARG	18.0
4	F	24	LYS	18.0
1	B	536	GLN	18.0
1	B	567	THR	17.9
1	A	564	ASP	17.9
2	H	13	GLU	17.9
1	A	565	ASP	17.9
1	A	716	VAL	17.9
3	C	36	PHE	17.9
1	A	507	VAL	17.9
2	G	146	VAL	17.8
2	G	113	ASN	17.8
1	A	263	GLU	17.8
1	B	295	LYS	17.8
2	G	324	TYR	17.7
1	B	283	HIS	17.7
1	B	230	SER	17.7
1	B	312	GLN	17.7
1	A	65	ALA	17.7
1	A	336	ALA	17.7
1	A	515	SER	17.7
2	H	200	ALA	17.7
1	A	289	HIS	17.6
3	D	30	THR	17.6
2	G	285	PRO	17.5
1	B	176	THR	17.5
3	D	31	ILE	17.5
1	A	600	ASP	17.5
1	A	538	TYR	17.5
1	A	687	LEU	17.5
2	H	112	ILE	17.4

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Mol	Chain	Res	Type	RSRZ
2	H	224	LEU	17.4
1	A	286	LEU	17.4
1	B	707	GLN	17.4
1	B	734	LEU	17.4
1	B	277	ASN	17.4
2	G	37	PRO	17.3
1	A	677	PHE	17.3
4	E	18	ILE	17.3
1	A	506	ALA	17.3
1	A	421	ASP	17.3
1	A	115	TYR	17.3
1	A	188	ASN	17.3
1	A	278	LEU	17.2
1	A	632	LYS	17.2
1	A	292	GLN	17.2
1	B	236	GLN	17.2
1	B	412	GLU	17.2
1	A	381	PHE	17.2
1	B	731	MET	17.2
1	B	410	THR	17.2
3	C	31	ILE	17.2
3	C	42	VAL	17.1
1	A	516	ARG	17.1
2	G	387	VAL	17.1
2	H	94	ILE	17.1
1	B	439	VAL	17.1
1	A	368	ALA	17.1
1	B	509	GLY	17.0
1	B	474	ALA	17.0
4	F	25	GLY	16.9
1	B	386	ASN	16.9
2	G	314	LEU	16.9
1	B	754	MET	16.9
2	H	29	ARG	16.9
1	B	503	GLY	16.9
1	B	269	ALA	16.9
2	H	278	ALA	16.9
2	G	280	ALA	16.9
2	H	173	ALA	16.9
1	A	235	VAL	16.8
2	H	174	ASP	16.8
1	A	277	ASN	16.8

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Mol	Chain	Res	Type	RSRZ
1	A	508	VAL	16.8
1	B	23	ALA	16.8
2	G	213	ILE	16.8
2	H	376	SER	16.8
1	A	459	LEU	16.7
2	G	342	LYS	16.7
2	G	238	ALA	16.7
1	A	189	MET	16.7
1	A	72	ALA	16.7
2	G	136	ARG	16.6
3	D	32	SER	16.6
1	A	434	VAL	16.6
2	G	95	PRO	16.6
4	F	26	ARG	16.6
1	B	34	GLU	16.5
2	H	361	GLU	16.5
1	B	671	LEU	16.5
1	A	467	GLU	16.5
1	A	736	GLN	16.5
1	B	359	ASN	16.5
1	A	705	LYS	16.5
1	A	446	SER	16.4
1	A	230	SER	16.4
1	B	464	HIS	16.4
1	B	22	ILE	16.4
1	A	733	GLN	16.4
2	G	344	GLY	16.4
1	B	183	ASP	16.4
1	A	709	ARG	16.4
2	G	368	ILE	16.3
4	F	59	GLY	16.3
1	A	511	GLU	16.3
1	B	148	LEU	16.3
1	A	742	ALA	16.3
1	B	623	LEU	16.3
1	B	332	GLY	16.2
1	A	468	ALA	16.2
4	E	67	LEU	16.2
1	B	413	GLY	16.2
1	A	179	GLU	16.2
2	H	228	ILE	16.2
1	A	735	ARG	16.2

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Mol	Chain	Res	Type	RSRZ
2	H	377	VAL	16.1
1	B	232	LYS	16.1
2	G	204	PHE	16.1
1	B	540	SER	16.1
1	A	337	ILE	16.1
1	B	335	GLN	16.1
1	A	377	GLU	16.1
1	B	555	MET	16.1
1	B	336	ALA	16.0
1	B	665	TYR	16.0
1	B	326	GLY	16.0
1	B	337	ILE	16.0
1	A	717	LEU	16.0
1	A	288	HIS	16.0
1	A	276	ASP	16.0
2	G	389	PHE	16.0
1	B	46	ILE	16.0
1	A	442	SER	16.0
1	A	71	GLU	15.9
1	B	111	THR	15.9
1	A	142	GLY	15.9
1	B	427	MET	15.9
2	G	388	TRP	15.9
1	B	504	GLY	15.8
1	A	625	GLU	15.8
2	G	269	PRO	15.8
2	H	379	ALA	15.8
2	H	326	TYR	15.8
1	B	311	GLY	15.8
2	H	322	PHE	15.8
2	G	115	TYR	15.8
2	G	307	GLY	15.8
1	A	469	GLN	15.8
1	B	184	TYR	15.8
1	A	599	TYR	15.7
1	B	774	PHE	15.7
1	B	662	ASN	15.7
2	G	353	GLY	15.7
1	A	87	MET	15.6
1	A	231	THR	15.6
2	G	15	ARG	15.6
1	A	43	HIS	15.6

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Mol	Chain	Res	Type	RSRZ
4	E	12	ILE	15.6
1	A	40	ALA	15.6
1	B	279	PHE	15.6
1	B	465	GLU	15.6
2	H	100	LEU	15.5
1	B	706	GLU	15.5
1	A	747	ASN	15.5
1	A	58	THR	15.5
1	B	373	THR	15.5
2	G	311	TYR	15.5
2	G	116	THR	15.5
1	A	382	ARG	15.5
1	A	205	VAL	15.5
2	G	125	THR	15.5
1	A	703	PHE	15.5
1	B	767	ILE	15.5
1	A	141	MET	15.5
2	G	16	GLN	15.4
1	B	622	ASN	15.4
1	A	556	ALA	15.4
1	B	47	GLU	15.4
2	H	129	LEU	15.4
2	G	19	ILE	15.4
1	A	178	ASN	15.4
2	H	300	ILE	15.4
2	H	306	PRO	15.4
1	A	758	ALA	15.4
1	B	722	SER	15.4
2	G	234	TYR	15.3
1	A	198	GLN	15.3
2	G	126	VAL	15.3
1	A	14	ARG	15.3
1	B	231	THR	15.3
1	A	572	LYS	15.3
1	B	233	LEU	15.2
2	G	231	GLY	15.2
3	D	61	LEU	15.2
4	E	60	ALA	15.2
1	B	777	LYS	15.2
1	A	118	ALA	15.2
2	G	325	PHE	15.2
2	G	96	SER	15.2

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Mol	Chain	Res	Type	RSRZ
1	B	425	ARG	15.2
1	B	651	GLU	15.2
1	B	48	PHE	15.2
2	G	88	GLN	15.2
1	B	409	ARG	15.2
2	G	70	LEU	15.2
4	E	69	LEU	15.2
1	B	289	HIS	15.1
2	G	410	THR	15.1
1	A	358	GLN	15.1
2	G	161	THR	15.1
1	A	311	GLY	15.1
1	A	755	GLU	15.1
1	A	140	GLN	15.0
1	B	736	GLN	15.0
1	B	683	GLU	15.0
2	G	155	ILE	14.9
2	H	11	LEU	14.9
1	B	436	THR	14.9
2	H	166	THR	14.9
2	G	321	PHE	14.9
2	G	201	VAL	14.9
2	G	91	THR	14.9
1	B	621	GLU	14.9
1	B	478	GLY	14.9
1	B	679	LYS	14.9
2	G	17	LYS	14.8
4	E	61	LEU	14.8
4	E	14	VAL	14.8
1	B	632	LYS	14.8
4	E	63	LEU	14.8
2	H	282	LEU	14.8
2	H	296	PHE	14.8
2	G	312	ASN	14.8
2	H	318	PHE	14.7
2	H	207	LYS	14.7
2	H	148	GLU	14.7
1	A	458	VAL	14.7
2	G	30	LEU	14.7
2	G	169	LEU	14.7
2	G	232	ILE	14.7
1	A	757	PHE	14.7

