



Full wwPDB X-ray Structure Validation Report ⓘ

Oct 9, 2023 – 02:49 PM EDT

PDB ID : 4V60
Title : The structure of rat liver vault at 3.5 angstrom resolution
Authors : Kato, K.; Zhou, Y.; Tanaka, H.; Yao, M.; Yamashita, E.; Yoshimura, M.;
Tsukihara, T.
Deposited on : 2008-10-24
Resolution : 3.50 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : 4.02b-467
Xtriage (Phenix) : 1.13
EDS : 2.35.1
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.35.1

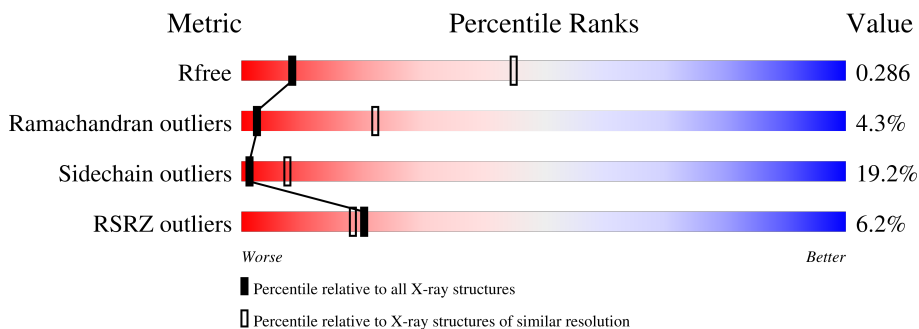
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.50 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	1659 (3.60-3.40)
Ramachandran outliers	138981	1005 (3.58-3.42)
Sidechain outliers	138945	1006 (3.58-3.42)
RSRZ outliers	127900	1559 (3.60-3.40)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. 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	861	
1	B	861	
1	C	861	
1	D	861	
1	E	861	
1	F	861	
1	G	861	

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Mol	Chain	Length	Quality of chain	
1	H	861	5%	77% 17% • 6%
1	I	861	6%	77% 16% • 6%
1	J	861	7%	77% 16% • 6%
1	K	861	7%	74% 18% • 6%
1	L	861	6%	77% 16% • 6%
1	M	861	5%	76% 17% • 6%
1	N	861	4%	76% 17% • 6%
1	O	861	4%	76% 17% • 6%
1	P	861	5%	75% 19% • 6%
1	Q	861	7%	75% 19% • 6%
1	R	861	7%	74% 19% • 6%
1	S	861	6%	76% 17% • 6%
1	T	861	6%	77% 16% • 6%
1	U	861	5%	76% 17% • 6%
1	V	861	6%	76% 17% • 6%
1	W	861	8%	77% 16% • 6%
1	X	861	7%	77% 17% • 6%
1	Y	861	6%	78% 16% • 6%
1	Z	861	7%	77% 16% • 6%
1	a	861	6%	77% 16% • 6%
1	b	861	5%	77% 16% • 6%
1	c	861	7%	76% 18% • 6%
1	d	861	6%	77% 16% • 6%
1	e	861	6%	77% 16% • 6%
1	f	861	6%	76% 17% • 6%

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Mol	Chain	Length	Quality of chain
1	g	861	5% 75% 18% • 6%
1	h	861	5% 76% 17% • 6%
1	i	861	5% 75% 18% • 6%
1	j	861	7% 76% 17% • 6%
1	k	861	6% 76% 17% • 6%
1	l	861	6% 77% 16% • 6%
1	m	861	6% 77% 16% • 6%

2 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 241956 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 vault protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	812	6204	3915	1101	1172	16	0	0	30
1	B	812	6204	3915	1101	1172	16	0	0	30
1	C	812	6204	3915	1101	1172	16	0	0	30
1	D	812	6204	3915	1101	1172	16	0	0	30
1	E	812	6204	3915	1101	1172	16	0	0	30
1	F	812	6204	3915	1101	1172	16	0	0	30
1	G	812	6204	3915	1101	1172	16	0	0	30
1	H	812	6204	3915	1101	1172	16	0	0	30
1	I	812	6204	3915	1101	1172	16	0	0	30
1	J	812	6204	3915	1101	1172	16	0	0	30
1	K	812	6204	3915	1101	1172	16	0	0	30
1	L	812	6204	3915	1101	1172	16	0	0	30
1	M	812	6204	3915	1101	1172	16	0	0	30
1	N	812	6204	3915	1101	1172	16	0	0	30
1	O	812	6204	3915	1101	1172	16	0	0	30
1	P	812	6204	3915	1101	1172	16	0	0	30

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	Q	812	Total 6204	C 3915	N 1101	O 1172	S 16	0	0	30
1	R	812	Total 6204	C 3915	N 1101	O 1172	S 16	0	0	30
1	S	812	Total 6204	C 3915	N 1101	O 1172	S 16	0	0	30
1	T	812	Total 6204	C 3915	N 1101	O 1172	S 16	0	0	30
1	U	812	Total 6204	C 3915	N 1101	O 1172	S 16	0	0	30
1	V	812	Total 6204	C 3915	N 1101	O 1172	S 16	0	0	30
1	W	812	Total 6204	C 3915	N 1101	O 1172	S 16	0	0	30
1	X	812	Total 6204	C 3915	N 1101	O 1172	S 16	0	0	30
1	Y	812	Total 6204	C 3915	N 1101	O 1172	S 16	0	0	30
1	Z	812	Total 6204	C 3915	N 1101	O 1172	S 16	0	0	30
1	a	812	Total 6204	C 3915	N 1101	O 1172	S 16	0	0	30
1	b	812	Total 6204	C 3915	N 1101	O 1172	S 16	0	0	30
1	c	812	Total 6204	C 3915	N 1101	O 1172	S 16	0	0	30
1	d	812	Total 6204	C 3915	N 1101	O 1172	S 16	0	0	30
1	e	812	Total 6204	C 3915	N 1101	O 1172	S 16	0	0	30
1	f	812	Total 6204	C 3915	N 1101	O 1172	S 16	0	0	30
1	g	812	Total 6204	C 3915	N 1101	O 1172	S 16	0	0	30
1	h	812	Total 6204	C 3915	N 1101	O 1172	S 16	0	0	30
1	i	812	Total 6204	C 3915	N 1101	O 1172	S 16	0	0	30
1	j	812	Total 6204	C 3915	N 1101	O 1172	S 16	0	0	30
1	k	812	Total 6204	C 3915	N 1101	O 1172	S 16	0	0	30

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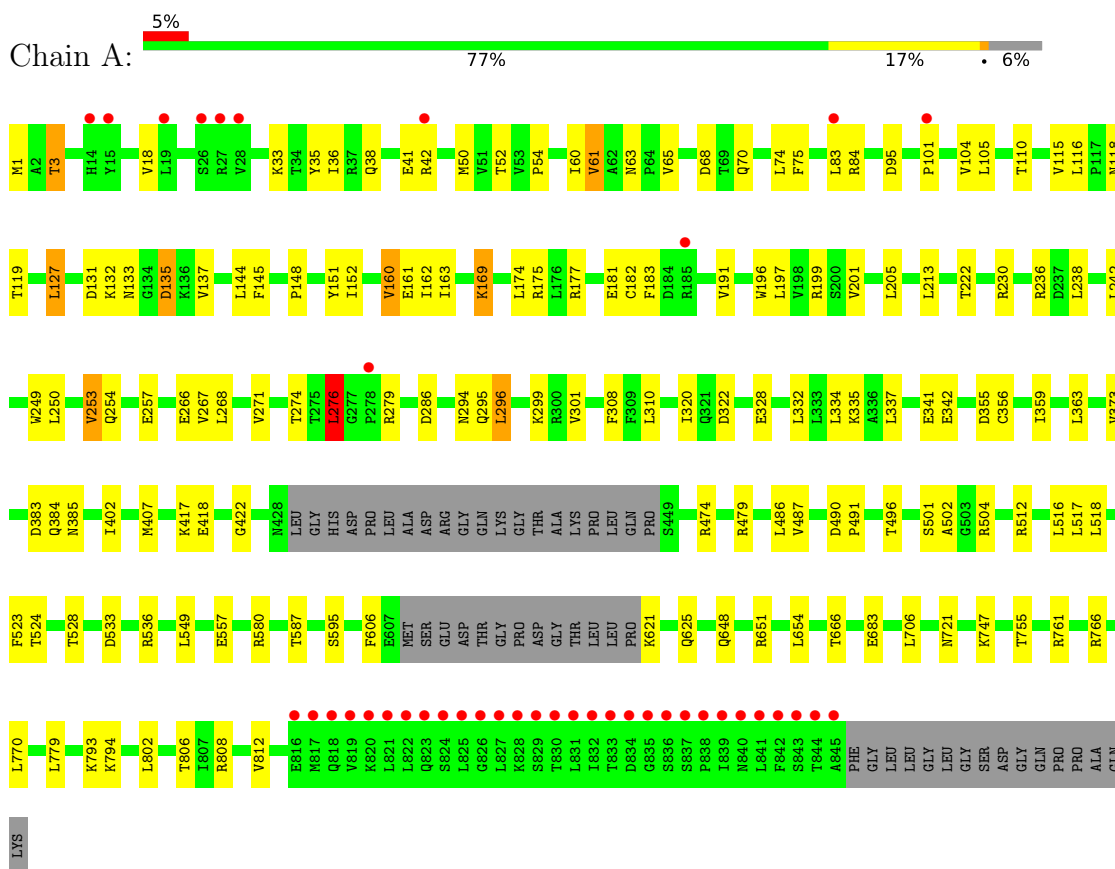
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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	l	812	Total 6204	C 3915	N 1101	O 1172	S 16	0	0	30
1	m	812	Total 6204	C 3915	N 1101	O 1172	S 16	0	0	30

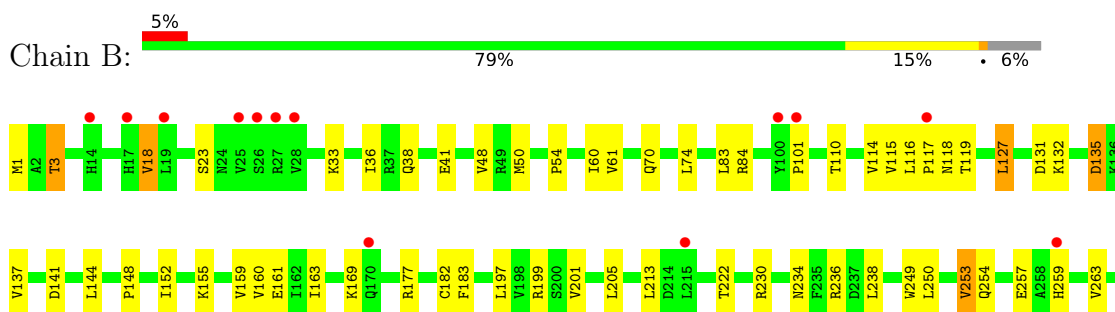
3 Residue-property plots

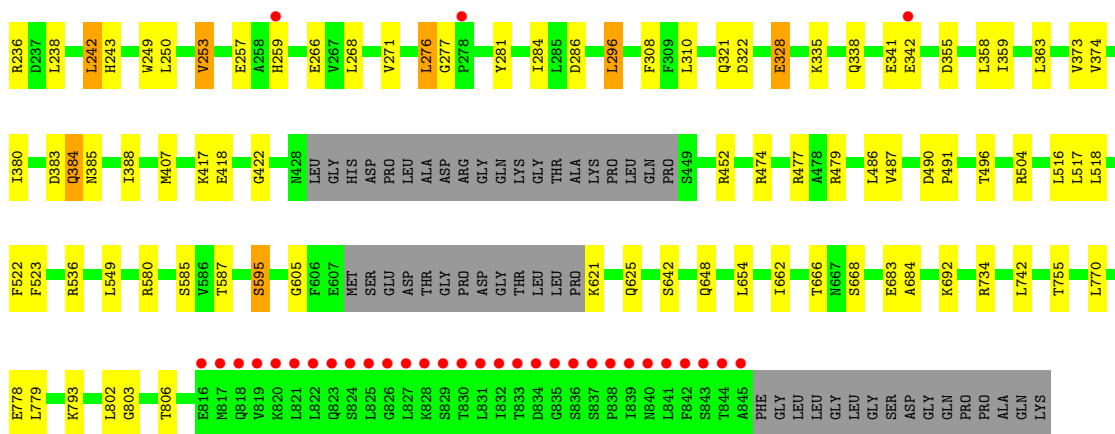
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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 vault protein

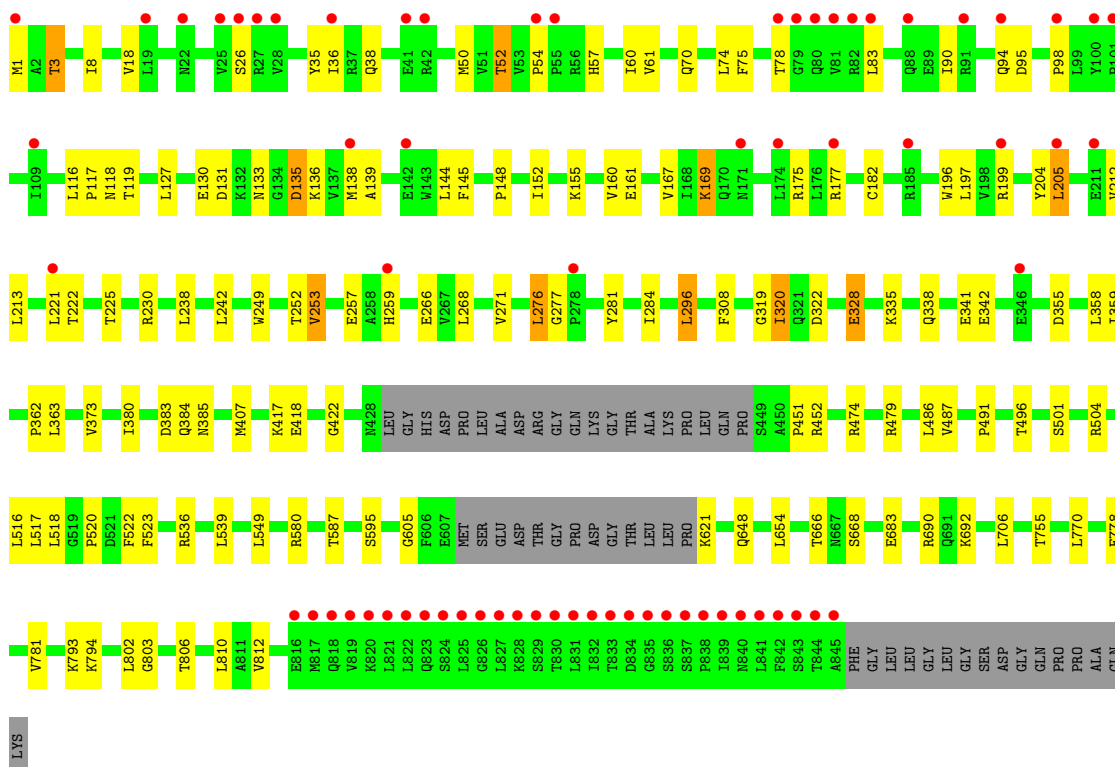
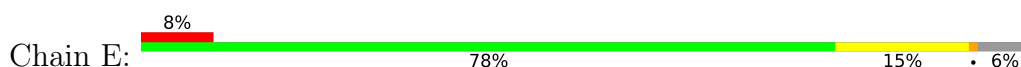


- Molecule 1: Major vault protein

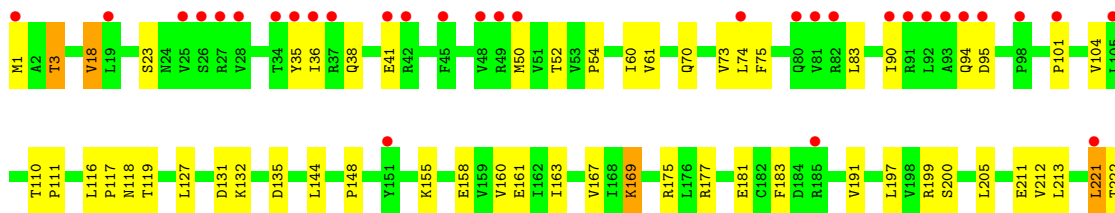
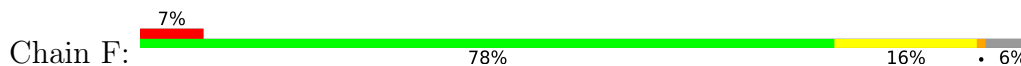


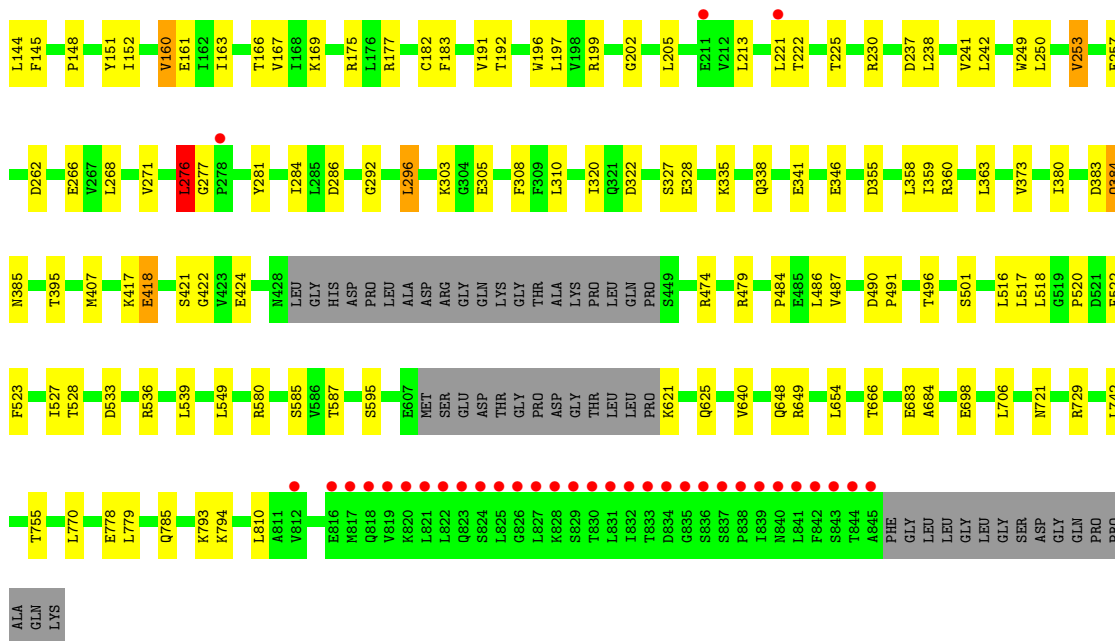


• Molecule 1: Major vault protein

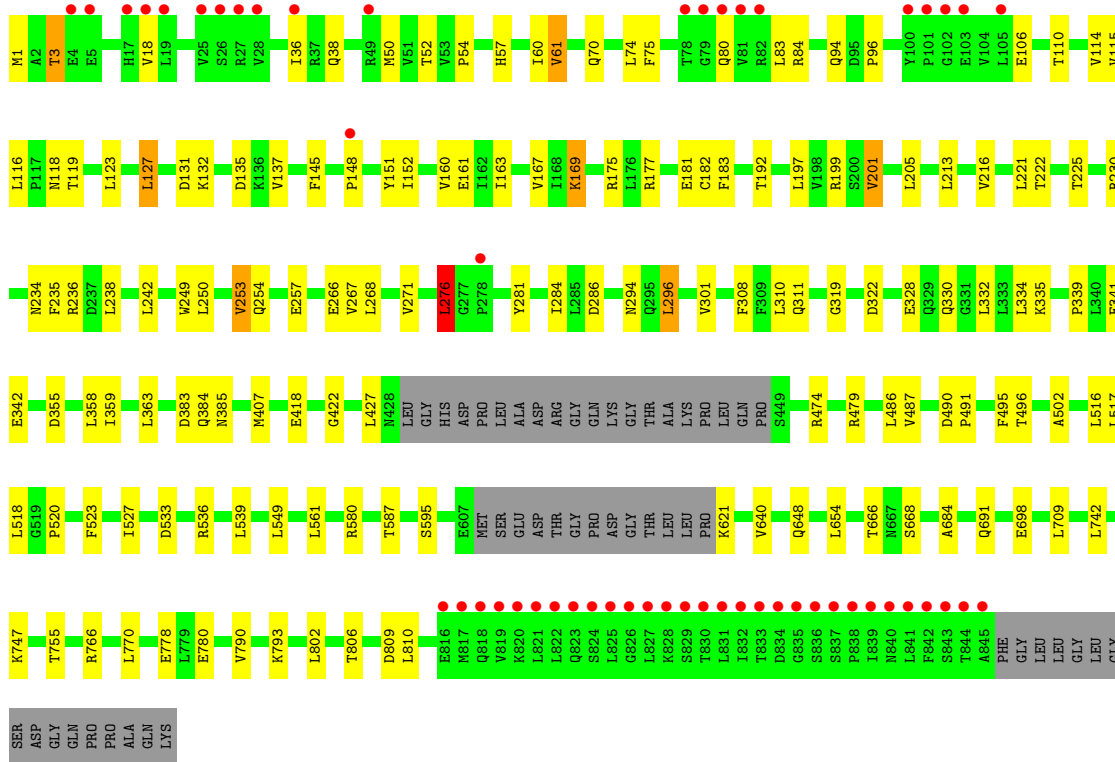
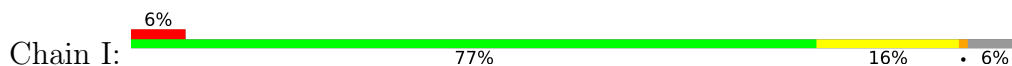