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Mol	Chain	Res	Type	RSRZ
1	B	681	PRO	14.7
1	B	224	SER	14.7
1	A	246	ALA	14.7
1	B	178	ASN	14.7
1	A	417	ALA	14.7
1	A	486	MET	14.7
1	A	571	SER	14.7
2	G	127	GLN	14.7
2	G	71	THR	14.7
4	E	59	GLY	14.7
1	B	285	ALA	14.6
2	H	111	LYS	14.6
1	A	539	LEU	14.6
1	A	50	GLU	14.6
1	A	504	GLY	14.5
2	G	380	LEU	14.5
2	H	113	ASN	14.5
2	H	214	GLY	14.5
4	E	10	VAL	14.5
2	H	120	THR	14.5
1	A	119	LEU	14.5
1	B	658	VAL	14.5
1	B	234	TYR	14.4
1	B	433	LEU	14.4
1	A	598	GLN	14.4
4	F	60	ALA	14.4
2	H	168	PHE	14.4
1	B	147	PHE	14.4
1	B	633	SER	14.4
2	G	317	THR	14.4
1	A	651	GLU	14.4
3	C	29	ALA	14.4
2	H	283	LEU	14.3
1	B	229	LYS	14.3
4	E	17	ILE	14.3
1	A	460	ASN	14.3
1	B	541	MET	14.3
1	A	18	ARG	14.3
2	G	332	ASN	14.3
2	G	114	GLU	14.3
2	H	381	ILE	14.3
1	B	87	MET	14.2

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Mol	Chain	Res	Type	RSRZ
1	A	383	ASN	14.2
1	A	732	ASP	14.2
1	B	203	PHE	14.2
1	B	600	ASP	14.2
1	A	126	VAL	14.2
1	B	476	GLN	14.2
1	A	69	VAL	14.2
1	B	480	VAL	14.2
1	B	595	GLN	14.2
1	A	333	LEU	14.2
1	A	606	GLN	14.2
1	B	142	GLY	14.1
2	G	209	LYS	14.1
1	B	186	ARG	14.1
2	H	201	VAL	14.1
1	B	144	ILE	14.1
1	A	268	LYS	14.1
1	B	339	ALA	14.1
1	A	756	GLY	14.1
1	A	712	GLU	14.1
2	H	227	ALA	14.1
1	A	117	ASN	14.1
2	G	121	LEU	14.1
2	G	202	ILE	14.0
1	B	36	LEU	14.0
1	A	116	LEU	14.0
1	B	69	VAL	14.0
1	B	378	GLU	14.0
1	A	359	ASN	13.9
1	B	287	ASN	13.9
2	G	315	TYR	13.9
2	H	291	PHE	13.9
1	B	616	GLU	13.9
1	A	229	LYS	13.9
1	B	276	ASP	13.9
4	E	70	SER	13.9
2	G	412	ARG	13.9
1	A	234	TYR	13.9
1	A	433	LEU	13.8
1	B	426	TYR	13.8
2	H	280	ALA	13.8
1	A	422	VAL	13.8

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Mol	Chain	Res	Type	RSRZ
1	B	297	HIS	13.8
2	H	204	PHE	13.8
1	A	385	TYR	13.8
4	F	15	VAL	13.8
1	B	145	PHE	13.8
2	G	184	GLY	13.8
1	B	479	ALA	13.8
1	A	371	THR	13.8
1	A	522	LEU	13.8
1	B	114	VAL	13.7
1	B	19	TYR	13.7
1	B	686	GLU	13.7
2	G	341	HIS	13.7
1	A	214	ILE	13.7
1	B	714	VAL	13.7
1	B	281	VAL	13.7
2	G	192	GLY	13.7
2	G	133	PHE	13.7
3	D	59	LEU	13.7
4	F	56	TYR	13.7
1	B	58	THR	13.7
4	F	17	ILE	13.7
1	B	355	ILE	13.7
1	A	737	GLY	13.7
2	G	322	PHE	13.7
2	G	386	SER	13.6
2	G	286	SER	13.6
1	A	604	ARG	13.6
2	G	265	ILE	13.6
1	B	181	GLY	13.6
1	A	266	MET	13.6
1	A	637	ARG	13.6
2	H	167	MET	13.6
1	B	187	ASP	13.6
1	A	595	GLN	13.6
1	B	381	PHE	13.6
1	A	109	THR	13.5
2	G	427	VAL	13.5
1	A	320	THR	13.5
2	G	261	THR	13.5
1	A	203	PHE	13.5
2	H	108	GLY	13.5

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Mol	Chain	Res	Type	RSRZ
1	B	235	VAL	13.5
1	A	768	GLU	13.5
1	B	225	GLY	13.5
1	B	294	LEU	13.5
1	B	601	ASP	13.5
1	B	71	GLU	13.5
2	G	134	TRP	13.5
2	H	172	ILE	13.5
2	G	207	LYS	13.5
4	E	21	LEU	13.5
1	B	565	ASP	13.5
1	A	776	MET	13.4
1	A	335	GLN	13.4
1	A	110	SER	13.4
2	G	264	PRO	13.4
1	A	334	HIS	13.4
1	B	261	LEU	13.4
1	B	179	GLU	13.4
1	A	603	LEU	13.4
1	A	70	ARG	13.3
1	B	505	LEU	13.3
2	H	116	THR	13.3
2	G	174	ASP	13.3
2	G	159	VAL	13.3
1	B	709	ARG	13.3
1	A	702	GLN	13.3
1	B	711	PHE	13.3
1	A	406	LEU	13.3
2	H	10	GLU	13.3
1	B	301	GLN	13.3
1	A	466	ARG	13.3
1	B	237	ALA	13.3
1	B	115	TYR	13.2
1	B	341	GLU	13.2
1	A	607	ARG	13.2
2	H	63	SER	13.2
2	G	32	SER	13.2
2	H	350	VAL	13.2
2	G	98	GLN	13.2
2	H	203	GLN	13.2
1	B	205	VAL	13.2
2	G	290	ASN	13.2

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Mol	Chain	Res	Type	RSRZ
2	G	233	VAL	13.2
2	G	313	PHE	13.2
2	H	202	ILE	13.1
1	A	265	GLY	13.1
1	A	146	GLU	13.1
2	H	119	LEU	13.1
1	B	733	GLN	13.1
1	A	723	LYS	13.1
1	A	404	PRO	13.1
1	B	271	LYS	13.1
1	A	641	ALA	13.1
1	B	744	ALA	13.0
2	H	132	ALA	13.0
1	A	63	VAL	13.0
2	G	160	LEU	13.0
2	G	230	VAL	13.0
1	A	137	ASP	13.0
2	H	122	PHE	13.0
1	A	274	GLY	13.0
2	G	33	HIS	13.0
1	A	272	ALA	13.0
1	B	751	GLU	13.0
4	E	28	ASP	13.0
1	B	759	MET	13.0
1	B	457	GLN	12.9
2	G	211	GLY	12.9
1	B	603	LEU	12.9
1	B	300	MET	12.9
1	A	379	GLU	12.9
2	H	310	PHE	12.9
1	A	386	ASN	12.9
1	B	188	ASN	12.9
2	G	287	THR	12.9
2	G	336	LEU	12.9
3	C	54	ILE	12.9
1	B	462	LYS	12.8
2	H	428	ARG	12.8
1	B	255	LYS	12.8
1	B	560	ARG	12.8
1	A	287	ASN	12.8
1	B	356	THR	12.8
1	A	47	GLU	12.8

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Mol	Chain	Res	Type	RSRZ
2	G	349	GLY	12.8
1	B	49	LYS	12.8
1	B	735	ARG	12.8
1	B	750	ARG	12.8
1	B	643	THR	12.8
1	A	734	LEU	12.8
2	H	329	VAL	12.8
2	G	38	GLY	12.8
1	B	380	GLU	12.8
1	B	299	ALA	12.8
1	B	776	MET	12.7
1	A	41	LEU	12.7
1	B	564	ASP	12.7
1	B	343	LEU	12.7
1	B	395	ASN	12.7
1	B	604	ARG	12.7
1	A	532	PRO	12.7
1	B	242	ARG	12.7
1	B	315	ILE	12.6
1	B	110	SER	12.6
1	A	640	ALA	12.6
2	H	87	MET	12.6
1	A	372	GLY	12.6
2	H	388	TRP	12.6
1	B	778	ALA	12.6
2	H	170	VAL	12.6
1	A	751	GLU	12.6
1	A	107	THR	12.6
2	G	210	THR	12.6
1	A	262	THR	12.6
1	B	149	GLY	12.6
1	A	566	SER	12.6
1	A	369	GLY	12.5
3	C	28	LYS	12.5
1	A	48	PHE	12.5
2	G	28	TYR	12.5
2	G	306	PRO	12.5
1	B	553	ARG	12.5
1	B	475	GLY	12.5
1	A	753	GLN	12.5
2	H	253	ARG	12.5
4	F	53	LYS	12.5