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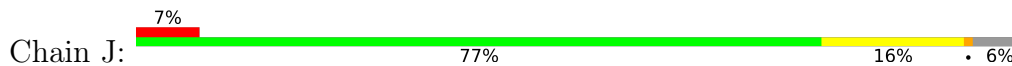


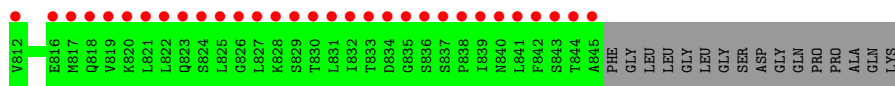


• Molecule 1: Major vault protein

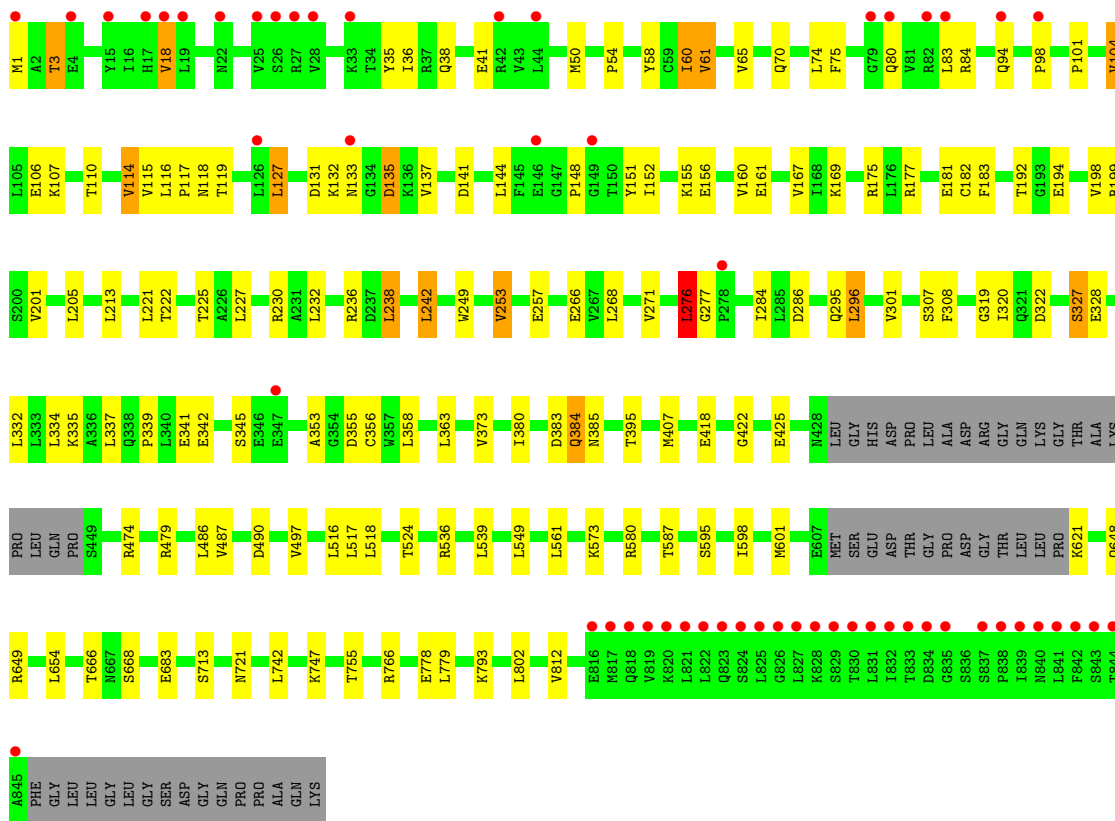
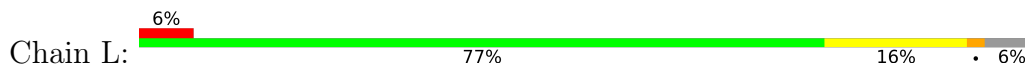


• Molecule 1: Major vault protein

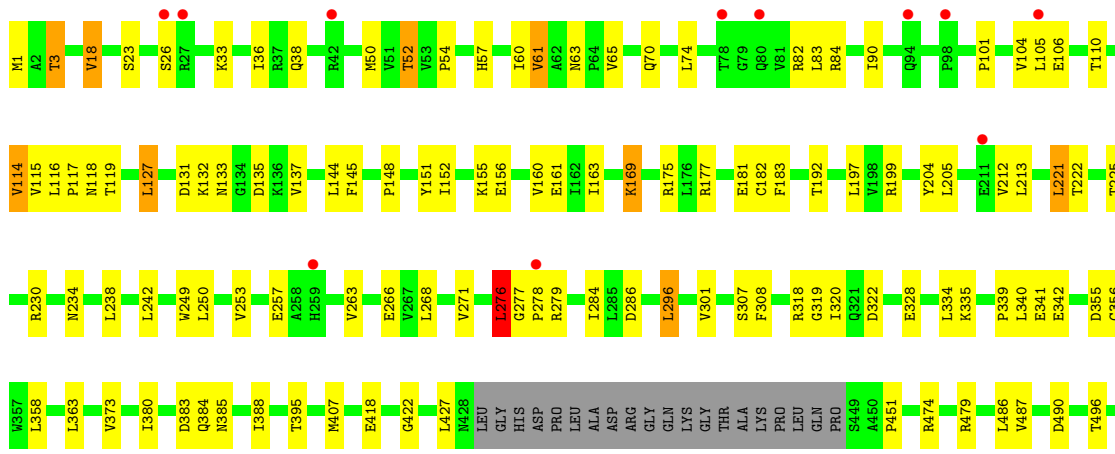
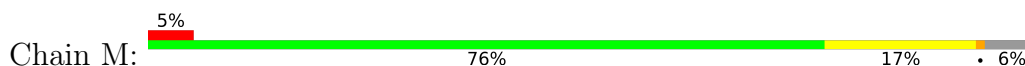


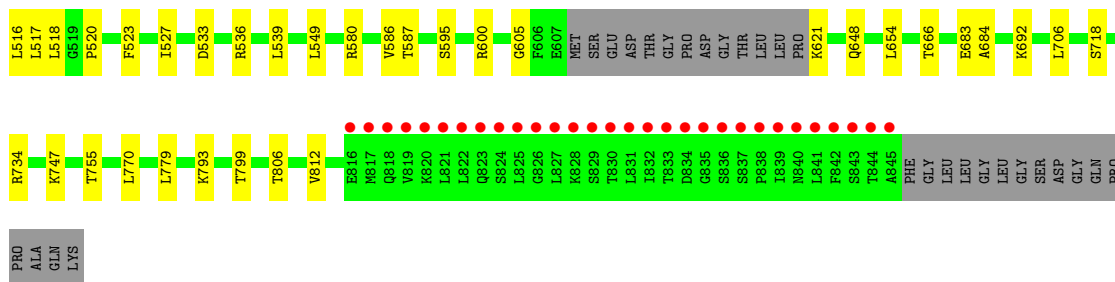


• Molecule 1: Major vault protein

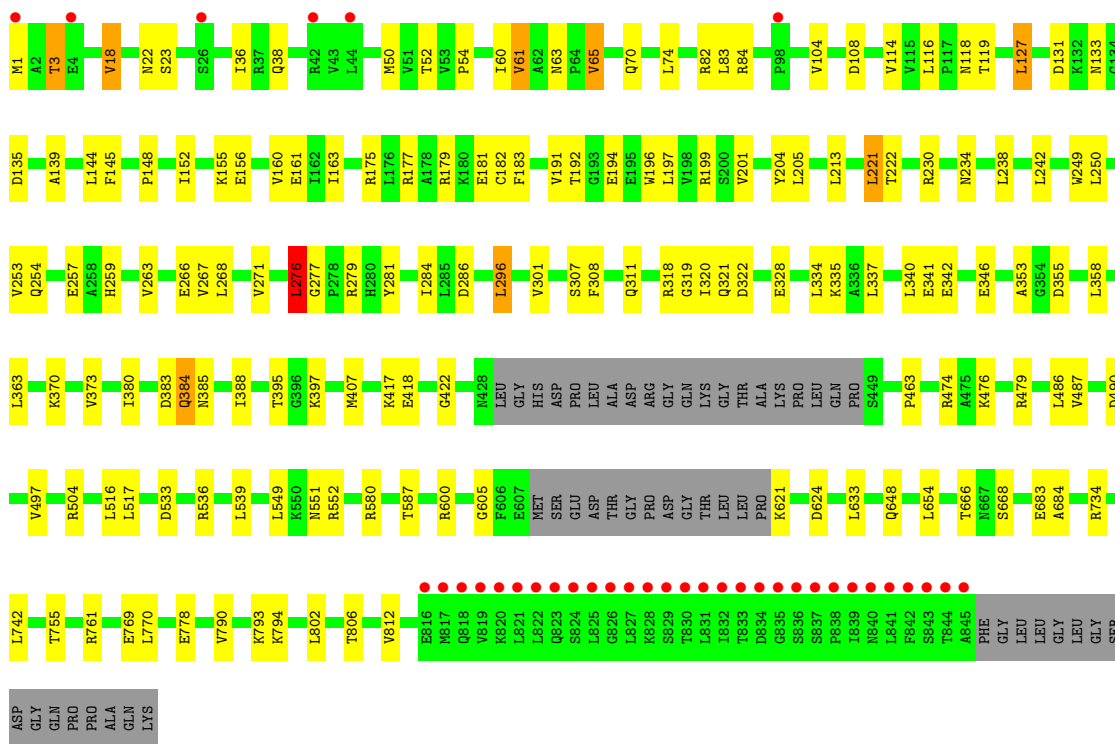
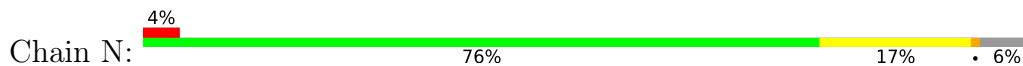


• Molecule 1: Major vault protein

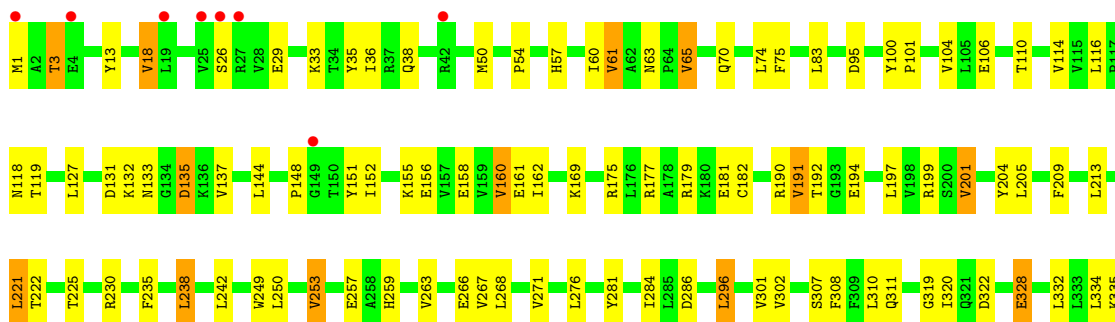
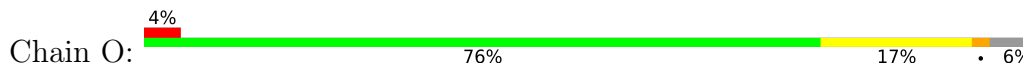


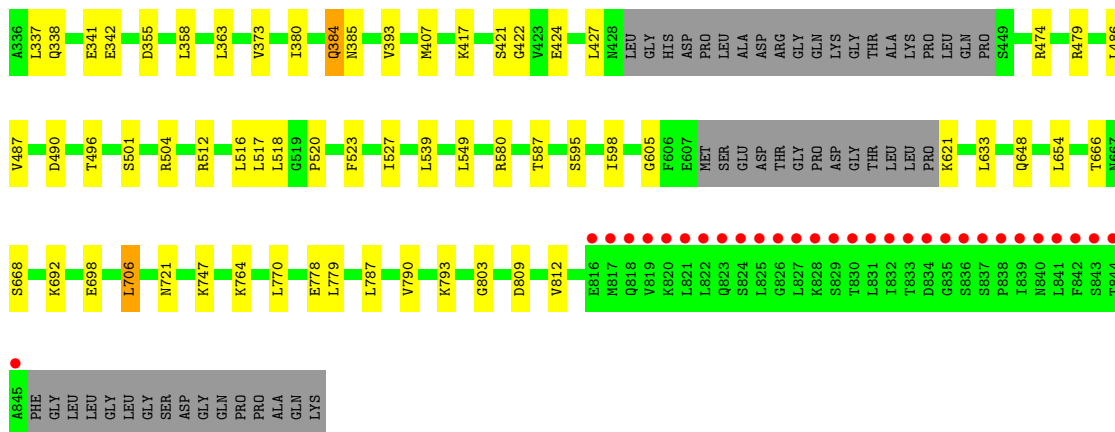


• Molecule 1: Major vault protein

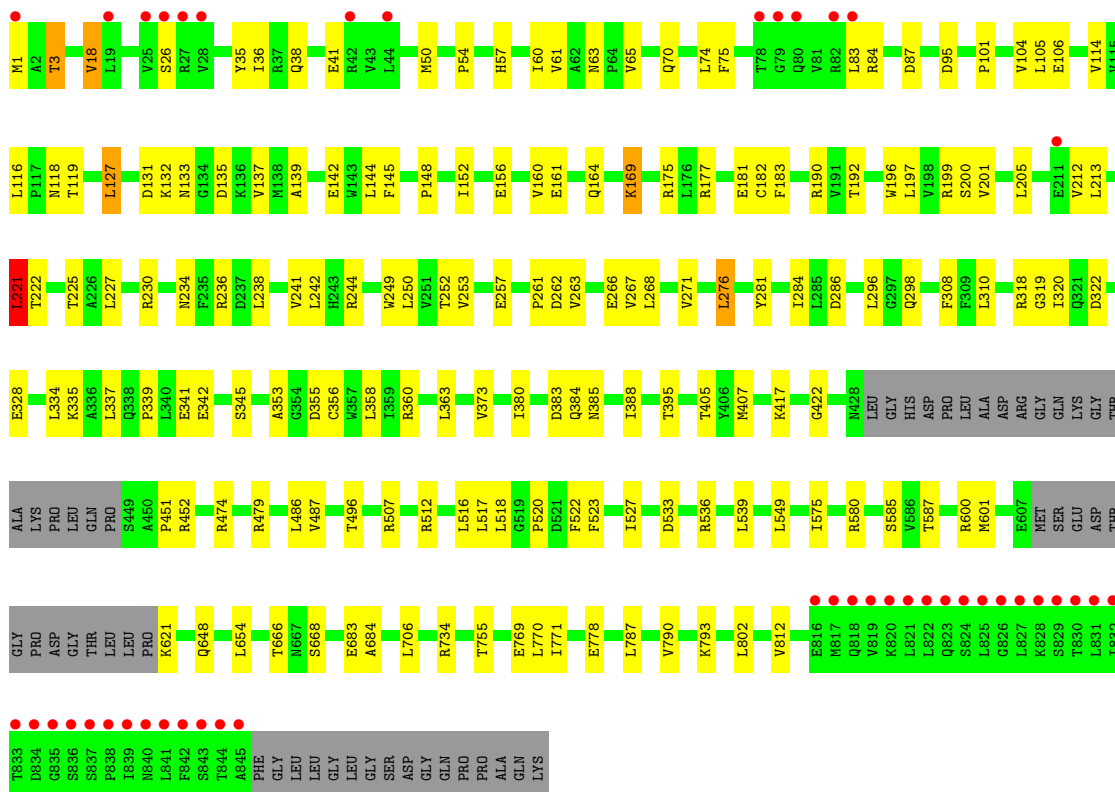


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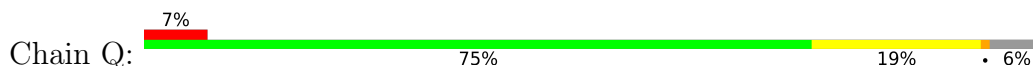