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Mol	Chain	Res	Type	RSRZ
2	G	182	GLY	12.5
1	B	435	GLY	12.5
1	B	562	GLY	12.5
1	A	440	GLU	12.4
4	F	55	THR	12.4
1	A	114	VAL	12.4
1	A	455	PRO	12.4
4	F	27	GLY	12.4
1	A	447	LYS	12.4
1	B	563	MET	12.4
1	B	477	LYS	12.4
1	A	237	ALA	12.4
1	A	713	LYS	12.4
1	A	49	LYS	12.4
2	G	235	VAL	12.4
2	G	193	ILE	12.3
1	B	494	LYS	12.3
1	B	307	VAL	12.3
2	G	166	THR	12.3
1	A	624	ARG	12.3
1	A	296	ALA	12.3
2	G	131	ILE	12.3
1	A	427	MET	12.3
1	B	72	ALA	12.3
1	B	556	ALA	12.3
1	A	378	GLU	12.2
1	A	517	ARG	12.2
1	A	90	VAL	12.2
2	H	175	ARG	12.2
2	H	378	ILE	12.2
1	A	313	VAL	12.2
1	B	481	THR	12.2
1	B	666	LEU	12.2
1	A	456	HIS	12.2
1	A	317	ASP	12.2
1	B	599	TYR	12.2
2	H	117	LYS	12.2
2	G	295	PRO	12.2
2	H	39	ILE	12.2
1	A	138	ALA	12.2
1	A	195	GLN	12.1
4	F	52	THR	12.1

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Mol	Chain	Res	Type	RSRZ
1	A	370	MET	12.1
2	G	191	ALA	12.1
2	G	186	SER	12.1
1	A	411	MET	12.1
1	B	430	GLN	12.1
1	A	594	LYS	12.1
1	B	385	TYR	12.1
2	H	97	LEU	12.0
1	B	762	HIS	12.0
2	H	199	ASN	12.0
1	A	601	ASP	12.0
2	G	171	TRP	12.0
1	A	602	VAL	12.0
1	A	777	LYS	12.0
1	B	417	ALA	12.0
1	A	394	THR	11.9
1	B	401	ASP	11.9
4	E	65	LEU	11.9
1	A	731	MET	11.9
1	A	418	VAL	11.9
1	A	523	ARG	11.9
1	A	470	ILE	11.9
1	A	605	GLN	11.9
1	B	424	GLN	11.9
2	H	92	VAL	11.9
1	A	243	THR	11.9
2	H	110	TYR	11.9
2	G	335	GLU	11.9
2	H	308	ALA	11.8
1	B	568	PRO	11.8
1	A	724	TRP	11.8
2	G	73	PHE	11.8
1	A	314	VAL	11.8
4	F	57	TRP	11.8
2	H	176	ILE	11.8
1	B	717	LEU	11.8
2	H	98	GLN	11.8
2	H	341	HIS	11.8
2	G	318	PHE	11.8
1	A	17	ASN	11.8
1	A	706	GLU	11.7
1	B	443	GLU	11.7

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Mol	Chain	Res	Type	RSRZ
2	H	76	GLY	11.7
2	G	21	THR	11.7
1	A	461	ALA	11.7
1	A	476	GLN	11.7
1	A	769	ASP	11.7
2	G	288	LEU	11.7
1	A	543	ASP	11.6
2	G	409	ASP	11.6
1	A	424	GLN	11.6
1	B	6	ASN	11.6
2	G	162	LEU	11.6
1	A	366	LYS	11.6
1	B	198	GLN	11.6
2	G	402	ILE	11.6
1	A	200	PRO	11.6
1	B	460	ASN	11.6
1	A	503	GLY	11.6
2	H	62	PHE	11.6
1	B	334	HIS	11.5
1	B	342	GLY	11.5
2	G	14	LEU	11.5
2	G	414	ILE	11.5
2	G	94	ILE	11.5
1	A	589	ASN	11.5
2	G	65	GLY	11.5
2	G	346	PHE	11.5
2	H	73	PHE	11.5
1	B	278	LEU	11.5
1	A	113	PRO	11.5
1	B	498	GLY	11.5
2	G	29	ARG	11.5
2	G	405	GLY	11.5
2	H	266	LYS	11.4
1	A	413	GLY	11.4
1	A	123	GLY	11.4
1	A	357	PHE	11.4
1	B	331	GLU	11.4
2	G	399	THR	11.4
2	H	147	VAL	11.4
1	B	210	ASP	11.4
1	A	437	VAL	11.4
1	A	714	VAL	11.4

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Mol	Chain	Res	Type	RSRZ
2	G	185	ALA	11.4
1	A	120	THR	11.4
2	H	15	ARG	11.4
1	B	202	HIS	11.4
2	H	285	PRO	11.4
1	A	330	SER	11.4
1	A	210	ASP	11.3
4	F	58	LEU	11.3
1	B	391	THR	11.3
2	H	114	GLU	11.3
1	A	108	LEU	11.3
1	B	344	GLU	11.3
2	G	20	PHE	11.3
3	C	56	SER	11.3
1	A	122	LYS	11.3
1	A	73	SER	11.3
1	B	403	ARG	11.2
2	H	284	ILE	11.2
4	E	64	VAL	11.2
1	A	443	GLU	11.2
2	H	93	ALA	11.2
2	G	391	ILE	11.2
1	A	445	ILE	11.2
4	E	51	LEU	11.2
1	B	50	GLU	11.2
1	A	609	VAL	11.2
1	B	421	ASP	11.2
2	H	72	VAL	11.2
1	B	764	ILE	11.2
1	A	255	LYS	11.2
2	G	208	VAL	11.2
4	F	62	PHE	11.2
2	H	16	GLN	11.1
2	G	347	ILE	11.1
1	A	180	LEU	11.1
1	A	765	GLU	11.1
1	B	650	GLU	11.1
1	B	596	LEU	11.1
2	H	309	ILE	11.1
1	A	401	ASP	11.1
2	G	308	ALA	11.1
1	A	739	HIS	11.1

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Mol	Chain	Res	Type	RSRZ
2	H	77	VAL	11.1
2	G	268	ASN	11.1
2	H	130	GLY	11.1
1	A	190	VAL	11.1
1	B	371	THR	11.0
1	A	136	ARG	11.0
1	B	77	THR	11.0
1	B	248	LYS	11.0
2	H	109	ARG	11.0
1	B	612	LYS	11.0
2	G	426	TYR	11.0
1	A	408	TYR	11.0
1	A	275	ILE	11.0
1	A	349	SER	11.0
1	A	46	ILE	11.0
1	A	748	PRO	10.9
2	H	272	VAL	10.9
2	H	281	LEU	10.9
2	H	374	PHE	10.9
1	A	407	ILE	10.9
1	B	379	GLU	10.9
1	B	634	SER	10.9
1	A	151	THR	10.9
1	A	772	ALA	10.9
2	G	165	GLY	10.9
1	A	636	GLU	10.8
2	H	335	GLU	10.8
1	B	571	SER	10.8
1	B	109	THR	10.8
4	E	40	SER	10.8
1	A	213	LEU	10.8
1	A	412	GLU	10.8
1	B	222	ILE	10.8
1	A	728	ILE	10.7
2	H	390	ASN	10.7
1	A	410	THR	10.7
1	B	251	THR	10.7
1	B	635	LEU	10.7
4	E	29	VAL	10.7
1	A	316	VAL	10.7
1	A	21	LYS	10.7
1	A	513	HIS	10.7

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Mol	Chain	Res	Type	RSRZ
2	G	69	ARG	10.7
2	G	327	THR	10.7
1	B	11	PRO	10.7
1	B	382	ARG	10.7
1	B	645	ARG	10.7
1	A	771	VAL	10.7
1	A	293	ALA	10.7
1	B	357	PHE	10.7
1	B	247	GLU	10.7
1	A	573	MET	10.7
1	B	543	ASP	10.7
1	A	145	PHE	10.6
2	H	99	ARG	10.6
1	B	88	GLY	10.6
3	C	60	SER	10.6
1	B	461	ALA	10.6
1	A	121	GLY	10.6
1	B	539	LEU	10.6
2	G	74	ALA	10.6
1	B	272	ALA	10.6
1	B	737	GLY	10.6
2	G	92	VAL	10.6
1	A	149	GLY	10.6
1	A	187	ASP	10.6
1	B	387	MET	10.5
1	B	745	GLN	10.5
2	G	177	THR	10.5
1	A	487	ALA	10.5
2	G	237	GLU	10.5
1	A	291	ASN	10.5
1	A	112	LEU	10.5
1	B	240	PHE	10.5
1	A	211	SER	10.5
2	G	302	ASP	10.5
1	A	225	GLY	10.5
1	B	615	PHE	10.5
2	G	112	ILE	10.4
2	H	171	TRP	10.4
1	A	332	GLY	10.4
1	B	669	GLY	10.4
2	G	326	TYR	10.4
1	A	62	LEU	10.4

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Mol	Chain	Res	Type	RSRZ
1	A	766	SER	10.4
1	B	377	GLU	10.4
2	G	89	LEU	10.4
1	A	711	PHE	10.4
1	B	330	SER	10.4
1	B	208	GLU	10.4
2	H	419	ILE	10.4
1	A	501	GLU	10.4
2	G	404	VAL	10.4
1	A	197	VAL	10.4
1	A	444	LEU	10.4
1	A	224	SER	10.4
1	B	21	LYS	10.4
2	G	320	VAL	10.4
2	H	118	TYR	10.3
2	H	340	LEU	10.3
1	A	764	ILE	10.3
1	A	148	LEU	10.3
1	B	275	ILE	10.3
2	H	28	TYR	10.3
1	B	552	GLU	10.3
1	B	81	PRO	10.3
2	H	198	PRO	10.3
2	H	358	LYS	10.2
1	A	581	SER	10.2
1	B	207	ASP	10.2
1	B	533	GLY	10.2
1	B	333	LEU	10.2
2	G	22	LEU	10.2
1	A	159	MET	10.2
2	G	369	PHE	10.2
2	H	414	ILE	10.2
1	B	8	MET	10.2
4	F	61	LEU	10.2
1	A	339	ALA	10.2
1	A	726	ASP	10.2
2	H	411	PHE	10.2
1	B	602	VAL	10.2
2	H	382	PRO	10.1
4	E	39	GLN	10.1
1	A	676	ILE	10.1
1	A	773	LYS	10.1

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Mol	Chain	Res	Type	RSRZ
1	B	551	ALA	10.1
1	A	147	PHE	10.1
2	G	173	ALA	10.1
1	B	302	LYS	10.1
4	E	38	GLY	10.1
1	B	408	TYR	10.1
2	H	265	ILE	10.1
1	A	514	GLU	10.1
2	G	407	ALA	10.0
4	F	50	ILE	10.0
2	H	375	LEU	10.0
2	G	415	GLU	10.0
2	G	328	ALA	10.0
1	A	770	GLU	10.0
1	B	376	THR	10.0
1	B	588	ASN	10.0
1	A	353	ALA	10.0
2	G	330	LEU	10.0
2	H	206	GLU	10.0
1	A	177	ASN	10.0
1	B	185	LEU	10.0
2	H	57	ALA	10.0
2	H	271	GLY	10.0
1	A	239	ALA	10.0
1	A	89	GLY	10.0
2	H	56	PHE	10.0
2	H	389	PHE	10.0
2	G	331	ILE	10.0
1	B	305	ASP	10.0
2	H	418	LEU	10.0
2	G	279	GLN	9.9
1	A	331	GLU	9.9
1	B	346	GLN	9.9
2	G	319	ILE	9.9
2	G	111	LYS	9.9
1	A	675	ASP	9.9
2	G	266	LYS	9.9
1	B	367	LEU	9.9
1	B	15	THR	9.9
1	B	211	SER	9.9
1	B	298	VAL	9.9
2	H	409	ASP	9.9

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Mol	Chain	Res	Type	RSRZ
1	A	271	LYS	9.9
2	H	101	ALA	9.9
1	B	606	GLN	9.9
2	G	406	VAL	9.9
2	H	387	VAL	9.8
2	G	72	VAL	9.8
1	B	420	GLU	9.8
1	B	598	GLN	9.8
2	G	86	MET	9.8
1	A	75	ARG	9.8
2	G	183	ASN	9.8
1	A	750	ARG	9.8
2	G	64	GLY	9.8
1	A	471	ILE	9.8
1	B	243	THR	9.8
1	B	724	TRP	9.8
1	B	644	PRO	9.8
2	G	76	GLY	9.8
1	A	590	PHE	9.8
3	D	29	ALA	9.8
2	G	400	ALA	9.7
1	A	183	ASP	9.7
1	A	531	ASP	9.7
4	F	28	ASP	9.7
1	A	240	PHE	9.7
1	A	761	GLU	9.7
1	B	129	VAL	9.7
1	A	39	ASP	9.7
1	B	354	THR	9.7
1	A	156	LEU	9.6
4	F	16	LEU	9.6
1	A	134	ALA	9.6
1	B	214	ILE	9.6
1	B	209	VAL	9.6
2	G	172	ILE	9.6
1	B	668	GLU	9.6
1	A	348	GLU	9.6
1	B	763	MET	9.6
1	B	57	THR	9.6
1	B	402	ASP	9.6
1	B	591	ASP	9.6
2	G	27	ILE	9.6

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Mol	Chain	Res	Type	RSRZ
1	B	416	LYS	9.6
1	A	597	LEU	9.6
1	A	741	ARG	9.6
1	B	20	GLU	9.6
2	H	88	GLN	9.6
1	A	57	THR	9.6
1	B	605	GLN	9.5
1	B	723	LYS	9.5
2	G	408	LEU	9.5
2	H	90	LEU	9.5
1	A	22	ILE	9.5
1	A	593	ARG	9.5
1	B	348	GLU	9.5
1	A	238	ASN	9.5
1	B	241	VAL	9.5
1	B	434	VAL	9.5
1	B	761	GLU	9.5
1	B	561	PHE	9.5
1	B	670	ALA	9.5
1	A	88	GLY	9.5
1	B	10	ASP	9.5
1	A	150	LEU	9.5
1	B	227	ALA	9.5
1	A	51	ARG	9.5
1	A	32	ASP	9.5
1	A	171	ASP	9.5
1	B	514	GLU	9.5
2	H	412	ARG	9.4
1	A	329	TYR	9.4
1	A	160	SER	9.4
2	G	392	PRO	9.4
2	G	13	GLU	9.4
1	A	67	ALA	9.4
1	A	298	VAL	9.4
1	A	135	SER	9.4
1	B	199	ARG	9.4
2	G	403	VAL	9.4
2	G	236	GLN	9.3
2	H	102	LYS	9.3
1	B	7	LYS	9.3
1	A	670	ALA	9.3
1	A	299	ALA	9.3

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Mol	Chain	Res	Type	RSRZ
1	A	767	ILE	9.3
1	A	423	ALA	9.3
4	E	30	GLY	9.3
2	H	229	ILE	9.3
2	H	397	GLY	9.3
1	B	358	GLN	9.3
1	B	12	THR	9.3
1	B	550	GLY	9.3
1	A	542	GLU	9.3
2	G	413	GLN	9.3
2	G	301	ALA	9.3
2	H	339	ASN	9.2
2	G	316	VAL	9.2
2	H	185	ALA	9.2
1	A	387	MET	9.2
2	H	86	MET	9.2
1	A	81	PRO	9.2
1	A	587	GLY	9.2
1	A	373	THR	9.2
1	B	325	LYS	9.2
1	B	340	LYS	9.2
1	B	117	ASN	9.2
1	A	582	GLN	9.2
1	B	141	MET	9.2
2	G	296	PHE	9.2
2	H	305	GLN	9.2
1	B	537	PHE	9.2
1	A	318	SER	9.1
2	G	239	GLU	9.1
1	B	496	GLY	9.1
1	A	438	ALA	9.1
2	H	78	MET	9.1
2	H	416	THR	9.1
1	B	431	PRO	9.1
1	A	227	ALA	9.1
2	G	401	LEU	9.1
1	A	83	LYS	9.1
1	A	488	GLY	9.1
1	A	360	TYR	9.1
2	G	329	VAL	9.1
1	B	18	ARG	9.0
1	A	416	LYS	9.0

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Mol	Chain	Res	Type	RSRZ
4	E	37	MET	9.0
1	A	319	PHE	9.0
1	A	738	ILE	9.0
2	G	18	PHE	9.0
2	H	121	LEU	9.0
1	A	384	ILE	9.0
1	B	713	LYS	9.0
4	E	41	ILE	9.0
1	B	130	ASN	9.0
1	B	139	GLU	9.0
1	B	746	THR	9.0
1	A	155	ASN	9.0
1	A	152	VAL	9.0
2	G	393	PHE	9.0
2	H	351	ARG	9.0
2	H	400	ALA	9.0
1	B	220	PRO	9.0
1	B	349	SER	8.9
1	B	360	TYR	8.9
1	A	295	LYS	8.9
1	A	596	LEU	8.9
1	B	345	ILE	8.9
2	G	68	GLY	8.9
1	B	173	THR	8.9
1	B	538	TYR	8.9
1	A	31	GLY	8.9
1	A	245	LYS	8.9
2	H	133	PHE	8.9
1	A	27	ASP	8.8
3	C	57	PHE	8.8
1	A	638	ALA	8.8
2	H	131	ILE	8.8
1	A	226	GLN	8.8
1	A	297	HIS	8.8
2	G	381	ILE	8.8
1	A	388	GLN	8.8
1	B	320	THR	8.8
1	A	29	ILE	8.8
1	A	269	ALA	8.8
4	F	39	GLN	8.8
1	A	635	LEU	8.8
1	B	492	ASP	8.8