• Molecule 1: Major vault protein

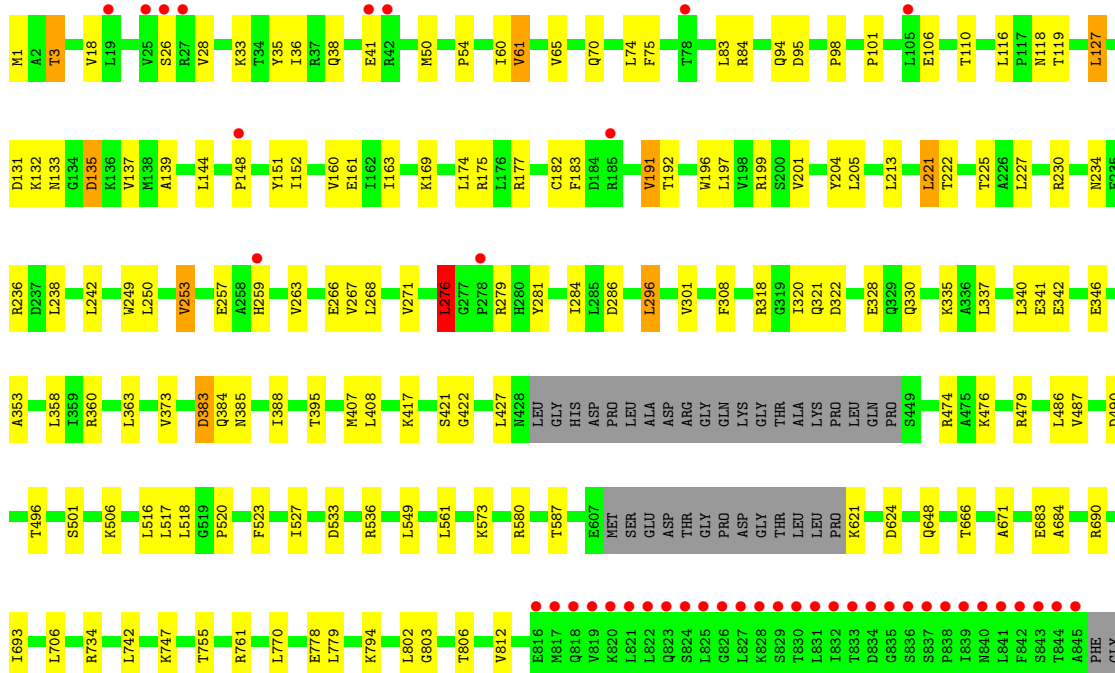
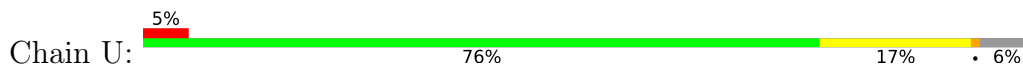


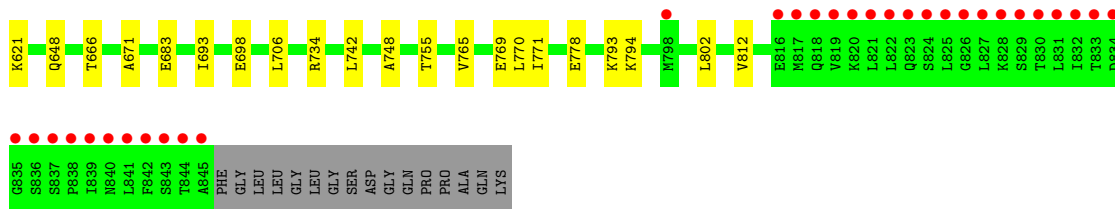
• Molecule 1: Major vault protein



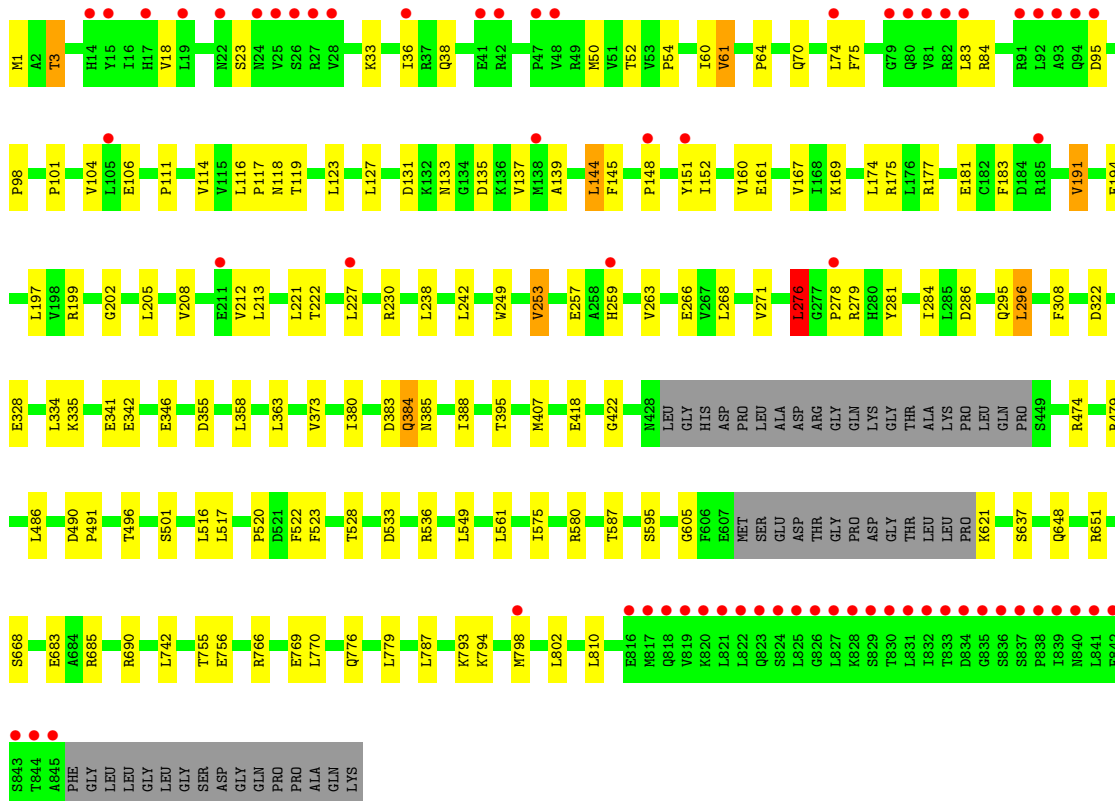
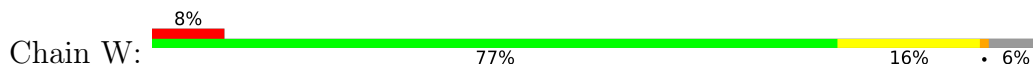
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GLY
SER
ASP
GLY
GLN
PRO
PRO
ALA
GLN
LYS

• Molecule 1: Major vault protein

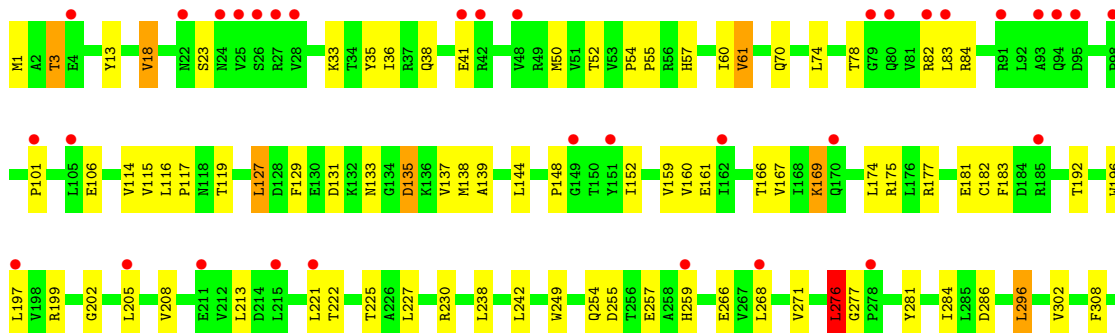
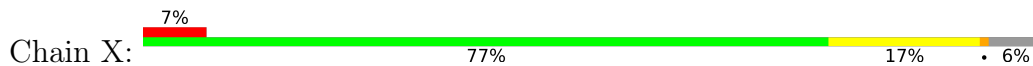


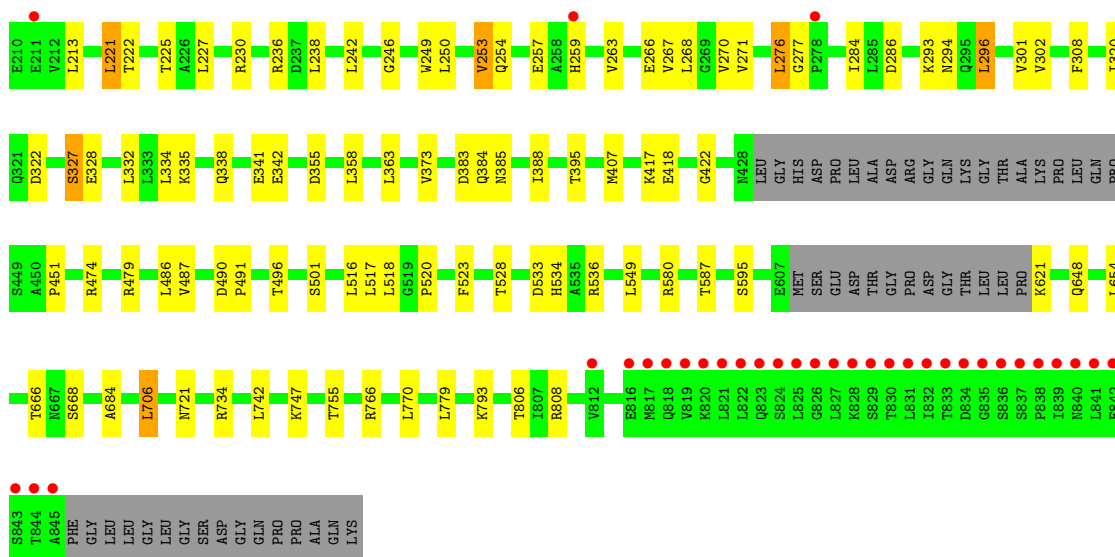


• Molecule 1: Major vault protein

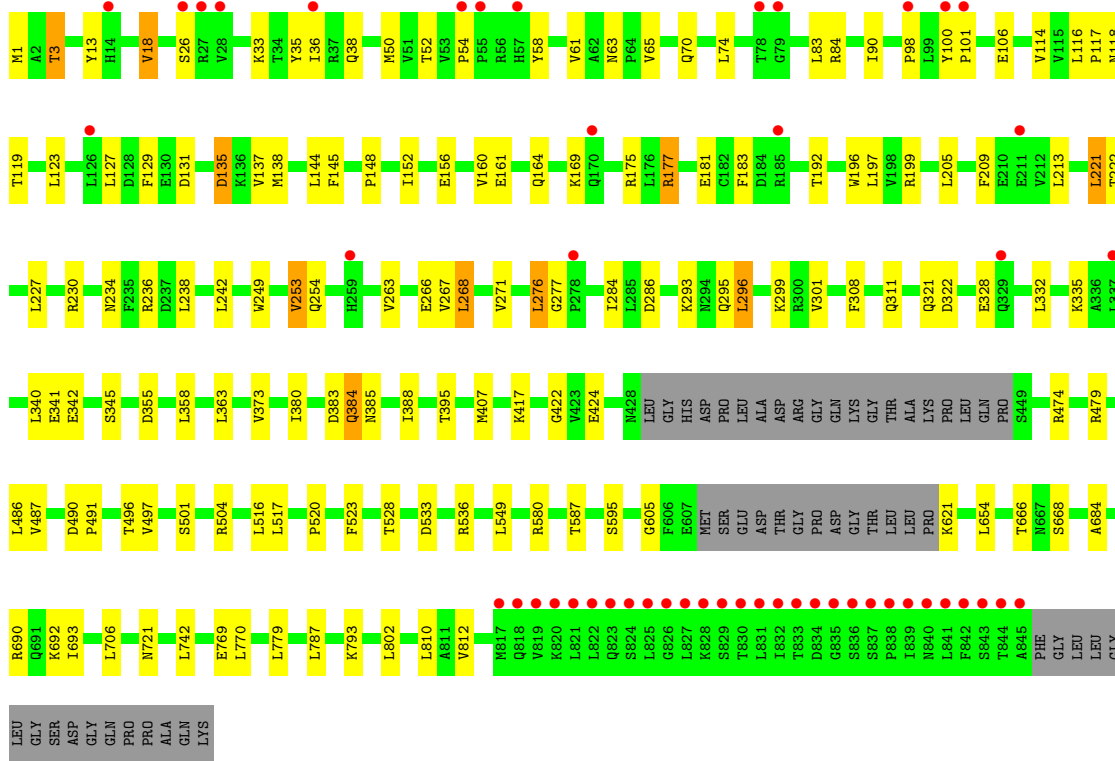
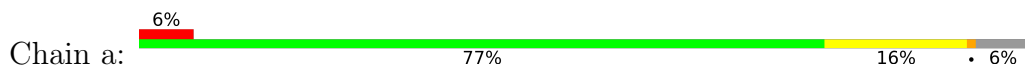


• Molecule 1: Major vault protein

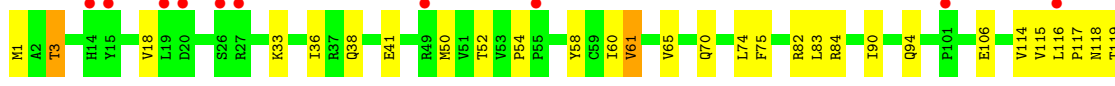
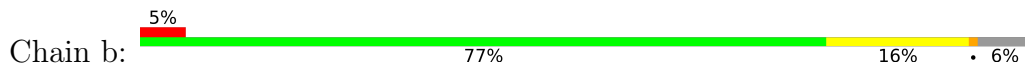


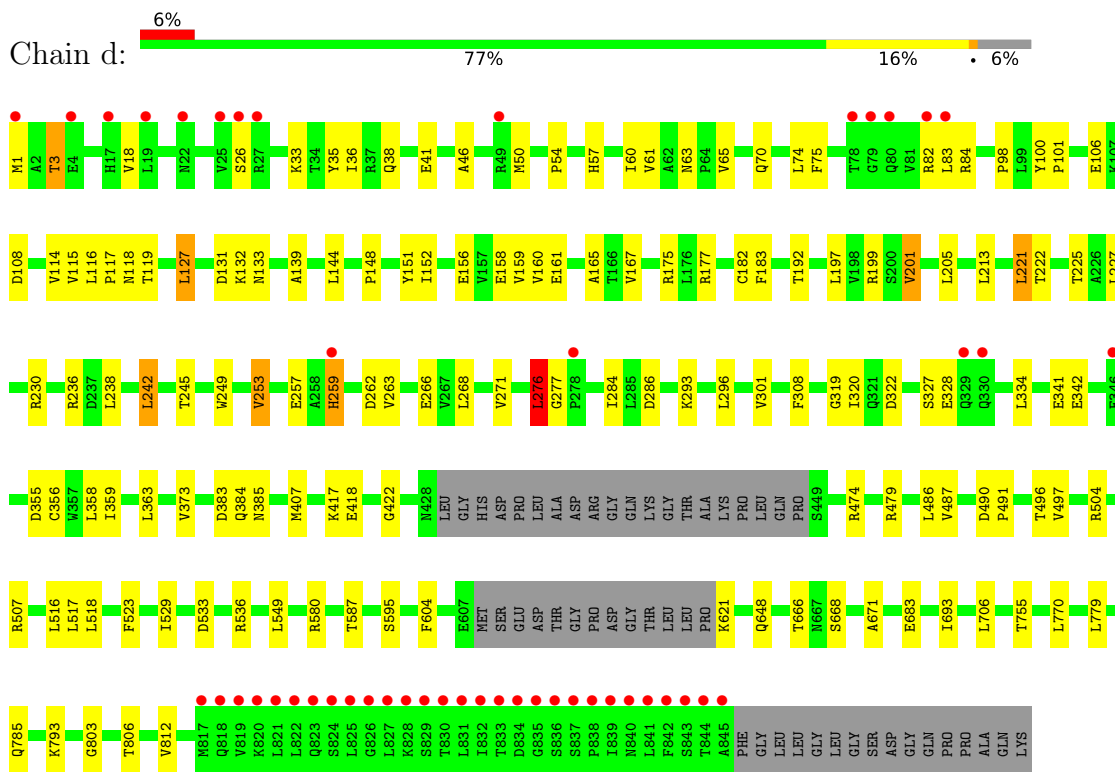


• Molecule 1: Major vault protein

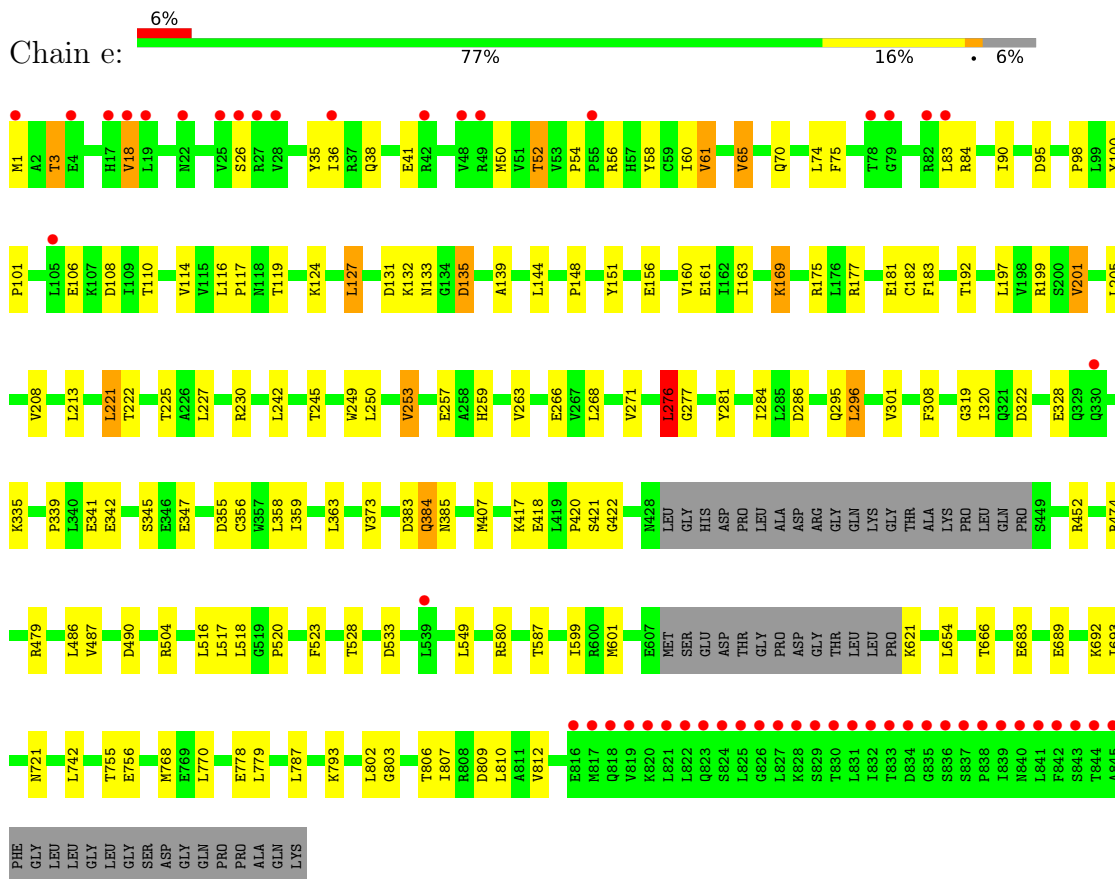


• Molecule 1: Major vault protein

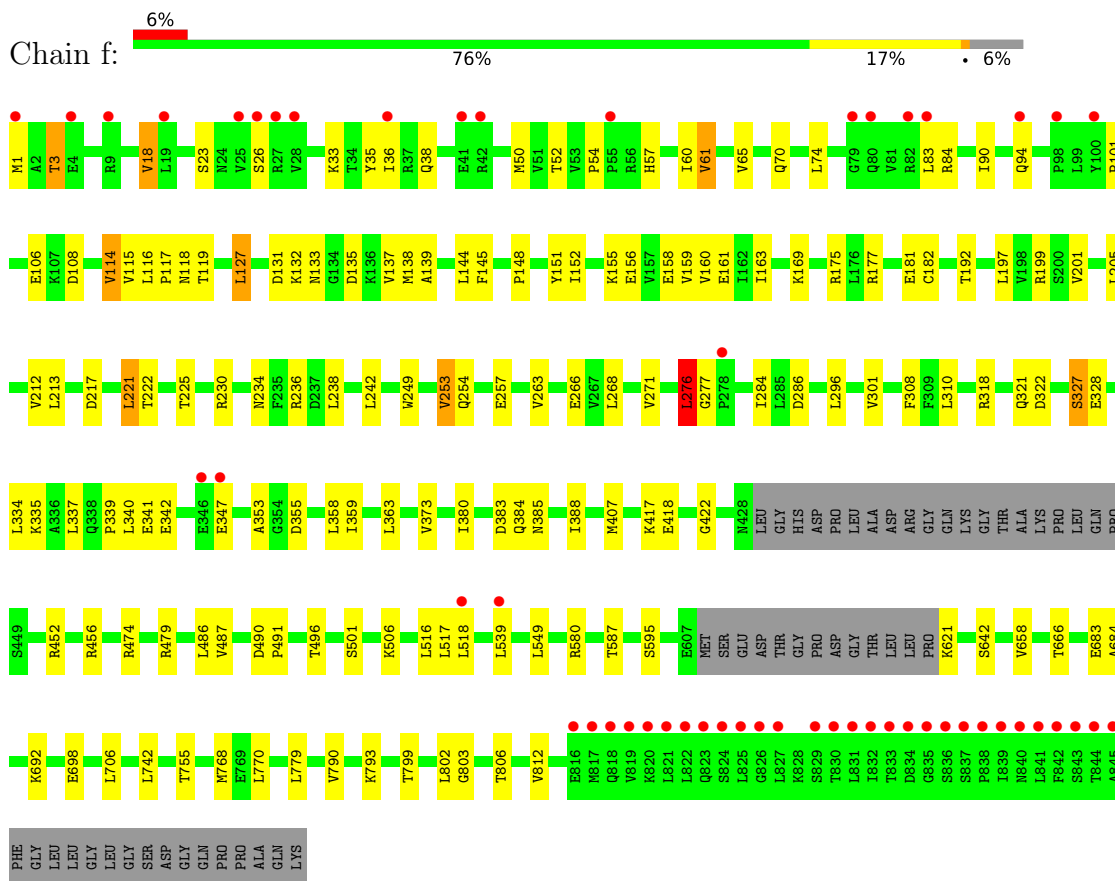




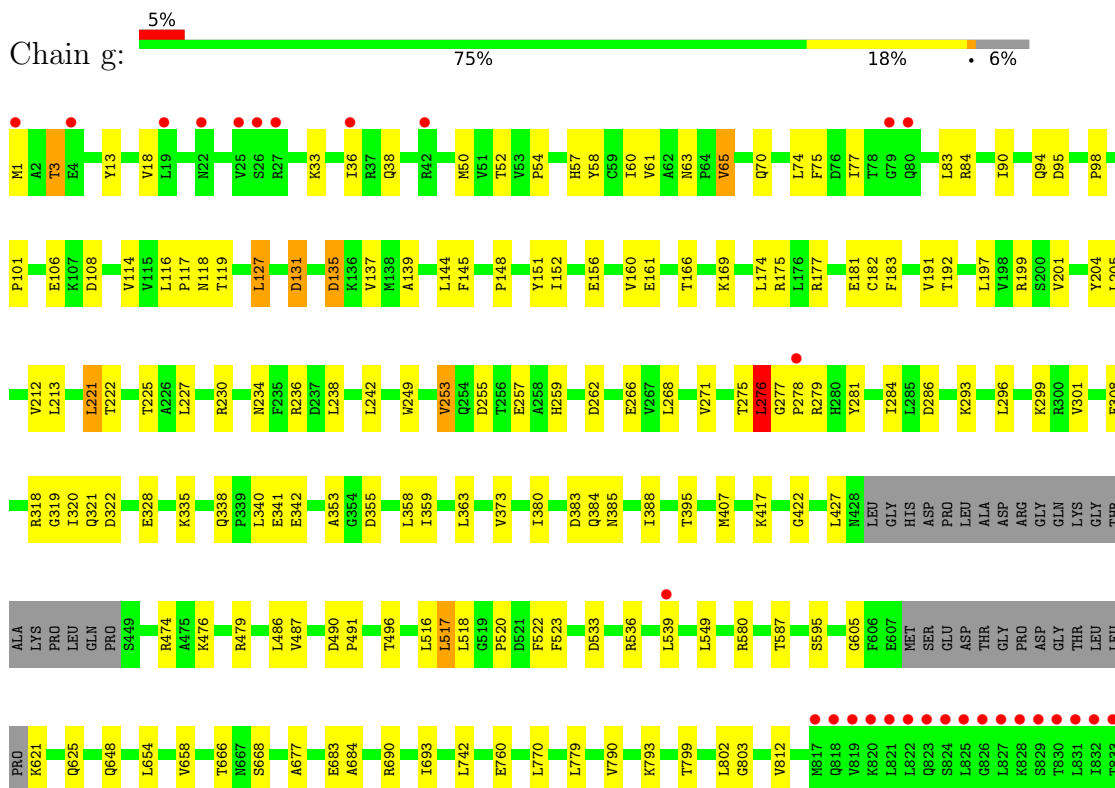
• Molecule 1: Major vault protein

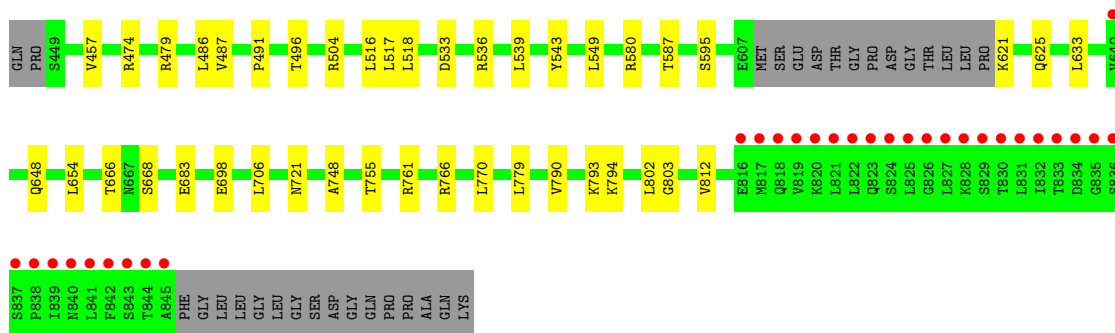


• Molecule 1: Major vault protein

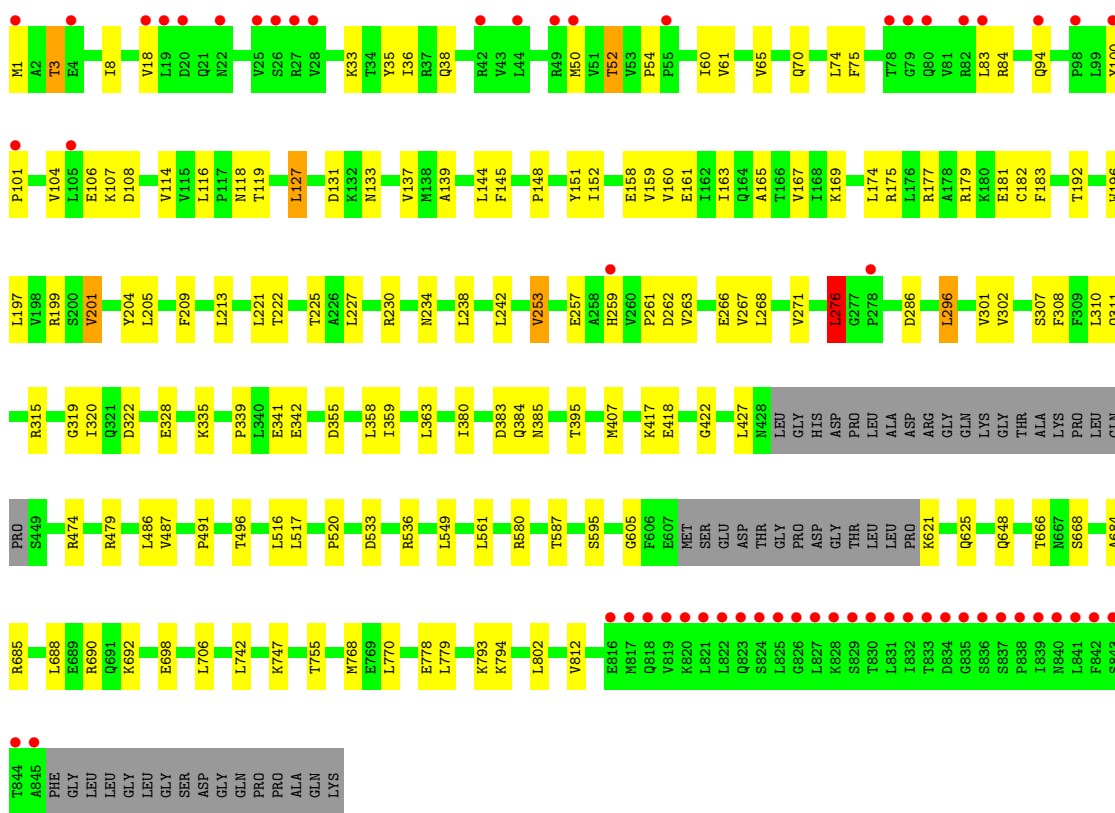
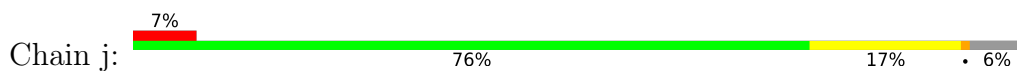


• Molecule 1: Major vault protein

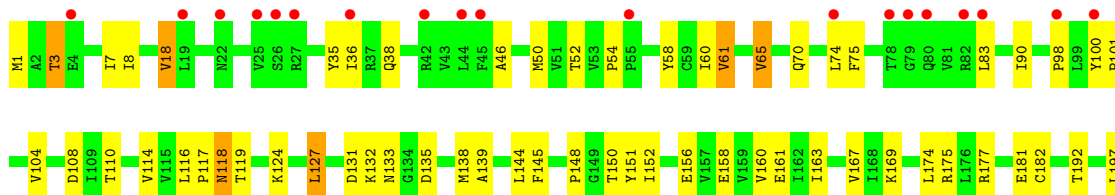
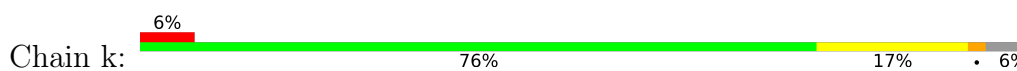


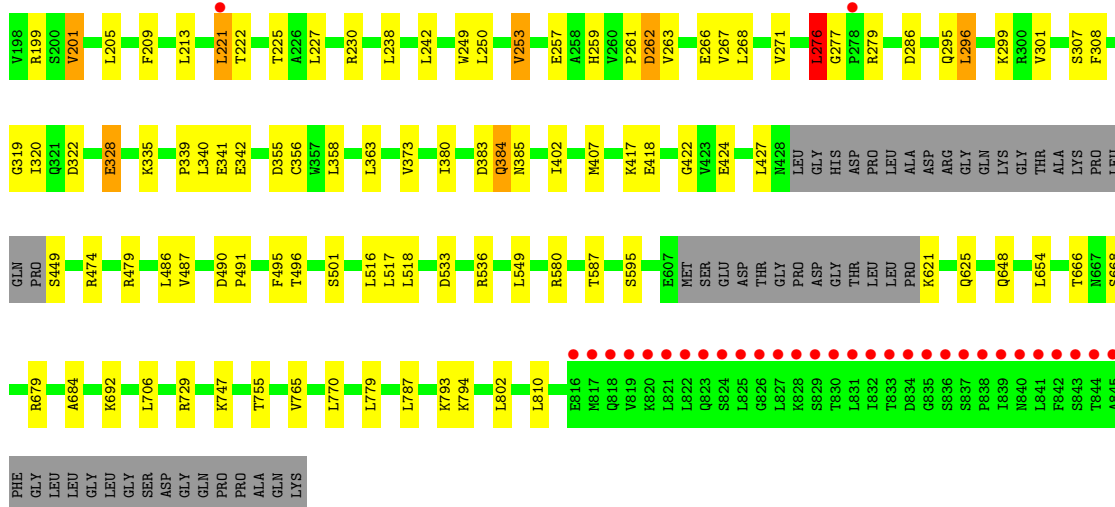


• Molecule 1: Major vault protein

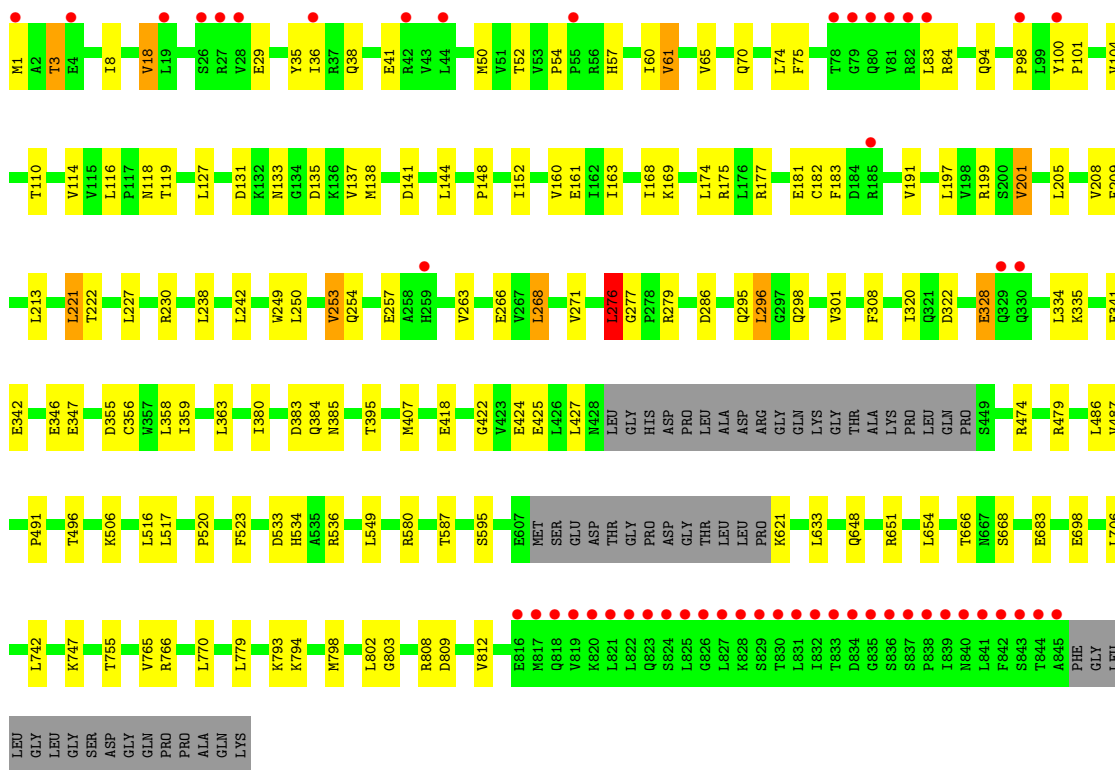
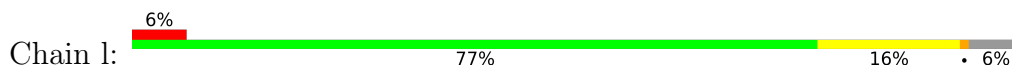


• Molecule 1: Major vault protein

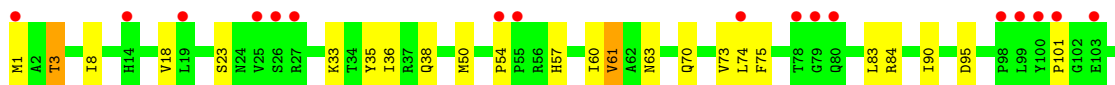
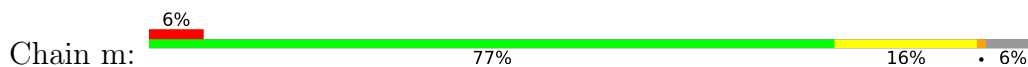