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Mol	Chain	Res	Type	RSRZ
1	A	744	ALA	8.8
2	H	252	GLY	8.8
1	A	774	PHE	8.8
2	G	23	LEU	8.8
1	A	414	LYS	8.8
1	A	176	THR	8.8
1	A	341	GLU	8.7
2	H	178	GLU	8.7
1	B	636	GLU	8.7
1	A	25	ASP	8.7
2	H	177	THR	8.7
1	B	175	SER	8.7
1	A	475	GLY	8.7
1	A	611	TYR	8.7
2	H	386	SER	8.7
1	B	324	MET	8.7
1	B	690	ASP	8.7
1	A	393	PRO	8.7
1	A	749	LEU	8.7
1	B	720	VAL	8.7
2	H	273	ILE	8.6
2	H	292	VAL	8.6
1	A	196	MET	8.6
2	G	99	ARG	8.6
2	G	416	THR	8.6
1	A	86	LEU	8.6
1	B	445	ILE	8.6
1	B	573	MET	8.6
1	B	372	GLY	8.6
1	A	727	HIS	8.6
1	B	685	LEU	8.6
3	D	28	LYS	8.6
2	H	380	LEU	8.6
1	B	70	ARG	8.6
4	F	49	THR	8.6
1	B	73	SER	8.6
1	A	28	ALA	8.6
1	A	153	GLY	8.6
1	A	270	GLU	8.6
1	A	419	ALA	8.6
1	B	511	GLU	8.6
2	G	377	VAL	8.6

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Mol	Chain	Res	Type	RSRZ
1	A	85	GLN	8.6
2	G	289	LEU	8.6
1	B	775	VAL	8.6
1	A	463	ASN	8.5
2	G	376	SER	8.5
2	H	295	PRO	8.5
1	A	315	ILE	8.5
2	H	410	THR	8.5
2	G	90	LEU	8.5
1	B	76	VAL	8.5
1	A	405	ASP	8.5
2	G	85	ILE	8.5
1	B	594	LYS	8.5
2	H	304	PHE	8.5
1	A	730	ALA	8.5
1	B	310	ASP	8.5
1	B	93	HIS	8.5
2	H	360	LEU	8.5
1	B	495	LEU	8.5
1	B	347	ASN	8.5
2	G	418	LEU	8.4
2	G	338	GLU	8.4
1	A	19	TYR	8.4
2	H	84	SER	8.4
1	A	725	MET	8.4
1	A	93	HIS	8.4
1	A	193	LYS	8.4
1	B	384	ILE	8.4
1	A	340	LYS	8.4
1	B	105	GLY	8.4
1	A	376	THR	8.4
1	B	228	ALA	8.4
1	A	760	PHE	8.4
2	G	398	THR	8.4
4	E	33	PHE	8.4
1	B	497	GLU	8.4
2	G	396	GLY	8.4
2	G	40	ASN	8.4
1	B	91	ALA	8.4
1	A	74	ARG	8.4
1	A	242	ARG	8.4
2	H	82	SER	8.3

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Mol	Chain	Res	Type	RSRZ
2	H	277	PHE	8.3
2	G	75	LEU	8.3
2	H	413	GLN	8.3
1	B	350	MET	8.3
1	A	740	LEU	8.3
1	B	597	LEU	8.3
2	G	87	MET	8.3
1	B	703	PHE	8.3
4	F	38	GLY	8.3
1	A	66	PHE	8.3
1	A	192	TYR	8.2
1	A	778	ALA	8.2
2	G	252	GLY	8.2
1	A	775	VAL	8.2
1	A	172	ILE	8.2
1	B	80	PHE	8.2
1	A	642	TYR	8.2
2	G	176	ILE	8.2
2	H	352	PRO	8.2
1	B	17	ASN	8.2
1	A	10	ASP	8.2
1	A	127	VAL	8.2
3	C	55	ILE	8.2
1	B	721	ASP	8.2
1	B	215	ASP	8.1
2	G	93	ALA	8.1
1	B	160	SER	8.1
1	B	458	VAL	8.1
1	A	209	VAL	8.1
1	B	422	VAL	8.1
2	G	175	ARG	8.1
2	G	26	VAL	8.1
1	B	286	LEU	8.1
1	B	396	ARG	8.1
1	A	639	ILE	8.1
1	A	309	GLU	8.1
2	H	64	GLY	8.1
1	B	14	ARG	8.0
2	H	14	LEU	8.0
2	G	305	GLN	8.0
1	B	760	PHE	8.0
2	H	186	SER	8.0

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Mol	Chain	Res	Type	RSRZ
1	B	694	THR	8.0
1	B	592	SER	8.0
1	A	321	GLY	8.0
1	A	674	SER	8.0
1	B	157	ASN	8.0
1	A	512	ARG	8.0
2	G	278	ALA	8.0
1	B	136	ARG	8.0
2	H	180	GLY	8.0
1	A	342	GLY	8.0
1	B	390	VAL	8.0
2	H	349	GLY	7.9
1	B	351	THR	7.9
2	G	337	ALA	7.9
1	A	157	ASN	7.9
1	B	383	ASN	7.9
2	H	179	LYS	7.9
2	G	181	ILE	7.9
1	A	588	ASN	7.9
2	H	398	THR	7.9
1	A	212	ILE	7.9
1	A	472	GLU	7.9
1	A	462	LYS	7.9
2	H	293	GLN	7.9
1	A	553	ARG	7.9
2	G	25	PHE	7.9
4	F	14	VAL	7.9
1	B	274	GLY	7.9
1	B	749	LEU	7.8
1	A	174	TYR	7.8
2	H	107	TYR	7.8
1	A	567	THR	7.8
1	A	454	ILE	7.8
2	H	138	GLN	7.8
1	A	273	PHE	7.8
1	B	221	LEU	7.8
1	B	607	ARG	7.8
2	G	417	TYR	7.8
1	B	646	GLU	7.8
1	A	16	LEU	7.8
1	B	182	PHE	7.8
1	B	252	TYR	7.7

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Mol	Chain	Res	Type	RSRZ
1	B	667	ASP	7.7
1	B	9	PHE	7.7
1	B	432	VAL	7.7
1	A	106	LYS	7.7
1	B	642	TYR	7.7
2	H	336	LEU	7.7
1	B	282	LYS	7.7
1	B	226	GLN	7.7
1	A	356	THR	7.7
1	B	246	ALA	7.7
1	A	247	GLU	7.7
1	B	151	THR	7.7
2	H	183	ASN	7.7
2	G	270	ALA	7.7
1	A	374	ALA	7.7
4	E	36	GLY	7.7
1	B	701	GLU	7.7
2	H	184	GLY	7.6
1	B	388	GLN	7.6
2	H	236	GLN	7.6
2	G	339	ASN	7.6
1	A	30	ARG	7.6
1	B	196	MET	7.6
2	G	397	GLY	7.6
4	E	71	VAL	7.6
1	A	586	GLU	7.6
4	F	29	VAL	7.6
1	B	366	LYS	7.6
2	G	291	PHE	7.6
1	A	228	ALA	7.6
1	B	620	SER	7.5
2	H	415	GLU	7.5
1	A	208	GLU	7.5
2	H	103	GLU	7.5
1	B	710	GLU	7.5
2	H	354	GLN	7.5
1	A	623	LEU	7.5
1	B	164	LYS	7.5
1	B	92	LEU	7.5
1	B	96	ASN	7.5
1	B	201	LEU	7.5
1	A	591	ASP	7.5

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Mol	Chain	Res	Type	RSRZ
1	A	13	LYS	7.5
1	B	375	LYS	7.5
1	B	569	ILE	7.5
1	A	671	LEU	7.5
1	B	303	ASP	7.5
1	B	150	LEU	7.5
1	A	206	ILE	7.5
2	H	58	LEU	7.5
1	A	650	GLU	7.4
1	B	453	GLY	7.4
1	B	641	ALA	7.4
1	A	95	GLY	7.4
1	B	74	ARG	7.4
2	G	109	ARG	7.4
2	G	411	PHE	7.4
1	B	165	ARG	7.4
2	H	85	ILE	7.4
1	B	306	TYR	7.4
1	A	290	ILE	7.4
1	A	301	GLN	7.4
1	B	316	VAL	7.4
1	A	622	ASN	7.4
1	B	223	ILE	7.4
1	B	695	LYS	7.4
2	H	417	TYR	7.4
1	A	215	ASP	7.4
1	A	489	ARG	7.4
1	B	687	LEU	7.4
1	A	752	TYR	7.3
1	B	730	ALA	7.3
1	B	404	PRO	7.3
1	A	34	GLU	7.3
2	H	146	VAL	7.3
2	H	83	ALA	7.3
1	B	702	GLN	7.3
2	G	425	SER	7.3
1	B	190	VAL	7.3
1	B	423	ALA	7.3
1	B	446	SER	7.3
1	B	618	ILE	7.3
1	B	640	ALA	7.3
3	D	62	ARG	7.3