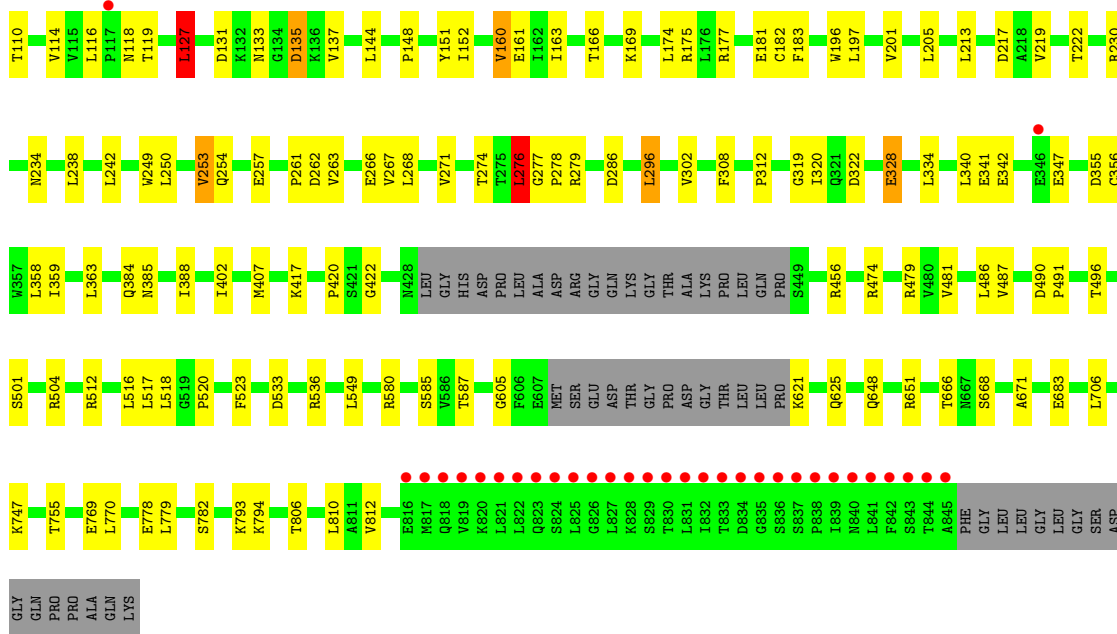


• Molecule 1: Major vault protein



• Molecule 1: Major vault protein





4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	702.25Å 383.80Å 598.48Å 90.00° 124.69° 90.00°	Depositor
Resolution (Å)	204.00 – 3.50 203.54 – 3.47	Depositor EDS
% Data completeness (in resolution range)	92.7 (204.00-3.50) 91.4 (203.54-3.47)	Depositor EDS
R_{merge}	0.23	Depositor
R_{sym}	0.21	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.51 (at 3.49Å)	Xtrriage
Refinement program	CNS	Depositor
R, R_{free}	0.311 , 0.330 0.286 , 0.286	Depositor DCC
R_{free} test set	76647 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å ²)	104.6	Xtrriage
Anisotropy	0.212	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 117.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.36$, $\langle L^2 \rangle = 0.19$	Xtrriage
Estimated twinning fraction	0.099 for h,-k,-h-l	Xtrriage
F_o, F_c correlation	0.85	EDS
Total number of atoms	241956	wwPDB-VP
Average B, all atoms (Å ²)	121.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.91% 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, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.50	0/6279	0.69	3/8506 (0.0%)
1	B	0.50	0/6279	0.68	4/8506 (0.0%)
1	C	0.50	0/6279	0.69	5/8506 (0.1%)
1	D	0.50	0/6279	0.69	5/8506 (0.1%)
1	E	0.51	0/6279	0.69	3/8506 (0.0%)
1	F	0.50	0/6279	0.68	2/8506 (0.0%)
1	G	0.49	0/6279	0.68	3/8506 (0.0%)
1	H	0.50	0/6279	0.68	4/8506 (0.0%)
1	I	0.51	0/6279	0.69	3/8506 (0.0%)
1	J	0.51	0/6279	0.71	4/8506 (0.0%)
1	K	0.53	0/6279	0.73	6/8506 (0.1%)
1	L	0.52	0/6279	0.72	4/8506 (0.0%)
1	M	0.52	0/6279	0.71	3/8506 (0.0%)
1	N	0.51	0/6279	0.71	3/8506 (0.0%)
1	O	0.52	0/6279	0.71	3/8506 (0.0%)
1	P	0.52	0/6279	0.73	7/8506 (0.1%)
1	Q	0.52	0/6279	0.72	6/8506 (0.1%)
1	R	0.53	0/6279	0.74	4/8506 (0.0%)
1	S	0.50	0/6279	0.70	4/8506 (0.0%)
1	T	0.50	0/6279	0.69	3/8506 (0.0%)
1	U	0.49	0/6279	0.68	5/8506 (0.1%)
1	V	0.50	0/6279	0.67	4/8506 (0.0%)
1	W	0.49	0/6279	0.68	5/8506 (0.1%)
1	X	0.49	0/6279	0.69	3/8506 (0.0%)
1	Y	0.50	0/6279	0.68	3/8506 (0.0%)
1	Z	0.50	0/6279	0.69	4/8506 (0.0%)
1	a	0.49	0/6279	0.69	3/8506 (0.0%)
1	b	0.51	0/6279	0.70	5/8506 (0.1%)
1	c	0.51	0/6279	0.70	5/8506 (0.1%)
1	d	0.50	0/6279	0.71	5/8506 (0.1%)
1	e	0.51	0/6279	0.71	4/8506 (0.0%)
1	f	0.51	0/6279	0.70	4/8506 (0.0%)
1	g	0.50	0/6279	0.70	6/8506 (0.1%)
1	h	0.49	0/6279	0.70	3/8506 (0.0%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	i	0.50	0/6279	0.70	4/8506 (0.0%)
1	j	0.50	0/6279	0.71	4/8506 (0.0%)
1	k	0.51	0/6279	0.72	4/8506 (0.0%)
1	l	0.50	0/6279	0.70	4/8506 (0.0%)
1	m	0.51	0/6279	0.69	4/8506 (0.0%)
All	All	0.51	0/244881	0.70	158/331734 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	1	1
1	B	1	0
1	C	1	1
1	D	1	1
1	E	1	1
1	F	1	0
1	G	1	0
1	H	1	0
1	I	1	0
1	J	1	1
1	K	1	1
1	L	1	0
1	M	1	0
1	N	1	0
1	O	1	0
1	P	1	0
1	Q	1	0
1	R	1	0
1	S	1	0
1	T	1	1
1	U	1	0
1	V	1	1
1	W	1	0
1	X	1	1
1	Y	1	0
1	Z	1	1
1	a	1	1
1	b	1	0
1	c	1	0

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Mol	Chain	#Chirality outliers	#Planarity outliers
1	d	1	0
1	e	1	1
1	f	1	0
1	g	1	0
1	h	1	0
1	i	1	1
1	j	1	0
1	k	1	0
1	l	1	0
1	m	1	1
All	All	39	14

There are no bond length outliers.

All (158) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	j	165	ALA	CB-CA-C	-7.38	99.03	110.10
1	E	276	LEU	CA-CB-CG	7.24	131.95	115.30
1	K	276	LEU	CA-CB-CG	7.10	131.64	115.30
1	l	276	LEU	CA-CB-CG	7.04	131.49	115.30
1	P	252	THR	CB-CA-C	-6.96	92.81	111.60
1	k	276	LEU	CA-CB-CG	6.91	131.19	115.30
1	B	276	LEU	CA-CB-CG	6.80	130.94	115.30
1	A	276	LEU	CA-CB-CG	6.78	130.90	115.30
1	T	276	LEU	CA-CB-CG	6.69	130.68	115.30
1	f	276	LEU	CA-CB-CG	6.66	130.61	115.30
1	b	276	LEU	CA-CB-CG	6.59	130.45	115.30
1	U	276	LEU	CA-CB-CG	6.53	130.32	115.30
1	F	276	LEU	CA-CB-CG	6.47	130.17	115.30
1	X	276	LEU	CA-CB-CG	6.41	130.05	115.30
1	H	276	LEU	CA-CB-CG	6.41	130.04	115.30
1	g	276	LEU	CA-CB-CG	6.38	129.96	115.30
1	Y	276	LEU	CA-CB-CG	6.38	129.96	115.30
1	M	276	LEU	CA-CB-CG	6.37	129.95	115.30
1	I	127	LEU	CA-CB-CG	6.31	129.81	115.30
1	Q	205	LEU	CA-CB-CG	6.26	129.70	115.30
1	h	221	LEU	CA-CB-CG	6.26	129.70	115.30
1	c	276	LEU	CA-CB-CG	6.20	129.57	115.30
1	a	276	LEU	CA-CB-CG	6.16	129.46	115.30
1	Y	221	LEU	CA-CB-CG	6.13	129.41	115.30
1	C	42	ARG	NE-CZ-NH2	-6.11	117.25	120.30
1	m	276	LEU	CA-CB-CG	6.08	129.29	115.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	Z	276	LEU	CA-CB-CG	6.07	129.27	115.30
1	L	276	LEU	CA-CB-CG	6.05	129.23	115.30
1	E	205	LEU	CA-CB-CG	6.05	129.22	115.30
1	h	276	LEU	CA-CB-CG	6.04	129.20	115.30
1	R	221	LEU	CA-CB-CG	6.04	129.18	115.30
1	I	276	LEU	CA-CB-CG	6.00	129.09	115.30
1	f	221	LEU	CA-CB-CG	6.00	129.09	115.30
1	W	221	LEU	CA-CB-CG	5.99	129.09	115.30
1	d	276	LEU	CA-CB-CG	5.99	129.08	115.30
1	U	221	LEU	CA-CB-CG	5.98	129.04	115.30
1	V	221	LEU	CA-CB-CG	5.97	129.02	115.30
1	D	221	LEU	CA-CB-CG	5.94	128.97	115.30
1	P	221	LEU	CA-CB-CG	5.93	128.94	115.30
1	a	221	LEU	CA-CB-CG	5.91	128.89	115.30
1	S	127	LEU	CA-CB-CG	5.90	128.88	115.30
1	L	127	LEU	CA-CB-CG	5.89	128.85	115.30
1	J	276	LEU	CA-CB-CG	5.89	128.85	115.30
1	U	127	LEU	CA-CB-CG	5.88	128.82	115.30
1	T	127	LEU	CA-CB-CG	5.87	128.79	115.30
1	d	221	LEU	CA-CB-CG	5.86	128.78	115.30
1	f	127	LEU	CA-CB-CG	5.85	128.75	115.30
1	g	127	LEU	CA-CB-CG	5.83	128.72	115.30
1	g	221	LEU	CA-CB-CG	5.83	128.71	115.30
1	Q	276	LEU	CA-CB-CG	5.80	128.64	115.30
1	d	165	ALA	CB-CA-C	-5.77	101.44	110.10
1	K	3	THR	OG1-CB-CG2	5.74	123.20	110.00
1	Y	3	THR	OG1-CB-CG2	5.73	123.18	110.00
1	M	127	LEU	CA-CB-CG	5.72	128.47	115.30
1	l	221	LEU	CA-CB-CG	5.72	128.45	115.30
1	b	221	LEU	CA-CB-CG	5.72	128.45	115.30
1	R	3	THR	OG1-CB-CG2	5.69	123.08	110.00
1	S	221	LEU	CA-CB-CG	5.67	128.34	115.30
1	l	3	THR	OG1-CB-CG2	5.66	123.01	110.00
1	N	3	THR	OG1-CB-CG2	5.65	123.00	110.00
1	L	3	THR	OG1-CB-CG2	5.65	123.00	110.00
1	k	3	THR	OG1-CB-CG2	5.65	122.99	110.00
1	X	706	LEU	CA-CB-CG	5.64	128.27	115.30
1	P	127	LEU	CA-CB-CG	5.63	128.26	115.30
1	G	3	THR	OG1-CB-CG2	5.63	122.95	110.00
1	O	3	THR	OG1-CB-CG2	5.63	122.95	110.00
1	m	3	THR	OG1-CB-CG2	5.63	122.95	110.00
1	c	706	LEU	CA-CB-CG	5.62	128.24	115.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	W	276	LEU	CA-CB-CG	5.62	128.23	115.30
1	d	127	LEU	CA-CB-CG	5.62	128.22	115.30
1	E	3	THR	OG1-CB-CG2	5.62	122.92	110.00
1	H	127	LEU	CA-CB-CG	5.59	128.17	115.30
1	P	276	LEU	CA-CB-CG	5.59	128.16	115.30
1	O	221	LEU	CA-CB-CG	5.57	128.11	115.30
1	j	276	LEU	CA-CB-CG	5.57	128.11	115.30
1	g	517	LEU	CA-CB-CG	5.56	128.10	115.30
1	M	3	THR	OG1-CB-CG2	5.56	122.79	110.00
1	X	3	THR	OG1-CB-CG2	5.55	122.76	110.00
1	G	276	LEU	CA-CB-CG	5.54	128.05	115.30
1	b	3	THR	OG1-CB-CG2	5.54	122.75	110.00
1	i	221	LEU	CA-CB-CG	5.53	128.03	115.30
1	e	3	THR	OG1-CB-CG2	5.53	122.72	110.00
1	P	164	GLN	C-N-CA	-5.53	107.88	121.70
1	U	3	THR	OG1-CB-CG2	5.53	122.71	110.00
1	k	221	LEU	CA-CB-CG	5.53	128.01	115.30
1	B	127	LEU	CA-CB-CG	5.50	127.96	115.30
1	I	3	THR	OG1-CB-CG2	5.50	122.65	110.00
1	j	3	THR	OG1-CB-CG2	5.50	122.65	110.00
1	P	3	THR	OG1-CB-CG2	5.49	122.64	110.00
1	Z	3	THR	OG1-CB-CG2	5.49	122.63	110.00
1	C	3	THR	OG1-CB-CG2	5.49	122.62	110.00
1	A	3	THR	OG1-CB-CG2	5.48	122.61	110.00
1	H	3	THR	OG1-CB-CG2	5.48	122.60	110.00
1	b	127	LEU	CA-CB-CG	5.48	127.89	115.30
1	m	340	LEU	CA-CB-CG	5.47	127.89	115.30
1	D	3	THR	OG1-CB-CG2	5.47	122.58	110.00
1	a	3	THR	OG1-CB-CG2	5.45	122.55	110.00
1	T	3	THR	OG1-CB-CG2	5.44	122.51	110.00
1	J	3	THR	OG1-CB-CG2	5.43	122.50	110.00
1	h	3	THR	OG1-CB-CG2	5.42	122.48	110.00
1	F	3	THR	OG1-CB-CG2	5.42	122.47	110.00
1	V	276	LEU	CA-CB-CG	5.42	127.77	115.30
1	f	3	THR	OG1-CB-CG2	5.41	122.45	110.00
1	S	3	THR	OG1-CB-CG2	5.40	122.42	110.00
1	e	276	LEU	CA-CB-CG	5.40	127.72	115.30
1	N	276	LEU	CA-CB-CG	5.39	127.70	115.30
1	K	221	LEU	CA-CB-CG	5.37	127.66	115.30
1	C	276	LEU	CA-CB-CG	5.35	127.60	115.30
1	B	3	THR	OG1-CB-CG2	5.34	122.28	110.00
1	D	276	LEU	CA-CB-CG	5.33	127.55	115.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	Q	127	LEU	CA-CB-CG	5.30	127.50	115.30
1	K	127	LEU	CA-CB-CG	5.30	127.48	115.30
1	k	127	LEU	CA-CB-CG	5.29	127.48	115.30
1	N	127	LEU	CA-CB-CG	5.29	127.46	115.30
1	R	276	LEU	CA-CB-CG	5.29	127.46	115.30
1	i	276	LEU	CA-CB-CG	5.26	127.40	115.30
1	V	3	THR	OG1-CB-CG2	5.26	122.09	110.00
1	i	3	THR	OG1-CB-CG2	5.26	122.09	110.00
1	g	3	THR	OG1-CB-CG2	5.24	122.06	110.00
1	W	144	LEU	CA-CB-CG	5.24	127.35	115.30
1	e	127	LEU	CA-CB-CG	5.24	127.35	115.30
1	d	3	THR	OG1-CB-CG2	5.24	122.04	110.00
1	i	127	LEU	CA-CB-CG	5.23	127.33	115.30
1	P	221	LEU	CB-CG-CD1	5.23	119.88	111.00
1	Z	221	LEU	CA-CB-CG	5.22	127.31	115.30
1	W	3	THR	CA-CB-OG1	5.22	119.96	109.00
1	L	104	VAL	N-CA-C	5.20	125.04	111.00
1	K	205	LEU	CA-CB-CG	5.20	127.25	115.30
1	A	127	LEU	CA-CB-CG	5.17	127.19	115.30
1	C	221	LEU	CA-CB-CG	5.17	127.19	115.30
1	C	127	LEU	CA-CB-CG	5.16	127.18	115.30
1	m	127	LEU	CA-CB-CG	5.16	127.16	115.30
1	K	104	VAL	N-CA-C	5.16	124.92	111.00
1	c	3	THR	OG1-CB-CG2	5.16	121.86	110.00
1	e	221	LEU	CA-CB-CG	5.15	127.15	115.30
1	c	127	LEU	CA-CB-CG	5.14	127.11	115.30
1	V	3	THR	CA-CB-OG1	5.12	119.75	109.00
1	J	221	LEU	CA-CB-CG	5.12	127.07	115.30
1	Z	706	LEU	CA-CB-CG	5.12	127.07	115.30
1	R	332	LEU	CA-CB-CG	5.11	127.05	115.30
1	j	221	LEU	CA-CB-CG	5.10	127.04	115.30
1	W	3	THR	OG1-CB-CG2	5.10	121.73	110.00
1	Q	706	LEU	CA-CB-CG	5.08	126.98	115.30
1	Q	3	THR	CA-CB-OG1	5.07	119.66	109.00
1	B	3	THR	CA-CB-OG1	5.07	119.64	109.00
1	O	706	LEU	CA-CB-CG	5.06	126.95	115.30
1	Q	3	THR	OG1-CB-CG2	5.06	121.65	110.00
1	l	268	LEU	CA-CB-CG	5.06	126.94	115.30
1	D	127	LEU	CA-CB-CG	5.06	126.94	115.30
1	g	3	THR	CA-CB-OG1	5.05	119.61	109.00
1	b	332	LEU	CA-CB-CG	5.03	126.87	115.30
1	c	3	THR	CA-CB-OG1	5.02	119.55	109.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	3	THR	CA-CB-OG1	5.02	119.54	109.00
1	H	3	THR	CA-CB-OG1	5.02	119.54	109.00
1	U	3	THR	CA-CB-OG1	5.01	119.52	109.00
1	G	127	LEU	CA-CB-CG	5.01	126.82	115.30
1	J	127	LEU	CA-CB-CG	5.00	126.80	115.30
1	S	276	LEU	CA-CB-CG	5.00	126.80	115.30

All (39) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	A	3	THR	CB
1	B	3	THR	CB
1	C	3	THR	CB
1	D	3	THR	CB
1	E	3	THR	CB
1	F	3	THR	CB
1	G	3	THR	CB
1	H	3	THR	CB
1	I	3	THR	CB
1	J	3	THR	CB
1	K	3	THR	CB
1	L	3	THR	CB
1	M	3	THR	CB
1	N	3	THR	CB
1	O	3	THR	CB
1	P	3	THR	CB
1	Q	3	THR	CB
1	R	3	THR	CB
1	S	3	THR	CB
1	T	3	THR	CB
1	U	3	THR	CB
1	V	3	THR	CB
1	W	3	THR	CB
1	X	3	THR	CB
1	Y	3	THR	CB
1	Z	3	THR	CB
1	a	3	THR	CB
1	b	3	THR	CB
1	c	3	THR	CB
1	d	3	THR	CB
1	e	3	THR	CB
1	f	3	THR	CB

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Mol	Chain	Res	Type	Atom
1	g	3	THR	CB
1	h	3	THR	CB
1	i	3	THR	CB
1	j	3	THR	CB
1	k	3	THR	CB
1	l	3	THR	CB
1	m	3	THR	CB

All (14) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	504	ARG	Peptide
1	C	504	ARG	Peptide
1	D	504	ARG	Peptide
1	E	504	ARG	Peptide
1	J	135	ASP	Peptide
1	K	135	ASP	Peptide
1	T	504	ARG	Peptide
1	V	504	ARG	Peptide
1	X	327	SER	Peptide
1	Z	302	VAL	Peptide
1	a	504	ARG	Peptide
1	e	504	ARG	Peptide
1	i	504	ARG	Peptide
1	m	504	ARG	Peptide

5.2 Too-close contacts [i](#)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

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	776/861 (90%)	634 (82%)	119 (15%)	23 (3%)	4	30
1	B	776/861 (90%)	640 (82%)	114 (15%)	22 (3%)	5	32
1	C	776/861 (90%)	639 (82%)	109 (14%)	28 (4%)	3	26
1	D	776/861 (90%)	635 (82%)	108 (14%)	33 (4%)	2	22
1	E	776/861 (90%)	637 (82%)	107 (14%)	32 (4%)	3	23
1	F	776/861 (90%)	627 (81%)	118 (15%)	31 (4%)	3	24
1	G	776/861 (90%)	648 (84%)	101 (13%)	27 (4%)	3	27
1	H	776/861 (90%)	636 (82%)	109 (14%)	31 (4%)	3	24
1	I	776/861 (90%)	650 (84%)	98 (13%)	28 (4%)	3	26
1	J	776/861 (90%)	637 (82%)	109 (14%)	30 (4%)	3	25
1	K	776/861 (90%)	631 (81%)	104 (13%)	41 (5%)	2	17
1	L	776/861 (90%)	637 (82%)	103 (13%)	36 (5%)	2	21
1	M	776/861 (90%)	633 (82%)	107 (14%)	36 (5%)	2	21
1	N	776/861 (90%)	639 (82%)	102 (13%)	35 (4%)	2	21
1	O	776/861 (90%)	637 (82%)	102 (13%)	37 (5%)	2	20
1	P	776/861 (90%)	627 (81%)	117 (15%)	32 (4%)	3	23
1	Q	776/861 (90%)	633 (82%)	104 (13%)	39 (5%)	2	19
1	R	776/861 (90%)	627 (81%)	109 (14%)	40 (5%)	2	18
1	S	776/861 (90%)	624 (80%)	115 (15%)	37 (5%)	2	20
1	T	776/861 (90%)	631 (81%)	113 (15%)	32 (4%)	3	23
1	U	776/861 (90%)	642 (83%)	100 (13%)	34 (4%)	2	21
1	V	776/861 (90%)	639 (82%)	110 (14%)	27 (4%)	3	27
1	W	776/861 (90%)	647 (83%)	96 (12%)	33 (4%)	2	22
1	X	776/861 (90%)	648 (84%)	97 (12%)	31 (4%)	3	24
1	Y	776/861 (90%)	644 (83%)	98 (13%)	34 (4%)	2	21
1	Z	776/861 (90%)	649 (84%)	97 (12%)	30 (4%)	3	25
1	a	776/861 (90%)	639 (82%)	108 (14%)	29 (4%)	3	26
1	b	776/861 (90%)	635 (82%)	112 (14%)	29 (4%)	3	26
1	c	776/861 (90%)	642 (83%)	101 (13%)	33 (4%)	2	22
1	d	776/861 (90%)	630 (81%)	118 (15%)	28 (4%)	3	26
1	e	776/861 (90%)	629 (81%)	113 (15%)	34 (4%)	2	21
1	f	776/861 (90%)	642 (83%)	99 (13%)	35 (4%)	2	21

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	g	776/861 (90%)	637 (82%)	98 (13%)	41 (5%)	2	17
1	h	776/861 (90%)	639 (82%)	97 (12%)	40 (5%)	2	18
1	i	776/861 (90%)	634 (82%)	104 (13%)	38 (5%)	2	19
1	j	776/861 (90%)	634 (82%)	107 (14%)	35 (4%)	2	21
1	k	776/861 (90%)	633 (82%)	105 (14%)	38 (5%)	2	19
1	l	776/861 (90%)	632 (81%)	107 (14%)	37 (5%)	2	20
1	m	776/861 (90%)	634 (82%)	108 (14%)	34 (4%)	2	21
All	All	30264/33579 (90%)	24831 (82%)	4143 (14%)	1290 (4%)	2	22

All (1290) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	135	ASP
1	A	148	PRO
1	A	169	LYS
1	A	253	VAL
1	A	296	LEU
1	A	328	GLU
1	A	355	ASP
1	B	54	PRO
1	B	148	PRO
1	B	169	LYS
1	B	201	VAL
1	B	253	VAL
1	B	279	ARG
1	B	328	GLU
1	B	355	ASP
1	C	116	LEU
1	C	148	PRO
1	C	169	LYS
1	C	253	VAL
1	C	296	LEU
1	C	328	GLU
1	C	355	ASP
1	D	54	PRO
1	D	61	VAL
1	D	148	PRO
1	D	169	LYS
1	D	182	CYS
1	D	201	VAL

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Mol	Chain	Res	Type
1	D	253	VAL
1	D	328	GLU
1	D	355	ASP
1	E	54	PRO
1	E	148	PRO
1	E	169	LYS
1	E	182	CYS
1	E	253	VAL
1	E	296	LEU
1	E	355	ASP
1	F	148	PRO
1	F	169	LYS
1	F	191	VAL
1	F	296	LEU
1	F	328	GLU
1	F	355	ASP
1	F	520	PRO
1	G	148	PRO
1	G	169	LYS
1	G	201	VAL
1	G	328	GLU
1	G	355	ASP
1	H	116	LEU
1	H	148	PRO
1	H	169	LYS
1	H	182	CYS
1	H	262	ASP
1	H	296	LEU
1	H	328	GLU
1	H	355	ASP
1	I	54	PRO
1	I	61	VAL
1	I	118	ASN
1	I	148	PRO
1	I	169	LYS
1	I	182	CYS
1	I	253	VAL
1	I	276	LEU
1	I	355	ASP
1	J	135	ASP
1	J	148	PRO
1	J	181	GLU

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Mol	Chain	Res	Type
1	J	182	CYS
1	J	296	LEU
1	J	328	GLU
1	J	355	ASP
1	K	52	THR
1	K	54	PRO
1	K	98	PRO
1	K	118	ASN
1	K	148	PRO
1	K	169	LYS
1	K	182	CYS
1	K	191	VAL
1	K	253	VAL
1	K	276	LEU
1	K	296	LEU
1	K	768	MET
1	L	58	TYR
1	L	61	VAL
1	L	98	PRO
1	L	133	ASN
1	L	148	PRO
1	L	169	LYS
1	L	182	CYS
1	L	242	LEU
1	L	253	VAL
1	L	327	SER
1	M	116	LEU
1	M	169	LYS
1	M	181	GLU
1	M	253	VAL
1	M	296	LEU
1	M	328	GLU
1	M	355	ASP
1	N	54	PRO
1	N	116	LEU
1	N	133	ASN
1	N	181	GLU
1	N	201	VAL
1	N	253	VAL
1	N	296	LEU
1	N	328	GLU
1	N	353	ALA

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Mol	Chain	Res	Type
1	N	355	ASP
1	O	148	PRO
1	O	169	LYS
1	O	201	VAL
1	O	253	VAL
1	O	319	GLY
1	O	328	GLU
1	O	422	GLY
1	P	54	PRO
1	P	148	PRO
1	P	169	LYS
1	P	181	GLU
1	P	201	VAL
1	P	328	GLU
1	P	353	ALA
1	P	355	ASP
1	Q	54	PRO
1	Q	169	LYS
1	Q	253	VAL
1	Q	296	LEU
1	Q	328	GLU
1	Q	353	ALA
1	R	26	SER
1	R	54	PRO
1	R	98	PRO
1	R	118	ASN
1	R	139	ALA
1	R	148	PRO
1	R	169	LYS
1	R	191	VAL
1	R	253	VAL
1	R	296	LEU
1	R	328	GLU
1	R	353	ALA
1	R	812	VAL
1	S	54	PRO
1	S	61	VAL
1	S	169	LYS
1	S	181	GLU
1	S	253	VAL
1	S	296	LEU
1	S	328	GLU

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Mol	Chain	Res	Type
1	T	169	LYS
1	T	296	LEU
1	T	422	GLY
1	U	169	LYS
1	U	182	CYS
1	U	201	VAL
1	U	253	VAL
1	U	296	LEU
1	U	353	ALA
1	U	506	LYS
1	V	54	PRO
1	V	169	LYS
1	V	182	CYS
1	V	253	VAL
1	V	418	GLU
1	W	61	VAL
1	W	148	PRO
1	W	169	LYS
1	W	191	VAL
1	W	253	VAL
1	W	296	LEU
1	W	328	GLU
1	W	355	ASP
1	X	148	PRO
1	X	169	LYS
1	X	182	CYS
1	X	296	LEU
1	X	355	ASP
1	Y	61	VAL
1	Y	117	PRO
1	Y	148	PRO
1	Y	194	GLU
1	Y	296	LEU
1	Y	355	ASP
1	Z	61	VAL
1	Z	116	LEU
1	Z	148	PRO
1	Z	169	LYS
1	Z	253	VAL
1	Z	296	LEU
1	Z	355	ASP
1	a	54	PRO

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Mol	Chain	Res	Type
1	a	148	PRO
1	a	169	LYS
1	a	181	GLU
1	a	253	VAL
1	a	296	LEU
1	a	328	GLU
1	b	54	PRO
1	b	116	LEU
1	b	135	ASP
1	b	148	PRO
1	b	169	LYS
1	b	253	VAL
1	b	328	GLU
1	c	116	LEU
1	c	118	ASN
1	c	169	LYS
1	c	182	CYS
1	c	253	VAL
1	c	296	LEU
1	c	327	SER
1	c	328	GLU
1	d	54	PRO
1	d	98	PRO
1	d	148	PRO
1	d	182	CYS
1	d	253	VAL
1	e	61	VAL
1	e	148	PRO
1	e	169	LYS
1	e	182	CYS
1	e	253	VAL
1	f	54	PRO
1	f	61	VAL
1	f	148	PRO
1	f	169	LYS
1	f	182	CYS
1	f	253	VAL
1	g	116	LEU
1	g	253	VAL
1	g	353	ALA
1	g	355	ASP
1	h	54	PRO

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Mol	Chain	Res	Type
1	h	116	LEU
1	h	182	CYS
1	h	201	VAL
1	h	253	VAL
1	h	296	LEU
1	h	319	GLY
1	h	328	GLU
1	h	355	ASP
1	i	54	PRO
1	i	116	LEU
1	i	148	PRO
1	i	169	LYS
1	i	182	CYS
1	i	201	VAL
1	i	253	VAL
1	i	296	LEU
1	i	328	GLU
1	i	355	ASP
1	j	116	LEU
1	j	148	PRO
1	j	169	LYS
1	j	253	VAL
1	j	328	GLU
1	j	422	GLY
1	k	52	THR
1	k	54	PRO
1	k	169	LYS
1	k	253	VAL
1	k	296	LEU
1	k	328	GLU
1	k	355	ASP
1	k	422	GLY
1	l	61	VAL
1	l	118	ASN
1	l	148	PRO
1	l	169	LYS
1	l	182	CYS
1	l	201	VAL
1	l	253	VAL
1	l	296	LEU
1	l	328	GLU
1	l	355	ASP

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Mol	Chain	Res	Type
1	m	54	PRO
1	m	116	LEU
1	m	148	PRO
1	m	169	LYS
1	m	201	VAL
1	m	279	ARG
1	m	296	LEU
1	m	328	GLU
1	m	355	ASP
1	A	54	PRO
1	A	116	LEU
1	A	182	CYS
1	A	201	VAL
1	A	812	VAL
1	B	116	LEU
1	B	296	LEU
1	C	54	PRO
1	C	61	VAL
1	C	181	GLU
1	C	277	GLY
1	C	319	GLY
1	C	346	GLU
1	D	94	GLN
1	D	116	LEU
1	D	296	LEU
1	D	422	GLY
1	D	605	GLY
1	E	116	LEU
1	E	319	GLY
1	E	328	GLU
1	E	422	GLY
1	E	491	PRO
1	E	803	GLY
1	F	54	PRO
1	F	116	LEU
1	F	181	GLU
1	F	211	GLU
1	F	212	VAL
1	F	276	LEU
1	F	319	GLY
1	F	422	GLY
1	F	769	GLU

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Mol	Chain	Res	Type
1	G	54	PRO
1	G	61	VAL
1	G	116	LEU
1	G	181	GLU
1	G	253	VAL
1	G	279	ARG
1	G	296	LEU
1	G	346	GLU
1	G	422	GLY
1	H	54	PRO
1	H	253	VAL
1	H	384	GLN
1	H	418	GLU
1	H	422	GLY
1	H	520	PRO
1	I	116	LEU
1	I	201	VAL
1	I	235	PHE
1	I	319	GLY
1	I	328	GLU
1	I	422	GLY
1	J	116	LEU
1	J	118	ASN
1	J	169	LYS
1	J	253	VAL
1	J	277	GLY
1	J	319	GLY
1	J	605	GLY
1	K	58	TYR
1	K	61	VAL
1	K	114	VAL
1	K	133	ASN
1	K	139	ALA
1	K	181	GLU
1	K	259	HIS
1	K	422	GLY
1	K	491	PRO
1	K	600	ARG
1	K	684	ALA
1	L	54	PRO
1	L	114	VAL
1	L	181	GLU

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Mol	Chain	Res	Type
1	L	276	LEU
1	L	277	GLY
1	L	296	LEU
1	L	319	GLY
1	L	328	GLU
1	L	353	ALA
1	L	422	GLY
1	L	573	LYS
1	L	812	VAL
1	M	54	PRO
1	M	61	VAL
1	M	118	ASN
1	M	182	CYS
1	M	276	LEU
1	M	277	GLY
1	M	319	GLY
1	M	339	PRO
1	M	422	GLY
1	M	605	GLY
1	M	684	ALA
1	N	61	VAL
1	N	148	PRO
1	N	182	CYS
1	N	221	LEU
1	N	263	VAL
1	N	276	LEU
1	N	319	GLY
1	N	422	GLY
1	O	54	PRO
1	O	116	LEU
1	O	135	ASP
1	O	181	GLU
1	O	182	CYS
1	O	191	VAL
1	O	238	LEU
1	O	296	LEU
1	O	803	GLY
1	P	116	LEU
1	P	139	ALA
1	P	182	CYS
1	P	298	GLN
1	P	422	GLY

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Mol	Chain	Res	Type
1	P	684	ALA
1	Q	52	THR
1	Q	61	VAL
1	Q	118	ASN
1	Q	133	ASN
1	Q	139	ALA
1	Q	181	GLU
1	Q	182	CYS
1	Q	191	VAL
1	Q	201	VAL
1	Q	319	GLY
1	Q	422	GLY
1	R	18	VAL
1	R	52	THR
1	R	61	VAL
1	R	101	PRO
1	R	182	CYS
1	R	221	LEU
1	R	339	PRO
1	R	491	PRO
1	R	803	GLY
1	S	148	PRO
1	S	201	VAL
1	S	422	GLY
1	S	803	GLY
1	S	812	VAL
1	T	54	PRO
1	T	61	VAL
1	T	116	LEU
1	T	201	VAL
1	T	328	GLU
1	T	355	ASP
1	T	803	GLY
1	U	26	SER
1	U	54	PRO
1	U	61	VAL
1	U	116	LEU
1	U	118	ASN
1	U	135	ASP
1	U	191	VAL
1	U	279	ARG
1	U	328	GLU

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Mol	Chain	Res	Type
1	U	383	ASP
1	U	422	GLY
1	U	671	ALA
1	U	803	GLY
1	U	812	VAL
1	V	61	VAL
1	V	116	LEU
1	V	181	GLU
1	V	190	ARG
1	V	346	GLU
1	V	422	GLY
1	V	605	GLY
1	W	54	PRO
1	W	116	LEU
1	W	418	GLU
1	W	422	GLY
1	X	61	VAL
1	X	116	LEU
1	X	135	ASP
1	X	139	ALA
1	X	276	LEU
1	X	277	GLY
1	X	328	GLU
1	X	422	GLY
1	X	605	GLY
1	Y	26	SER
1	Y	54	PRO
1	Y	169	LYS
1	Y	319	GLY
1	Y	327	SER
1	Y	328	GLU
1	Z	26	SER
1	Z	54	PRO
1	Z	181	GLU
1	Z	182	CYS
1	Z	263	VAL
1	Z	277	GLY
1	Z	327	SER
1	Z	338	GLN
1	Z	422	GLY
1	Z	520	PRO
1	a	26	SER

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Mol	Chain	Res	Type
1	a	61	VAL
1	a	116	LEU
1	a	277	GLY
1	a	422	GLY
1	a	605	GLY
1	b	118	ASN
1	b	181	GLU
1	b	422	GLY
1	b	427	LEU
1	b	803	GLY
1	c	181	GLU
1	c	277	GLY
1	c	355	ASP
1	c	803	GLY
1	c	812	VAL
1	d	61	VAL
1	d	101	PRO
1	d	276	LEU
1	d	327	SER
1	d	355	ASP
1	d	422	GLY
1	d	812	VAL
1	e	52	THR
1	e	54	PRO
1	e	98	PRO
1	e	117	PRO
1	e	277	GLY
1	e	296	LEU
1	e	319	GLY
1	e	328	GLU
1	e	355	ASP
1	e	422	GLY
1	e	803	GLY
1	f	94	GLN
1	f	116	LEU
1	f	118	ASN
1	f	201	VAL
1	f	277	GLY
1	f	355	ASP
1	f	506	LYS
1	f	803	GLY
1	f	812	VAL

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Mol	Chain	Res	Type
1	g	54	PRO
1	g	61	VAL
1	g	148	PRO
1	g	169	LYS
1	g	181	GLU
1	g	255	ASP
1	g	276	LEU
1	g	279	ARG
1	g	319	GLY
1	g	328	GLU
1	g	422	GLY
1	g	605	GLY
1	g	684	ALA
1	g	803	GLY
1	g	812	VAL
1	h	61	VAL
1	h	84	ARG
1	h	94	GLN
1	h	148	PRO
1	h	169	LYS
1	h	384	GLN
1	h	422	GLY
1	h	803	GLY
1	i	61	VAL
1	i	276	LEU
1	i	277	GLY
1	i	803	GLY
1	j	54	PRO
1	j	61	VAL
1	j	118	ASN
1	j	139	ALA
1	j	181	GLU
1	j	182	CYS
1	j	201	VAL
1	j	263	VAL
1	j	296	LEU
1	j	311	GLN
1	j	319	GLY
1	j	418	GLU
1	j	605	GLY
1	k	116	LEU
1	k	148	PRO

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Mol	Chain	Res	Type
1	k	182	CYS
1	k	276	LEU
1	l	52	THR
1	l	54	PRO
1	l	101	PRO
1	l	116	LEU
1	l	803	GLY
1	m	118	ASN
1	m	181	GLU
1	m	253	VAL
1	A	118	ASN
1	A	276	LEU
1	A	279	ARG
1	A	502	ALA
1	B	101	PRO
1	B	117	PRO
1	B	118	ASN
1	B	327	SER
1	C	101	PRO
1	D	101	PRO
1	D	135	ASP
1	D	277	GLY
1	D	384	GLN
1	D	684	ALA
1	E	52	THR
1	E	338	GLN
1	E	451	PRO
1	E	605	GLY
1	F	61	VAL
1	F	94	GLN
1	F	135	ASP
1	F	221	LEU
1	F	384	GLN
1	H	135	ASP
1	H	276	LEU
1	H	277	GLY
1	H	327	SER
1	I	296	LEU
1	I	311	GLN
1	I	640	VAL
1	J	26	SER
1	J	54	PRO

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Mol	Chain	Res	Type
1	J	139	ALA
1	J	259	HIS
1	J	294	ASN
1	J	327	SER
1	J	684	ALA
1	K	18	VAL
1	K	26	SER
1	K	116	LEU
1	K	279	ARG
1	K	339	PRO
1	K	769	GLU
1	L	117	PRO
1	M	52	THR
1	M	148	PRO
1	M	279	ARG
1	M	427	LEU
1	M	520	PRO
1	M	812	VAL
1	N	194	GLU
1	N	384	GLN
1	O	26	SER
1	O	61	VAL
1	O	118	ASN
1	O	194	GLU
1	O	427	LEU
1	O	520	PRO
1	P	118	ASN
1	P	221	LEU
1	P	263	VAL
1	P	319	GLY
1	P	520	PRO
1	P	600	ARG
1	P	769	GLU
1	Q	18	VAL
1	Q	26	SER
1	Q	116	LEU
1	Q	148	PRO
1	Q	221	LEU
1	Q	263	VAL
1	Q	355	ASP
1	Q	605	GLY
1	Q	684	ALA

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Mol	Chain	Res	Type
1	R	181	GLU
1	R	259	HIS
1	R	319	GLY
1	R	422	GLY
1	R	427	LEU
1	R	520	PRO
1	R	684	ALA
1	S	26	SER
1	S	52	THR
1	S	116	LEU
1	S	118	ASN
1	S	190	ARG
1	S	212	VAL
1	S	346	GLU
1	S	491	PRO
1	T	118	ASN
1	T	148	PRO
1	T	319	GLY
1	T	427	LEU
1	T	520	PRO
1	T	812	VAL
1	U	148	PRO
1	V	105	LEU
1	V	355	ASP
1	W	135	ASP
1	W	276	LEU
1	W	346	GLU
1	W	520	PRO
1	X	54	PRO
1	X	101	PRO
1	X	117	PRO
1	X	181	GLU
1	X	338	GLN
1	X	384	GLN
1	X	418	GLU
1	Y	116	LEU
1	Y	130	GLU
1	Y	276	LEU
1	Y	491	PRO
1	Y	605	GLY
1	Y	684	ALA
1	Z	139	ALA

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Mol	Chain	Res	Type
1	Z	684	ALA
1	a	135	ASP
1	a	177	ARG
1	a	268	LEU
1	a	491	PRO
1	b	94	GLN
1	b	182	CYS
1	b	201	VAL
1	b	268	LEU
1	b	296	LEU
1	b	355	ASP
1	c	26	SER
1	c	105	LEU
1	c	148	PRO
1	c	202	GLY
1	c	262	ASP
1	c	276	LEU
1	c	384	GLN
1	d	116	LEU
1	d	139	ALA
1	d	259	HIS
1	d	671	ALA
1	e	181	GLU
1	e	339	PRO
1	e	384	GLN
1	e	768	MET
1	e	812	VAL
1	f	117	PRO
1	f	139	ALA
1	f	181	GLU
1	f	276	LEU
1	f	327	SER
1	f	328	GLU
1	f	353	ALA
1	f	422	GLY
1	g	58	TYR
1	g	98	PRO
1	g	131	ASP
1	g	182	CYS
1	g	212	VAL
1	g	491	PRO
1	h	26	SER