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Mol	Chain	Res	Type	RSRZ
1	B	159	MET	7.3
1	A	20	GLU	7.3
1	B	329	TYR	7.3
1	A	173	THR	7.3
1	A	308	VAL	7.3
4	F	54	ALA	7.3
2	G	84	SER	7.2
1	A	304	VAL	7.2
1	A	375	LYS	7.2
2	G	102	LYS	7.2
1	A	220	PRO	7.2
2	H	137	GLY	7.2
1	B	140	GLN	7.2
2	G	39	ILE	7.2
1	B	86	LEU	7.2
2	G	292	VAL	7.2
1	A	181	GLY	7.2
1	A	420	GLU	7.2
1	A	347	ASN	7.2
2	G	385	ILE	7.2
1	B	574	VAL	7.2
1	A	570	GLN	7.2
1	A	307	VAL	7.2
1	B	393	PRO	7.2
2	G	348	PRO	7.2
2	G	382	PRO	7.1
1	A	448	LEU	7.1
2	H	237	GLU	7.1
1	A	490	GLY	7.1
1	A	592	SER	7.1
1	B	135	SER	7.1
2	H	254	GLN	7.1
1	A	346	GLN	7.1
1	A	610	ILE	7.1
1	B	727	HIS	7.1
1	A	451	ASN	7.1
2	H	182	GLY	7.1
2	G	137	GLY	7.1
1	A	11	PRO	7.1
2	G	309	ILE	7.1
2	G	110	TYR	7.1
1	B	206	ILE	7.1

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Mol	Chain	Res	Type	RSRZ
1	B	197	VAL	7.1
1	B	319	PHE	7.1
1	B	729	ASP	7.1
2	G	164	ALA	7.1
3	C	59	LEU	7.1
1	B	290	ILE	7.1
1	B	407	ILE	7.0
1	A	94	ASP	7.0
1	B	548	ARG	7.0
1	B	593	ARG	7.0
1	B	167	ALA	7.0
2	H	134	TRP	7.0
2	G	56	PHE	7.0
1	A	409	ARG	7.0
1	B	137	ASP	7.0
1	B	327	ARG	7.0
1	A	26	ILE	7.0
1	B	728	ILE	7.0
1	A	124	VAL	7.0
2	H	140	SER	7.0
2	H	9	PHE	6.9
1	A	35	ASN	6.9
2	H	251	VAL	6.9
1	A	710	GLU	6.9
2	G	63	SER	6.9
1	B	485	ASN	6.9
1	A	76	VAL	6.9
1	A	158	SER	6.9
2	H	188	ILE	6.9
1	A	154	LEU	6.9
1	B	213	LEU	6.9
4	F	71	VAL	6.9
1	A	207	ASP	6.8
1	A	345	ILE	6.8
2	H	420	GLN	6.8
1	B	189	MET	6.8
4	F	51	LEU	6.8
2	G	370	PHE	6.8
2	H	61	ILE	6.8
2	H	359	TYR	6.8
2	H	392	PRO	6.8
4	F	31	ALA	6.8

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Mol	Chain	Res	Type	RSRZ
1	B	107	THR	6.8
2	G	106	ASP	6.8
4	F	72	ILE	6.8
1	A	248	LYS	6.8
2	G	240	ARG	6.8
2	H	197	PHE	6.8
1	B	168	TYR	6.8
1	B	153	GLY	6.8
1	B	78	GLY	6.8
1	B	374	ALA	6.7
1	A	612	LYS	6.7
2	H	276	ILE	6.7
1	A	439	VAL	6.7
1	A	98	ALA	6.7
1	B	484	THR	6.7
1	A	133	LEU	6.7
1	B	684	MET	6.7
1	A	652	TRP	6.7
2	H	68	GLY	6.7
1	B	414	LYS	6.7
1	B	444	LEU	6.7
1	B	75	ARG	6.7
1	B	116	LEU	6.7
1	A	33	TYR	6.7
1	A	361	PHE	6.7
1	B	321	GLY	6.7
1	A	241	VAL	6.7
1	B	138	ALA	6.7
2	G	163	VAL	6.7
1	B	368	ALA	6.7
2	G	294	ASN	6.7
2	G	293	GLN	6.7
1	B	613	GLN	6.6
1	A	583	LYS	6.6
2	H	357	VAL	6.6
2	H	355	ASP	6.6
1	A	99	GLU	6.6
2	G	297	ILE	6.6
2	H	17	LYS	6.6
1	B	56	ALA	6.6
1	A	97	ILE	6.6
2	H	79	PRO	6.6

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Mol	Chain	Res	Type	RSRZ
2	G	247	PRO	6.6
1	A	530	GLY	6.6
1	A	743	TYR	6.6
1	A	256	THR	6.6
2	G	24	MET	6.6
1	A	555	MET	6.6
2	H	181	ILE	6.6
1	B	200	PRO	6.6
2	H	25	PHE	6.6
1	B	580	SER	6.6
2	H	396	GLY	6.6
4	E	34	GLY	6.6
1	B	589	ASN	6.6
2	H	81	ILE	6.6
1	A	202	HIS	6.5
1	B	370	MET	6.5
2	G	271	GLY	6.5
4	F	13	ALA	6.5
1	B	619	ASP	6.5
1	A	344	GLU	6.5
1	B	94	ASP	6.5
1	A	143	LYS	6.5
2	G	267	ILE	6.5
1	B	97	ILE	6.5
1	B	691	ARG	6.5
1	B	614	ARG	6.5
2	H	195	ALA	6.5
1	A	465	GLU	6.5
1	B	317	ASP	6.5
2	H	391	ILE	6.5
1	A	350	MET	6.5
2	H	191	ALA	6.5
1	B	16	LEU	6.5
1	A	580	SER	6.4
2	G	248	GLY	6.4
1	B	450	LYS	6.4
1	B	639	ILE	6.4
3	C	58	ILE	6.4
1	B	353	ALA	6.4
2	G	253	ARG	6.4
1	A	452	LYS	6.4
2	H	256	TYR	6.4

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Mol	Chain	Res	Type	RSRZ
1	A	8	MET	6.4
2	H	270	ALA	6.4
4	F	63	LEU	6.4
1	B	419	ALA	6.4
1	B	389	VAL	6.4
1	A	473	GLU	6.4
1	B	124	VAL	6.4
1	A	144	ILE	6.3
1	A	324	MET	6.3
1	A	55	GLY	6.3
2	H	267	ILE	6.3
1	A	450	LYS	6.3
1	B	13	LYS	6.3
1	A	500	LYS	6.3
2	G	104	GLU	6.3
2	G	130	GLY	6.3
1	B	590	PHE	6.3
2	G	66	ASN	6.3
1	A	77	THR	6.3
1	A	23	ALA	6.3
1	A	92	LEU	6.2
1	A	362	ARG	6.2
1	B	486	MET	6.2
1	A	80	PHE	6.2
1	A	613	GLN	6.2
1	B	547	ARG	6.2
1	B	174	TYR	6.2
1	B	523	ARG	6.2
2	G	77	VAL	6.2
2	H	106	ASP	6.2
2	H	268	ASN	6.2
1	B	617	VAL	6.2
1	B	95	GLY	6.2
2	H	261	THR	6.1
1	A	194	GLU	6.1
2	H	196	ASN	6.1
1	B	529	GLN	6.1
1	B	318	SER	6.1
2	G	383	ILE	6.1
1	B	549	PHE	6.1
1	A	191	LEU	6.1
2	H	399	THR	6.1

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Mol	Chain	Res	Type	RSRZ
2	H	238	ALA	6.1
2	H	145	PRO	6.1
1	B	309	GLU	6.1
2	G	262	TYR	6.1
1	A	729	ASP	6.1
2	H	348	PRO	6.1
1	A	24	ASN	6.0
1	A	759	MET	6.0
1	B	647	GLU	6.0
1	A	250	TYR	6.0
1	A	395	ASN	6.0
4	F	11	ILE	6.0
1	A	453	GLY	6.0
1	B	118	ALA	6.0
1	A	7	LYS	6.0
1	B	108	LEU	6.0
1	B	696	TYR	6.0
4	E	42	PHE	6.0
2	G	167	MET	5.9
2	H	27	ILE	5.9
1	A	56	ALA	5.9
1	A	6	ASN	5.9
2	H	401	LEU	5.9
1	A	12	THR	5.9
1	B	491	THR	5.9
2	G	138	GLN	5.9
1	A	38	ASP	5.9
1	A	186	ARG	5.9
1	B	212	ILE	5.9
1	A	96	ASN	5.9
2	H	405	GLY	5.9
2	H	275	ILE	5.9
4	E	50	ILE	5.9
1	A	326	GLY	5.9
2	G	144	ILE	5.9
1	B	743	TYR	5.9
2	H	192	GLY	5.9
2	G	371	GLY	5.8
2	H	70	LEU	5.8
1	A	261	LEU	5.8
1	A	502	LEU	5.8
1	B	637	ARG	5.8