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Mol	Chain	Res	Type
1	h	105	LEU
1	h	118	ASN
1	h	139	ALA
1	i	135	ASP
1	i	139	ALA
1	i	181	GLU
1	i	265	GLU
1	j	52	THR
1	j	101	PRO
1	j	127	LEU
1	k	98	PRO
1	k	118	ASN
1	k	139	ALA
1	k	150	THR
1	k	181	GLU
1	k	262	ASP
1	k	684	ALA
1	l	181	GLU
1	l	279	ARG
1	l	346	GLU
1	l	418	GLU
1	l	422	GLY
1	m	61	VAL
1	m	84	ARG
1	m	135	ASP
1	m	182	CYS
1	m	262	ASP
1	m	276	LEU
1	m	312	PRO
1	m	422	GLY
1	m	491	PRO
1	m	671	ALA
1	A	181	GLU
1	A	418	GLU
1	A	491	PRO
1	B	61	VAL
1	B	605	GLY
1	C	26	SER
1	C	133	ASN
1	C	139	ALA
1	C	384	GLN
1	D	374	VAL

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Mol	Chain	Res	Type
1	D	595	SER
1	E	26	SER
1	E	117	PRO
1	F	118	ASN
1	F	418	GLU
1	F	491	PRO
1	G	101	PRO
1	G	117	PRO
1	H	29	GLU
1	H	640	VAL
1	H	684	ALA
1	I	181	GLU
1	I	502	ALA
1	J	339	PRO
1	J	506	LYS
1	J	595	SER
1	K	242	LEU
1	K	319	GLY
1	L	355	ASP
1	L	384	GLN
1	M	26	SER
1	M	105	LEU
1	M	221	LEU
1	M	600	ARG
1	N	118	ASN
1	N	139	ALA
1	N	397	LYS
1	N	605	GLY
1	N	684	ALA
1	O	209	PHE
1	O	338	GLN
1	O	355	ASP
1	O	384	GLN
1	P	18	VAL
1	P	87	ASP
1	P	261	PRO
1	P	339	PRO
1	Q	98	PRO
1	Q	262	ASP
1	R	87	ASP
1	R	116	LEU
1	R	133	ASN

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Mol	Chain	Res	Type
1	R	276	LEU
1	R	463	PRO
1	S	58	TYR
1	S	159	VAL
1	S	279	ARG
1	S	427	LEU
1	S	684	ALA
1	S	761	ARG
1	T	127	LEU
1	T	253	VAL
1	T	418	GLU
1	T	491	PRO
1	T	563	SER
1	U	94	GLN
1	U	101	PRO
1	U	139	ALA
1	U	346	GLU
1	U	427	LEU
1	U	684	ALA
1	V	328	GLU
1	V	671	ALA
1	V	748	ALA
1	W	98	PRO
1	W	194	GLU
1	W	202	GLY
1	W	279	ARG
1	X	127	LEU
1	X	684	ALA
1	Y	139	ALA
1	Y	191	VAL
1	Y	202	GLY
1	Y	221	LEU
1	Z	101	PRO
1	Z	135	ASP
1	Z	328	GLU
1	a	101	PRO
1	a	311	GLN
1	a	355	ASP
1	a	384	GLN
1	b	276	LEU
1	b	418	GLU
1	c	422	GLY

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Mol	Chain	Res	Type
1	c	563	SER
1	c	595	SER
1	c	671	ALA
1	d	26	SER
1	d	117	PRO
1	d	242	LEU
1	d	263	VAL
1	e	26	SER
1	e	58	TYR
1	e	116	LEU
1	e	139	ALA
1	e	276	LEU
1	f	26	SER
1	f	52	THR
1	f	101	PRO
1	f	684	ALA
1	g	101	PRO
1	g	118	ASN
1	g	384	GLN
1	g	427	LEU
1	g	677	ALA
1	h	163	ILE
1	h	263	VAL
1	h	276	LEU
1	i	26	SER
1	i	101	PRO
1	i	193	GLY
1	i	255	ASP
1	i	346	GLU
1	i	422	GLY
1	i	812	VAL
1	j	262	ASP
1	j	276	LEU
1	j	684	ALA
1	k	61	VAL
1	k	101	PRO
1	k	279	ARG
1	k	384	GLN
1	k	418	GLU
1	k	491	PRO
1	l	94	GLN
1	l	98	PRO

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Mol	Chain	Res	Type
1	l	276	LEU
1	l	491	PRO
1	l	812	VAL
1	m	101	PRO
1	m	127	LEU
1	B	135	ASP
1	C	18	VAL
1	C	111	PRO
1	C	117	PRO
1	C	135	ASP
1	C	427	LEU
1	C	491	PRO
1	C	671	ALA
1	D	26	SER
1	D	127	LEU
1	D	139	ALA
1	D	242	LEU
1	D	338	GLN
1	D	418	GLU
1	D	803	GLY
1	E	61	VAL
1	E	94	GLN
1	E	98	PRO
1	E	135	ASP
1	E	418	GLU
1	F	374	VAL
1	G	520	PRO
1	G	684	ALA
1	H	26	SER
1	H	338	GLN
1	I	94	GLN
1	I	491	PRO
1	I	595	SER
1	I	684	ALA
1	K	277	GLY
1	K	292	GLY
1	K	294	ASN
1	K	520	PRO
1	L	60	ILE
1	L	94	GLN
1	L	116	LEU
1	L	118	ASN

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Mol	Chain	Res	Type
1	L	135	ASP
1	L	238	LEU
1	L	339	PRO
1	M	18	VAL
1	M	101	PRO
1	N	279	ARG
1	N	346	GLU
1	N	600	ARG
1	O	101	PRO
1	O	812	VAL
1	P	190	ARG
1	P	212	VAL
1	P	262	ASP
1	Q	87	ASP
1	Q	101	PRO
1	Q	190	ARG
1	Q	212	VAL
1	Q	276	LEU
1	Q	311	GLN
1	R	263	VAL
1	R	311	GLN
1	S	94	GLN
1	S	150	THR
1	S	769	GLU
1	T	181	GLU
1	T	212	VAL
1	T	279	ARG
1	T	346	GLU
1	U	276	LEU
1	U	573	LYS
1	V	139	ALA
1	V	296	LEU
1	W	101	PRO
1	W	111	PRO
1	W	117	PRO
1	W	139	ALA
1	W	181	GLU
1	W	212	VAL
1	W	491	PRO
1	X	55	PRO
1	X	319	GLY
1	X	600	ARG

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Mol	Chain	Res	Type
1	Y	94	GLN
1	Y	181	GLU
1	Y	418	GLU
1	Z	491	PRO
1	Z	534	HIS
1	a	117	PRO
1	a	684	ALA
1	b	457	VAL
1	b	520	PRO
1	b	563	SER
1	c	54	PRO
1	c	263	VAL
1	c	362	PRO
1	d	100	TYR
1	d	803	GLY
1	e	135	ASP
1	f	491	PRO
1	g	135	ASP
1	g	520	PRO
1	h	101	PRO
1	h	127	LEU
1	h	427	LEU
1	h	491	PRO
1	h	768	MET
1	i	99	LEU
1	i	279	ARG
1	i	311	GLN
1	i	748	ALA
1	j	100	TYR
1	j	355	ASP
1	j	427	LEU
1	j	491	PRO
1	k	100	TYR
1	k	201	VAL
1	k	209	PHE
1	k	427	LEU
1	l	18	VAL
1	l	29	GLU
1	l	100	TYR
1	l	298	GLN
1	l	427	LEU
1	l	520	PRO

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Mol	Chain	Res	Type
1	l	534	HIS
1	m	261	PRO
1	A	61	VAL
1	A	422	GLY
1	D	111	PRO
1	E	139	ALA
1	E	277	GLY
1	F	277	GLY
1	G	118	ASN
1	G	491	PRO
1	H	94	GLN
1	H	160	VAL
1	H	346	GLU
1	I	339	PRO
1	I	427	LEU
1	J	117	PRO
1	J	491	PRO
1	J	520	PRO
1	K	65	VAL
1	K	263	VAL
1	K	278	PRO
1	L	65	VAL
1	L	194	GLU
1	N	18	VAL
1	N	65	VAL
1	O	29	GLU
1	O	160	VAL
1	O	190	ARG
1	O	311	GLN
1	P	26	SER
1	P	812	VAL
1	Q	339	PRO
1	R	100	TYR
1	S	101	PRO
1	T	26	SER
1	T	29	GLU
1	T	684	ALA
1	U	520	PRO
1	V	491	PRO
1	W	118	ASN
1	W	384	GLN
1	W	605	GLY

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Mol	Chain	Res	Type
1	W	637	SER
1	Y	320	ILE
1	Z	294	ASN
1	a	263	VAL
1	a	812	VAL
1	b	61	VAL
1	b	263	VAL
1	c	491	PRO
1	d	319	GLY
1	d	491	PRO
1	f	768	MET
1	g	94	GLN
1	g	139	ALA
1	g	201	VAL
1	h	279	ARG
1	h	520	PRO
1	i	191	VAL
1	j	94	GLN
1	j	159	VAL
1	k	18	VAL
1	l	209	PHE
1	l	506	LYS
1	m	520	PRO
1	C	812	VAL
1	E	781	VAL
1	F	117	PRO
1	G	338	GLN
1	G	605	GLY
1	G	640	VAL
1	H	491	PRO
1	I	520	PRO
1	J	18	VAL
1	L	18	VAL
1	L	101	PRO
1	M	114	VAL
1	M	117	PRO
1	M	278	PRO
1	N	277	GLY
1	N	311	GLN
1	O	263	VAL
1	Q	100	TYR
1	Q	812	VAL

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Mol	Chain	Res	Type
1	R	117	PRO
1	S	18	VAL
1	S	117	PRO
1	U	28	VAL
1	U	263	VAL
1	V	201	VAL
1	X	159	VAL
1	X	520	PRO
1	Y	338	GLN
1	Z	55	PRO
1	Z	451	PRO
1	b	319	GLY
1	c	101	PRO
1	e	65	VAL
1	e	101	PRO
1	e	263	VAL
1	e	520	PRO
1	f	212	VAL
1	f	263	VAL
1	g	65	VAL
1	g	117	PRO
1	h	605	GLY
1	i	263	VAL
1	i	491	PRO
1	k	117	PRO
1	k	319	GLY
1	l	263	VAL
1	l	277	GLY
1	m	160	VAL
1	m	263	VAL
1	m	278	PRO
1	D	491	PRO
1	E	320	ILE
1	E	362	PRO
1	F	803	GLY
1	G	98	PRO
1	G	160	VAL
1	K	117	PRO
1	K	640	VAL
1	M	212	VAL
1	M	263	VAL
1	M	451	PRO

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Mol	Chain	Res	Type
1	O	18	VAL
1	P	451	PRO
1	R	65	VAL
1	S	311	GLN
1	T	77	ILE
1	T	191	VAL
1	T	263	VAL
1	X	18	VAL
1	X	202	GLY
1	Y	77	ILE
1	Y	277	GLY
1	b	491	PRO
1	b	812	VAL
1	c	261	PRO
1	c	278	PRO
1	d	159	VAL
1	d	201	VAL
1	f	18	VAL
1	f	114	VAL
1	f	339	PRO
1	g	277	GLY
1	g	278	PRO
1	g	338	GLN
1	h	96	PRO
1	h	98	PRO
1	h	338	GLN
1	i	111	PRO
1	i	212	VAL
1	i	339	PRO
1	k	263	VAL
1	m	277	GLY
1	B	18	VAL
1	B	48	VAL
1	B	159	VAL
1	B	263	VAL
1	B	278	PRO
1	C	803	GLY
1	E	812	VAL
1	F	18	VAL
1	F	111	PRO
1	G	374	VAL
1	H	292	GLY

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Mol	Chain	Res	Type
1	N	812	VAL
1	O	100	TYR
1	P	101	PRO
1	Q	261	PRO
1	R	605	GLY
1	S	263	VAL
1	S	277	GLY
1	S	520	PRO
1	V	98	PRO
1	V	212	VAL
1	X	451	PRO
1	Y	18	VAL
1	Y	55	PRO
1	Z	18	VAL
1	Z	117	PRO
1	Z	246	GLY
1	a	18	VAL
1	a	98	PRO
1	a	520	PRO
1	c	339	PRO
1	d	277	GLY
1	e	100	TYR
1	g	77	ILE
1	h	191	VAL
1	j	339	PRO
1	j	520	PRO
1	j	812	VAL
1	k	277	GLY
1	k	339	PRO
1	l	65	VAL
1	m	73	VAL
1	m	319	GLY
1	m	605	GLY
1	m	812	VAL
1	A	101	PRO
1	A	160	VAL
1	D	18	VAL
1	D	159	VAL
1	D	191	VAL
1	E	212	VAL
1	E	520	PRO
1	F	101	PRO

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Mol	Chain	Res	Type
1	G	65	VAL
1	H	202	GLY
1	I	96	PRO
1	J	263	VAL
1	K	605	GLY
1	N	463	PRO
1	O	605	GLY
1	Q	463	PRO
1	S	339	PRO
1	T	117	PRO
1	U	98	PRO
1	V	159	VAL
1	V	451	PRO
1	V	520	PRO
1	W	263	VAL
1	W	278	PRO
1	Y	98	PRO
1	Y	101	PRO
1	a	100	TYR
1	b	117	PRO
1	c	605	GLY
1	h	65	VAL
1	h	159	VAL
1	i	18	VAL
1	i	457	VAL
1	j	261	PRO
1	k	46	ALA
1	k	65	VAL
1	k	261	PRO
1	C	163	ILE
1	H	60	ILE
1	H	65	VAL
1	J	61	VAL
1	N	504	ARG
1	O	65	VAL
1	V	812	VAL
1	Y	263	VAL
1	d	46	ALA
1	e	18	VAL
1	e	201	VAL
1	f	159	VAL
1	h	100	TYR

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Mol	Chain	Res	Type
1	h	261	PRO
1	i	100	TYR

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain 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 sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	663/727 (91%)	527 (80%)	136 (20%)	1	6
1	B	663/727 (91%)	545 (82%)	118 (18%)	2	10
1	C	663/727 (91%)	536 (81%)	127 (19%)	1	7
1	D	663/727 (91%)	543 (82%)	120 (18%)	1	9
1	E	663/727 (91%)	550 (83%)	113 (17%)	2	12
1	F	663/727 (91%)	543 (82%)	120 (18%)	1	9
1	G	663/727 (91%)	533 (80%)	130 (20%)	1	7
1	H	663/727 (91%)	533 (80%)	130 (20%)	1	7
1	I	663/727 (91%)	537 (81%)	126 (19%)	1	8
1	J	663/727 (91%)	532 (80%)	131 (20%)	1	7
1	K	663/727 (91%)	519 (78%)	144 (22%)	1	5
1	L	663/727 (91%)	536 (81%)	127 (19%)	1	7
1	M	663/727 (91%)	537 (81%)	126 (19%)	1	8
1	N	663/727 (91%)	535 (81%)	128 (19%)	1	7
1	O	663/727 (91%)	528 (80%)	135 (20%)	1	6
1	P	663/727 (91%)	527 (80%)	136 (20%)	1	6
1	Q	663/727 (91%)	528 (80%)	135 (20%)	1	6
1	R	663/727 (91%)	521 (79%)	142 (21%)	1	5
1	S	663/727 (91%)	539 (81%)	124 (19%)	1	8
1	T	663/727 (91%)	540 (81%)	123 (19%)	1	8
1	U	663/727 (91%)	532 (80%)	131 (20%)	1	7
1	V	663/727 (91%)	530 (80%)	133 (20%)	1	6

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	W	663/727 (91%)	545 (82%)	118 (18%)	2	10
1	X	663/727 (91%)	534 (80%)	129 (20%)	1	7
1	Y	663/727 (91%)	547 (82%)	116 (18%)	2	10
1	Z	663/727 (91%)	535 (81%)	128 (19%)	1	7
1	a	663/727 (91%)	538 (81%)	125 (19%)	1	8
1	b	663/727 (91%)	534 (80%)	129 (20%)	1	7
1	c	663/727 (91%)	531 (80%)	132 (20%)	1	7
1	d	663/727 (91%)	542 (82%)	121 (18%)	1	8
1	e	663/727 (91%)	534 (80%)	129 (20%)	1	7
1	f	663/727 (91%)	536 (81%)	127 (19%)	1	7
1	g	663/727 (91%)	533 (80%)	130 (20%)	1	7
1	h	663/727 (91%)	535 (81%)	128 (19%)	1	7
1	i	663/727 (91%)	533 (80%)	130 (20%)	1	7
1	j	663/727 (91%)	540 (81%)	123 (19%)	1	8
1	k	663/727 (91%)	531 (80%)	132 (20%)	1	7
1	l	663/727 (91%)	541 (82%)	122 (18%)	1	8
1	m	663/727 (91%)	541 (82%)	122 (18%)	1	8
All	All	25857/28353 (91%)	20881 (81%)	4976 (19%)	1	7

All (4976) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	MET
1	A	3	THR
1	A	18	VAL
1	A	33	LYS
1	A	35	TYR
1	A	36	ILE
1	A	38	GLN
1	A	41	GLU
1	A	42	ARG
1	A	50	MET
1	A	52	THR
1	A	60	ILE
1	A	61	VAL
1	A	63	ASN

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Mol	Chain	Res	Type
1	A	65	VAL
1	A	68	ASP
1	A	70	GLN
1	A	74	LEU
1	A	75	PHE
1	A	83	LEU
1	A	84	ARG
1	A	95	ASP
1	A	104	VAL
1	A	105	LEU
1	A	110	THR
1	A	115	VAL
1	A	119	THR
1	A	127	LEU
1	A	131	ASP
1	A	132	LYS
1	A	133	ASN
1	A	135	ASP
1	A	137	VAL
1	A	144	LEU
1	A	145	PHE
1	A	151	TYR
1	A	152	ILE
1	A	160	VAL
1	A	161	GLU
1	A	162	ILE
1	A	163	ILE
1	A	169	LYS
1	A	174	LEU
1	A	175	ARG
1	A	177	ARG
1	A	183	PHE
1	A	191	VAL
1	A	196	TRP
1	A	197	LEU
1	A	199	ARG
1	A	205	LEU
1	A	213	LEU
1	A	222	THR
1	A	230	ARG
1	A	236	ARG
1	A	238	LEU

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Mol	Chain	Res	Type
1	A	242	LEU
1	A	249	TRP
1	A	250	LEU
1	A	253	VAL
1	A	254	GLN
1	A	257	GLU
1	A	266	GLU
1	A	267	VAL
1	A	268	LEU
1	A	271	VAL
1	A	274	THR
1	A	276	LEU
1	A	286	ASP
1	A	294	ASN
1	A	295	GLN
1	A	296	LEU
1	A	299	LYS
1	A	301	VAL
1	A	308	PHE
1	A	310	LEU
1	A	320	ILE
1	A	322	ASP
1	A	332	LEU
1	A	334	LEU
1	A	335	LYS
1	A	337	LEU
1	A	341	GLU
1	A	342	GLU
1	A	356	CYS
1	A	359	ILE
1	A	363	LEU
1	A	373	VAL
1	A	383	ASP
1	A	384	GLN
1	A	385	ASN
1	A	402	ILE
1	A	407	MET
1	A	417	LYS
1	A	474	ARG
1	A	479	ARG
1	A	486	LEU
1	A	487	VAL