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Mol	Chain	Res	Type	RSRZ
1	A	365	GLU	5.8
1	A	579	GLU	5.8
4	F	70	SER	5.8
1	A	91	ALA	5.8
1	A	184	TYR	5.8
2	H	427	VAL	5.8
1	A	554	THR	5.8
2	G	179	LYS	5.8
1	B	449	LEU	5.8
2	G	263	LEU	5.8
2	H	294	ASN	5.8
1	B	51	ARG	5.8
1	B	133	LEU	5.8
1	A	746	THR	5.8
1	B	193	LYS	5.8
1	B	392	ILE	5.8
2	H	26	VAL	5.8
1	B	570	GLN	5.7
1	A	528	ARG	5.7
1	A	82	PHE	5.7
1	B	697	ASN	5.7
1	A	294	LEU	5.7
4	F	37	MET	5.7
1	A	175	SER	5.7
1	A	253	ASP	5.7
2	G	139	VAL	5.7
1	A	669	GLY	5.7
1	A	53	GLU	5.7
1	B	698	GLU	5.7
4	F	48	GLU	5.7
1	B	490	GLY	5.7
1	A	303	ASP	5.7
1	A	584	ARG	5.7
2	G	103	GLU	5.7
2	G	259	ARG	5.7
1	A	84	VAL	5.7
2	H	80	TYR	5.7
1	B	219	THR	5.7
4	E	68	LEU	5.7
2	G	108	GLY	5.6
1	A	100	MET	5.6
2	H	383	ILE	5.6

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Mol	Chain	Res	Type	RSRZ
1	B	98	ALA	5.6
2	H	255	LEU	5.6
3	C	62	ARG	5.6
1	A	552	GLU	5.6
2	H	332	ASN	5.6
4	E	31	ALA	5.6
1	A	216	GLU	5.6
1	A	355	ILE	5.6
2	H	89	LEU	5.6
1	B	100	MET	5.6
1	A	763	MET	5.6
1	A	328	ARG	5.6
2	H	242	ILE	5.5
1	B	726	ASP	5.5
1	B	394	THR	5.5
2	G	299	VAL	5.5
1	A	130	ASN	5.5
1	A	524	GLY	5.5
1	A	541	MET	5.5
1	B	328	ARG	5.5
1	A	169	ALA	5.5
1	B	405	ASP	5.5
1	B	608	GLU	5.5
1	A	745	GLN	5.5
1	A	78	GLY	5.4
1	A	305	ASP	5.4
1	B	55	GLY	5.4
2	H	8	LEU	5.4
2	H	342	LYS	5.4
1	A	223	ILE	5.4
1	B	369	GLY	5.4
2	G	180	GLY	5.4
2	G	250	GLN	5.4
2	G	384	LEU	5.4
1	B	106	LYS	5.4
1	B	192	TYR	5.4
1	B	451	ASN	5.4
1	A	649	PRO	5.4
1	A	322	ARG	5.4
1	B	587	GLY	5.4
2	G	189	ILE	5.4
1	B	218	ARG	5.4

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Mol	Chain	Res	Type	RSRZ
1	B	546	MET	5.4
2	G	105	GLY	5.4
2	G	129	LEU	5.4
1	A	162	ASP	5.4
1	A	643	THR	5.4
2	H	241	ARG	5.4
2	H	330	LEU	5.3
2	G	178	GLU	5.3
2	H	235	VAL	5.3
1	A	389	VAL	5.3
1	B	217	ALA	5.3
1	B	163	GLU	5.3
1	B	152	VAL	5.3
1	A	217	ALA	5.3
1	B	418	VAL	5.3
2	G	101	ALA	5.3
1	B	742	ALA	5.3
4	F	12	ILE	5.3
2	G	168	PHE	5.3
1	A	244	LEU	5.3
1	B	253	ASP	5.3
1	A	351	THR	5.3
1	A	499	VAL	5.3
2	G	107	TYR	5.3
2	H	141	PRO	5.3
2	H	69	ARG	5.2
1	A	251	THR	5.2
2	H	353	GLY	5.2
2	H	394	TYR	5.2
1	B	352	LEU	5.2
1	B	725	MET	5.2
2	G	340	LEU	5.2
2	G	298	LYS	5.2
1	A	574	VAL	5.2
2	G	254	GLN	5.2
2	G	300	ILE	5.2
1	A	762	HIS	5.2
1	A	464	HIS	5.2
1	A	254	ILE	5.2
2	H	20	PHE	5.2
1	B	195	GLN	5.2
1	A	568	PRO	5.1

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Mol	Chain	Res	Type	RSRZ
2	H	269	PRO	5.1
1	B	611	TYR	5.1
2	H	233	VAL	5.1
1	B	520	ASN	5.1
1	A	327	ARG	5.1
2	H	264	PRO	5.1
1	A	496	GLY	5.1
2	H	230	VAL	5.1
1	A	182	PHE	5.0
1	B	166	GLU	5.0
1	B	415	PHE	5.0
1	B	172	ILE	5.0
1	B	156	LEU	5.0
4	F	36	GLY	5.0
1	B	482	ILE	5.0
1	B	524	GLY	5.0
1	A	415	PHE	5.0
1	B	194	GLU	5.0
1	A	249	ASP	5.0
1	A	577	ALA	5.0
1	A	400	ARG	5.0
1	B	738	ILE	5.0
2	H	385	ILE	5.0
1	B	406	LEU	5.0
1	B	273	PHE	5.0
1	A	161	LYS	5.0
4	F	64	VAL	5.0
2	H	259	ARG	5.0
1	A	569	ILE	4.9
2	G	251	VAL	4.9
1	B	361	PHE	4.9
1	A	323	LEU	4.9
1	A	343	LEU	4.9
2	G	83	ALA	4.9
2	G	375	LEU	4.9
2	H	408	LEU	4.9
1	B	577	ALA	4.9
1	A	131	GLU	4.9
2	G	61	ILE	4.9
2	G	57	ALA	4.9
1	B	103	GLY	4.9
2	G	241	ARG	4.8

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Mol	Chain	Res	Type	RSRZ
1	A	306	TYR	4.8
1	B	517	ARG	4.8
1	A	449	LEU	4.8
1	A	474	ALA	4.8
2	G	277	PHE	4.8
2	H	356	THR	4.8
4	F	32	ALA	4.8
1	B	638	ALA	4.8
4	F	35	GLY	4.8
4	F	46	GLY	4.8
1	A	132	TYR	4.8
2	H	136	ARG	4.8
4	E	43	GLY	4.8
2	H	347	ILE	4.8
4	F	40	SER	4.8
2	H	258	GLY	4.7
1	B	256	THR	4.7
1	A	621	GLU	4.7
1	A	363	MET	4.7
2	H	21	THR	4.7
1	A	352	LEU	4.7
1	A	477	LYS	4.7
2	H	337	ALA	4.7
2	H	402	ILE	4.7
1	B	699	LYS	4.7
1	B	649	PRO	4.7
1	B	304	VAL	4.7
1	B	260	GLN	4.7
4	E	72	ILE	4.7
2	G	272	VAL	4.7
1	B	245	LYS	4.7
2	H	135	ILE	4.6
2	H	395	PHE	4.6
2	G	273	ILE	4.6
2	H	189	ILE	4.6
1	B	448	LEU	4.6
2	H	338	GLU	4.6
1	B	162	ASP	4.6
2	G	419	ILE	4.6
2	H	426	TYR	4.6
2	H	71	THR	4.6
4	E	32	ALA	4.6

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Mol	Chain	Res	Type	RSRZ
2	G	100	LEU	4.6
2	H	193	ILE	4.6
1	B	521	GLN	4.6
1	B	483	ALA	4.6
1	A	354	THR	4.6
1	A	364	TYR	4.5
1	A	494	LYS	4.5
2	H	274	PRO	4.5
1	A	105	GLY	4.5
4	F	30	GLY	4.5
1	B	171	ASP	4.5
1	B	748	PRO	4.5
1	B	79	MET	4.5
1	A	170	ALA	4.5
1	B	132	TYR	4.5
2	H	260	LYS	4.5
1	B	747	ASN	4.5
4	E	48	GLU	4.5
1	B	739	HIS	4.5
1	A	392	ILE	4.5
1	B	581	SER	4.4
2	G	188	ILE	4.4
1	B	576	ARG	4.4
4	E	45	GLY	4.4
1	A	585	VAL	4.4
1	A	37	SER	4.4
1	B	119	LEU	4.4
3	C	61	LEU	4.4
1	B	362	ARG	4.4
2	H	139	VAL	4.4
1	B	586	GLU	4.4
1	B	688	ILE	4.4
1	B	544	GLU	4.4
2	G	260	LYS	4.4
2	H	257	ALA	4.4
2	G	67	LEU	4.4
2	H	240	ARG	4.4
1	B	365	GLU	4.4
1	A	219	THR	4.3
2	G	190	PHE	4.3
1	B	447	LYS	4.3
4	E	49	THR	4.3

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Mol	Chain	Res	Type	RSRZ
1	B	493	ILE	4.3
1	B	254	ILE	4.3
2	H	232	ILE	4.3
1	B	515	SER	4.3
1	A	497	GLU	4.3
2	H	24	MET	4.3
2	H	67	LEU	4.2
1	B	161	LYS	4.2
2	G	303	MET	4.2
1	B	489	ARG	4.2
2	H	250	GLN	4.2
1	B	530	GLY	4.2
1	B	689	MET	4.2
2	H	105	GLY	4.2
2	G	420	GLN	4.2
4	E	46	GLY	4.2
1	B	53	GLU	4.2
2	G	81	ILE	4.2
2	G	256	TYR	4.2
1	A	9	PHE	4.2
1	A	54	LYS	4.1
1	B	154	LEU	4.1
1	B	134	ALA	4.1
1	A	222	ILE	4.1
1	A	550	GLY	4.1
1	B	526	SER	4.1
2	G	60	ASP	4.1
1	B	452	LYS	4.1
2	G	62	PHE	4.1
1	A	36	LEU	4.1
1	B	155	ASN	4.1
1	A	101	LYS	4.1
1	A	218	ARG	4.1
1	B	123	GLY	4.1
1	A	544	GLU	4.1
1	B	158	SER	4.1
1	B	131	GLU	4.1
1	A	129	VAL	4.0
1	A	578	VAL	4.0
2	G	246	TYR	4.0
4	E	35	GLY	4.0
2	H	66	ASN	4.0

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Mol	Chain	Res	Type	RSRZ
1	A	257	LYS	4.0
1	B	169	ALA	4.0
1	B	518	ILE	4.0
1	A	168	TYR	4.0
2	G	143	GLY	4.0
1	A	391	THR	4.0
1	A	258	ALA	4.0
1	B	575	SER	4.0
4	F	45	GLY	4.0
1	A	614	ARG	4.0
1	B	700	GLU	4.0
1	A	672	GLU	4.0
2	G	82	SER	4.0
2	H	393	PHE	4.0
1	B	459	LEU	4.0
1	A	668	GLU	4.0
1	A	164	LYS	4.0
1	B	170	ALA	4.0
1	B	398	VAL	4.0
1	A	79	MET	3.9
1	A	667	ASP	3.9
2	H	234	TYR	3.9
1	A	201	LEU	3.9
2	H	343	ALA	3.9
1	B	516	ARG	3.9
1	B	85	GLN	3.9
1	B	364	TYR	3.9
1	B	323	LEU	3.8
2	H	244	ILE	3.8
1	A	103	GLY	3.8
1	B	740	LEU	3.8
2	G	255	LEU	3.8
1	A	300	MET	3.8
2	H	194	VAL	3.8
1	A	529	GLN	3.8
1	A	325	LYS	3.8
1	B	101	LYS	3.8
2	G	12	LYS	3.8
1	B	487	ALA	3.8
1	A	221	LEU	3.8
1	A	575	SER	3.8
1	B	579	GLU	3.7

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Mol	Chain	Res	Type	RSRZ
2	H	65	GLY	3.7
2	G	258	GLY	3.7
1	B	52	LEU	3.7
1	B	120	THR	3.7
2	G	80	TYR	3.7
2	H	384	LEU	3.7
1	B	525	ARG	3.7
2	H	143	GLY	3.7
1	B	363	MET	3.7
4	F	8	LEU	3.7
2	G	242	ILE	3.6
1	B	397	PRO	3.6
1	A	619	ASP	3.6
1	A	128	THR	3.6
2	G	79	PRO	3.6
1	B	191	LEU	3.6
2	G	187	LEU	3.6
2	G	423	TYR	3.6
1	B	216	GLU	3.5
2	H	142	LYS	3.5
2	H	239	GLU	3.5
2	G	422	LYS	3.5
2	H	248	GLY	3.5
1	A	104	GLU	3.5
1	A	185	LEU	3.5
1	B	522	LEU	3.5
1	A	302	LYS	3.5
1	A	491	THR	3.4
1	B	54	LYS	3.4
1	A	495	LEU	3.4
2	H	345	ALA	3.4
1	B	400	ARG	3.4
1	A	390	VAL	3.4
1	A	545	LEU	3.4
2	G	395	PHE	3.4
2	H	404	VAL	3.3
2	H	344	GLY	3.3
2	G	140	SER	3.3
4	E	47	VAL	3.3
1	B	693	ILE	3.3
2	G	245	GLN	3.3
2	H	187	LEU	3.3

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Mol	Chain	Res	Type	RSRZ
1	A	644	PRO	3.3
2	H	243	PRO	3.3
1	A	576	ARG	3.3
2	G	243	PRO	3.3
2	H	331	ILE	3.3
1	A	498	GLY	3.3
2	H	23	LEU	3.3
4	F	47	VAL	3.3
1	A	526	SER	3.3
1	B	99	GLU	3.3
2	H	407	ALA	3.3
1	A	252	TYR	3.3
1	A	615	PHE	3.3
4	F	33	PHE	3.3
4	F	68	LEU	3.2
1	B	244	LEU	3.2
1	B	585	VAL	3.2
2	G	249	ARG	3.2
1	B	102	THR	3.2
1	B	578	VAL	3.2
2	G	304	PHE	3.2
1	B	519	ASP	3.2
2	G	11	LEU	3.2
4	E	44	VAL	3.2
1	B	322	ARG	3.2
4	F	10	VAL	3.1
1	B	83	LYS	3.1
1	A	102	THR	3.1
1	B	82	PHE	3.1
1	B	648	LEU	3.1
2	G	58	LEU	3.1
2	G	257	ALA	3.1
2	G	141	PRO	3.1
2	H	190	PHE	3.1
4	F	69	LEU	3.1
1	B	545	LEU	3.1
2	G	394	TYR	3.1
4	F	66	ALA	3.0
2	H	231	GLY	3.0
1	A	492	ASP	3.0
4	F	42	PHE	3.0
2	G	276	ILE	3.0

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Mol	Chain	Res	Type	RSRZ
1	A	551	ALA	3.0
2	H	425	SER	3.0
2	G	374	PHE	3.0
2	H	144	ILE	2.9
1	A	620	SER	2.9
1	B	121	GLY	2.9
2	G	421	LYS	2.9
2	G	424	LYS	2.9
2	H	19	ILE	2.8
1	B	584	ARG	2.8
4	F	44	VAL	2.8
1	B	513	HIS	2.8
1	A	260	GLN	2.7
1	A	673	LYS	2.7
1	B	488	GLY	2.7
4	F	65	LEU	2.7
1	A	52	LEU	2.7
1	B	531	ASP	2.7
2	G	372	ALA	2.7
1	A	549	PHE	2.7
1	B	609	VAL	2.7
1	A	548	ARG	2.6
2	G	78	MET	2.6
2	G	10	GLU	2.6
1	A	617	VAL	2.6
1	B	692	ILE	2.6
2	H	406	VAL	2.6
1	A	396	ARG	2.5
2	H	246	TYR	2.5
2	H	262	TYR	2.5
2	H	104	GLU	2.5
4	F	34	GLY	2.5
2	H	346	PHE	2.5
4	F	43	GLY	2.5
1	B	259	VAL	2.4
1	A	547	ARG	2.4
2	H	22	LEU	2.4
1	A	653	LYS	2.4
1	A	655	ASP	2.4
1	A	616	GLU	2.3
2	H	334	VAL	2.3
1	A	165	ARG	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	163	GLU	2.3
1	A	618	ILE	2.3
2	H	249	ARG	2.3
2	H	403	VAL	2.3
1	B	532	PRO	2.3
4	F	67	LEU	2.2
1	A	525	ARG	2.2
4	F	9	PHE	2.2
1	A	493	ILE	2.2
2	G	373	LEU	2.2
2	G	9	PHE	2.2
1	B	512	ARG	2.1
2	H	333	PRO	2.1
4	F	41	ILE	2.1
1	B	528	ARG	2.1

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.