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Mol	Chain	Res	Type
1	A	490	ASP
1	A	496	THR
1	A	501	SER
1	A	512	ARG
1	A	516	LEU
1	A	517	LEU
1	A	518	LEU
1	A	523	PHE
1	A	524	THR
1	A	528	THR
1	A	533	ASP
1	A	536	ARG
1	A	549	LEU
1	A	557	GLU
1	A	580	ARG
1	A	587	THR
1	A	595	SER
1	A	606	PHE
1	A	621	LYS
1	A	625	GLN
1	A	648	GLN
1	A	651	ARG
1	A	654	LEU
1	A	666	THR
1	A	683	GLU
1	A	706	LEU
1	A	721	ASN
1	A	747	LYS
1	A	755	THR
1	A	761	ARG
1	A	766	ARG
1	A	770	LEU
1	A	779	LEU
1	A	793	LYS
1	A	794	LYS
1	A	802	LEU
1	A	806	THR
1	A	808	ARG
1	B	1	MET
1	B	3	THR
1	B	18	VAL
1	B	23	SER

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Mol	Chain	Res	Type
1	B	33	LYS
1	B	36	ILE
1	B	38	GLN
1	B	41	GLU
1	B	50	MET
1	B	60	ILE
1	B	70	GLN
1	B	74	LEU
1	B	83	LEU
1	B	84	ARG
1	B	110	THR
1	B	114	VAL
1	B	115	VAL
1	B	119	THR
1	B	127	LEU
1	B	131	ASP
1	B	132	LYS
1	B	135	ASP
1	B	137	VAL
1	B	141	ASP
1	B	144	LEU
1	B	152	ILE
1	B	155	LYS
1	B	160	VAL
1	B	161	GLU
1	B	163	ILE
1	B	177	ARG
1	B	182	CYS
1	B	183	PHE
1	B	197	LEU
1	B	199	ARG
1	B	205	LEU
1	B	213	LEU
1	B	222	THR
1	B	230	ARG
1	B	234	ASN
1	B	236	ARG
1	B	238	LEU
1	B	249	TRP
1	B	250	LEU
1	B	253	VAL
1	B	254	GLN

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Mol	Chain	Res	Type
1	B	257	GLU
1	B	259	HIS
1	B	266	GLU
1	B	268	LEU
1	B	271	VAL
1	B	276	LEU
1	B	286	ASP
1	B	296	LEU
1	B	301	VAL
1	B	302	VAL
1	B	308	PHE
1	B	322	ASP
1	B	328	GLU
1	B	335	LYS
1	B	341	GLU
1	B	342	GLU
1	B	345	SER
1	B	356	CYS
1	B	358	LEU
1	B	359	ILE
1	B	363	LEU
1	B	370	LYS
1	B	373	VAL
1	B	380	ILE
1	B	383	ASP
1	B	384	GLN
1	B	385	ASN
1	B	407	MET
1	B	420	PRO
1	B	474	ARG
1	B	479	ARG
1	B	486	LEU
1	B	487	VAL
1	B	496	THR
1	B	497	VAL
1	B	501	SER
1	B	516	LEU
1	B	517	LEU
1	B	518	LEU
1	B	522	PHE
1	B	523	PHE
1	B	528	THR

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Mol	Chain	Res	Type
1	B	533	ASP
1	B	536	ARG
1	B	549	LEU
1	B	580	ARG
1	B	585	SER
1	B	587	THR
1	B	599	ILE
1	B	601	MET
1	B	621	LYS
1	B	633	LEU
1	B	648	GLN
1	B	651	ARG
1	B	654	LEU
1	B	666	THR
1	B	683	GLU
1	B	698	GLU
1	B	706	LEU
1	B	721	ASN
1	B	734	ARG
1	B	742	LEU
1	B	747	LYS
1	B	755	THR
1	B	766	ARG
1	B	770	LEU
1	B	778	GLU
1	B	779	LEU
1	B	782	SER
1	B	793	LYS
1	B	794	LYS
1	B	810	LEU
1	C	1	MET
1	C	3	THR
1	C	18	VAL
1	C	23	SER
1	C	35	TYR
1	C	36	ILE
1	C	38	GLN
1	C	50	MET
1	C	56	ARG
1	C	57	HIS
1	C	60	ILE
1	C	61	VAL

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Mol	Chain	Res	Type
1	C	63	ASN
1	C	65	VAL
1	C	70	GLN
1	C	74	LEU
1	C	75	PHE
1	C	83	LEU
1	C	84	ARG
1	C	90	ILE
1	C	110	THR
1	C	114	VAL
1	C	119	THR
1	C	127	LEU
1	C	131	ASP
1	C	132	LYS
1	C	135	ASP
1	C	137	VAL
1	C	144	LEU
1	C	151	TYR
1	C	160	VAL
1	C	161	GLU
1	C	167	VAL
1	C	169	LYS
1	C	175	ARG
1	C	177	ARG
1	C	183	PHE
1	C	191	VAL
1	C	192	THR
1	C	196	TRP
1	C	197	LEU
1	C	199	ARG
1	C	201	VAL
1	C	205	LEU
1	C	213	LEU
1	C	221	LEU
1	C	222	THR
1	C	225	THR
1	C	230	ARG
1	C	234	ASN
1	C	238	LEU
1	C	242	LEU
1	C	243	HIS
1	C	249	TRP

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Mol	Chain	Res	Type
1	C	250	LEU
1	C	253	VAL
1	C	254	GLN
1	C	257	GLU
1	C	259	HIS
1	C	266	GLU
1	C	268	LEU
1	C	271	VAL
1	C	276	LEU
1	C	286	ASP
1	C	296	LEU
1	C	302	VAL
1	C	308	PHE
1	C	320	ILE
1	C	322	ASP
1	C	328	GLU
1	C	335	LYS
1	C	337	LEU
1	C	341	GLU
1	C	342	GLU
1	C	345	SER
1	C	358	LEU
1	C	359	ILE
1	C	363	LEU
1	C	373	VAL
1	C	383	ASP
1	C	384	GLN
1	C	385	ASN
1	C	407	MET
1	C	417	LYS
1	C	418	GLU
1	C	474	ARG
1	C	479	ARG
1	C	486	LEU
1	C	487	VAL
1	C	490	ASP
1	C	496	THR
1	C	501	SER
1	C	516	LEU
1	C	517	LEU
1	C	518	LEU
1	C	522	PHE

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Mol	Chain	Res	Type
1	C	523	PHE
1	C	528	THR
1	C	533	ASP
1	C	536	ARG
1	C	539	LEU
1	C	549	LEU
1	C	580	ARG
1	C	585	SER
1	C	587	THR
1	C	621	LYS
1	C	633	LEU
1	C	666	THR
1	C	668	SER
1	C	683	GLU
1	C	688	LEU
1	C	690	ARG
1	C	692	LYS
1	C	698	GLU
1	C	706	LEU
1	C	721	ASN
1	C	742	LEU
1	C	755	THR
1	C	770	LEU
1	C	771	ILE
1	C	778	GLU
1	C	779	LEU
1	C	787	LEU
1	C	793	LYS
1	C	794	LYS
1	C	806	THR
1	C	808	ARG
1	D	1	MET
1	D	3	THR
1	D	18	VAL
1	D	27	ARG
1	D	35	TYR
1	D	36	ILE
1	D	38	GLN
1	D	41	GLU
1	D	50	MET
1	D	57	HIS
1	D	60	ILE

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Mol	Chain	Res	Type
1	D	65	VAL
1	D	70	GLN
1	D	75	PHE
1	D	78	THR
1	D	83	LEU
1	D	90	ILE
1	D	106	GLU
1	D	110	THR
1	D	118	ASN
1	D	119	THR
1	D	127	LEU
1	D	131	ASP
1	D	132	LYS
1	D	135	ASP
1	D	138	MET
1	D	141	ASP
1	D	144	LEU
1	D	145	PHE
1	D	151	TYR
1	D	152	ILE
1	D	160	VAL
1	D	161	GLU
1	D	166	THR
1	D	177	ARG
1	D	183	PHE
1	D	191	VAL
1	D	197	LEU
1	D	204	TYR
1	D	205	LEU
1	D	209	PHE
1	D	213	LEU
1	D	221	LEU
1	D	222	THR
1	D	225	THR
1	D	230	ARG
1	D	236	ARG
1	D	238	LEU
1	D	242	LEU
1	D	243	HIS
1	D	249	TRP
1	D	250	LEU
1	D	253	VAL

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Mol	Chain	Res	Type
1	D	257	GLU
1	D	259	HIS
1	D	266	GLU
1	D	268	LEU
1	D	271	VAL
1	D	276	LEU
1	D	281	TYR
1	D	284	ILE
1	D	286	ASP
1	D	296	LEU
1	D	308	PHE
1	D	310	LEU
1	D	321	GLN
1	D	322	ASP
1	D	328	GLU
1	D	335	LYS
1	D	341	GLU
1	D	342	GLU
1	D	358	LEU
1	D	359	ILE
1	D	363	LEU
1	D	373	VAL
1	D	380	ILE
1	D	383	ASP
1	D	384	GLN
1	D	385	ASN
1	D	388	ILE
1	D	407	MET
1	D	417	LYS
1	D	452	ARG
1	D	474	ARG
1	D	477	ARG
1	D	479	ARG
1	D	486	LEU
1	D	487	VAL
1	D	490	ASP
1	D	496	THR
1	D	516	LEU
1	D	517	LEU
1	D	518	LEU
1	D	522	PHE
1	D	523	PHE

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Mol	Chain	Res	Type
1	D	536	ARG
1	D	549	LEU
1	D	580	ARG
1	D	585	SER
1	D	587	THR
1	D	595	SER
1	D	621	LYS
1	D	625	GLN
1	D	642	SER
1	D	648	GLN
1	D	654	LEU
1	D	662	ILE
1	D	666	THR
1	D	668	SER
1	D	683	GLU
1	D	692	LYS
1	D	734	ARG
1	D	742	LEU
1	D	755	THR
1	D	770	LEU
1	D	778	GLU
1	D	779	LEU
1	D	793	LYS
1	D	802	LEU
1	D	806	THR
1	E	1	MET
1	E	3	THR
1	E	8	ILE
1	E	18	VAL
1	E	35	TYR
1	E	36	ILE
1	E	38	GLN
1	E	50	MET
1	E	52	THR
1	E	57	HIS
1	E	60	ILE
1	E	70	GLN
1	E	74	LEU
1	E	75	PHE
1	E	78	THR
1	E	83	LEU
1	E	90	ILE

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Mol	Chain	Res	Type
1	E	95	ASP
1	E	118	ASN
1	E	119	THR
1	E	127	LEU
1	E	130	GLU
1	E	131	ASP
1	E	133	ASN
1	E	135	ASP
1	E	136	LYS
1	E	138	MET
1	E	144	LEU
1	E	145	PHE
1	E	152	ILE
1	E	155	LYS
1	E	160	VAL
1	E	161	GLU
1	E	167	VAL
1	E	169	LYS
1	E	175	ARG
1	E	177	ARG
1	E	196	TRP
1	E	197	LEU
1	E	199	ARG
1	E	204	TYR
1	E	205	LEU
1	E	213	LEU
1	E	221	LEU
1	E	222	THR
1	E	225	THR
1	E	230	ARG
1	E	238	LEU
1	E	242	LEU
1	E	249	TRP
1	E	252	THR
1	E	253	VAL
1	E	257	GLU
1	E	259	HIS
1	E	266	GLU
1	E	268	LEU
1	E	271	VAL
1	E	276	LEU
1	E	281	TYR

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Mol	Chain	Res	Type
1	E	284	ILE
1	E	296	LEU
1	E	308	PHE
1	E	320	ILE
1	E	322	ASP
1	E	328	GLU
1	E	335	LYS
1	E	341	GLU
1	E	342	GLU
1	E	358	LEU
1	E	359	ILE
1	E	363	LEU
1	E	373	VAL
1	E	380	ILE
1	E	383	ASP
1	E	384	GLN
1	E	385	ASN
1	E	407	MET
1	E	417	LYS
1	E	452	ARG
1	E	474	ARG
1	E	479	ARG
1	E	486	LEU
1	E	487	VAL
1	E	496	THR
1	E	501	SER
1	E	516	LEU
1	E	517	LEU
1	E	518	LEU
1	E	522	PHE
1	E	523	PHE
1	E	536	ARG
1	E	539	LEU
1	E	549	LEU
1	E	580	ARG
1	E	587	THR
1	E	595	SER
1	E	621	LYS
1	E	648	GLN
1	E	654	LEU
1	E	666	THR
1	E	668	SER

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Mol	Chain	Res	Type
1	E	683	GLU
1	E	690	ARG
1	E	692	LYS
1	E	706	LEU
1	E	755	THR
1	E	770	LEU
1	E	778	GLU
1	E	793	LYS
1	E	794	LYS
1	E	802	LEU
1	E	806	THR
1	E	810	LEU
1	F	1	MET
1	F	3	THR
1	F	18	VAL
1	F	23	SER
1	F	35	TYR
1	F	36	ILE
1	F	38	GLN
1	F	41	GLU
1	F	50	MET
1	F	52	THR
1	F	60	ILE
1	F	70	GLN
1	F	73	VAL
1	F	74	LEU
1	F	75	PHE
1	F	83	LEU
1	F	90	ILE
1	F	95	ASP
1	F	104	VAL
1	F	110	THR
1	F	119	THR
1	F	127	LEU
1	F	131	ASP
1	F	132	LYS
1	F	144	LEU
1	F	155	LYS
1	F	158	GLU
1	F	160	VAL
1	F	161	GLU
1	F	163	ILE

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Mol	Chain	Res	Type
1	F	167	VAL
1	F	169	LYS
1	F	175	ARG
1	F	177	ARG
1	F	183	PHE
1	F	197	LEU
1	F	199	ARG
1	F	200	SER
1	F	205	LEU
1	F	213	LEU
1	F	221	LEU
1	F	222	THR
1	F	225	THR
1	F	230	ARG
1	F	234	ASN
1	F	236	ARG
1	F	238	LEU
1	F	242	LEU
1	F	249	TRP
1	F	250	LEU
1	F	257	GLU
1	F	259	HIS
1	F	266	GLU
1	F	268	LEU
1	F	271	VAL
1	F	276	LEU
1	F	281	TYR
1	F	284	ILE
1	F	286	ASP
1	F	294	ASN
1	F	295	GLN
1	F	296	LEU
1	F	301	VAL
1	F	302	VAL
1	F	308	PHE
1	F	320	ILE
1	F	322	ASP
1	F	332	LEU
1	F	335	LYS
1	F	340	LEU
1	F	341	GLU
1	F	342	GLU

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Mol	Chain	Res	Type
1	F	358	LEU
1	F	359	ILE
1	F	363	LEU
1	F	383	ASP
1	F	384	GLN
1	F	385	ASN
1	F	402	ILE
1	F	407	MET
1	F	417	LYS
1	F	418	GLU
1	F	474	ARG
1	F	479	ARG
1	F	486	LEU
1	F	487	VAL
1	F	496	THR
1	F	501	SER
1	F	516	LEU
1	F	517	LEU
1	F	518	LEU
1	F	524	THR
1	F	527	ILE
1	F	528	THR
1	F	533	ASP
1	F	536	ARG
1	F	539	LEU
1	F	549	LEU
1	F	580	ARG
1	F	587	THR
1	F	595	SER
1	F	601	MET
1	F	621	LYS
1	F	648	GLN
1	F	654	LEU
1	F	666	THR
1	F	668	SER
1	F	683	GLU
1	F	690	ARG
1	F	692	LYS
1	F	755	THR
1	F	766	ARG
1	F	770	LEU
1	F	771	ILE

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Mol	Chain	Res	Type
1	F	778	GLU
1	F	779	LEU
1	F	790	VAL
1	F	793	LYS
1	F	794	LYS
1	F	806	THR
1	G	1	MET
1	G	3	THR
1	G	18	VAL
1	G	23	SER
1	G	35	TYR
1	G	36	ILE
1	G	38	GLN
1	G	50	MET
1	G	60	ILE
1	G	65	VAL
1	G	70	GLN
1	G	74	LEU
1	G	75	PHE
1	G	83	LEU
1	G	84	ARG
1	G	101	PRO
1	G	106	GLU
1	G	108	ASP
1	G	114	VAL
1	G	115	VAL
1	G	119	THR
1	G	127	LEU
1	G	131	ASP
1	G	132	LYS
1	G	135	ASP
1	G	138	MET
1	G	144	LEU
1	G	145	PHE
1	G	152	ILE
1	G	160	VAL
1	G	161	GLU
1	G	163	ILE
1	G	175	ARG
1	G	177	ARG
1	G	183	PHE
1	G	191	VAL

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Mol	Chain	Res	Type
1	G	196	TRP
1	G	197	LEU
1	G	199	ARG
1	G	200	SER
1	G	205	LEU
1	G	208	VAL
1	G	209	PHE
1	G	213	LEU
1	G	221	LEU
1	G	222	THR
1	G	227	LEU
1	G	230	ARG
1	G	236	ARG
1	G	238	LEU
1	G	242	LEU
1	G	249	TRP
1	G	250	LEU
1	G	253	VAL
1	G	257	GLU
1	G	259	HIS
1	G	266	GLU
1	G	268	LEU
1	G	271	VAL
1	G	276	LEU
1	G	281	TYR
1	G	284	ILE
1	G	296	LEU
1	G	301	VAL
1	G	306	LYS
1	G	308	PHE
1	G	310	LEU
1	G	318	ARG
1	G	320	ILE
1	G	321	GLN
1	G	322	ASP
1	G	335	LYS
1	G	341	GLU
1	G	342	GLU
1	G	358	LEU
1	G	359	ILE
1	G	360	ARG
1	G	363	LEU

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Mol	Chain	Res	Type
1	G	373	VAL
1	G	383	ASP
1	G	384	GLN
1	G	385	ASN
1	G	395	THR
1	G	402	ILE
1	G	407	MET
1	G	418	GLU
1	G	452	ARG
1	G	474	ARG
1	G	479	ARG
1	G	486	LEU
1	G	487	VAL
1	G	496	THR
1	G	501	SER
1	G	516	LEU
1	G	517	LEU
1	G	518	LEU
1	G	522	PHE
1	G	523	PHE
1	G	524	THR
1	G	527	ILE
1	G	528	THR
1	G	533	ASP
1	G	536	ARG
1	G	549	LEU
1	G	580	ARG
1	G	587	THR
1	G	601	MET
1	G	621	LYS
1	G	627	VAL
1	G	648	GLN
1	G	654	LEU
1	G	666	THR
1	G	668	SER
1	G	683	GLU
1	G	690	ARG
1	G	692	LYS
1	G	698	GLU
1	G	713	SER
1	G	721	ASN
1	G	734	ARG

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Mol	Chain	Res	Type
1	G	742	LEU
1	G	755	THR
1	G	756	GLU
1	G	764	LYS
1	G	766	ARG
1	G	770	LEU
1	G	790	VAL
1	G	793	LYS
1	G	794	LYS
1	G	802	LEU
1	H	1	MET
1	H	3	THR
1	H	18	VAL
1	H	36	ILE
1	H	38	GLN
1	H	50	MET
1	H	52	THR
1	H	57	HIS
1	H	60	ILE
1	H	61	VAL
1	H	70	GLN
1	H	74	LEU
1	H	75	PHE
1	H	83	LEU
1	H	84	ARG
1	H	104	VAL
1	H	106	GLU
1	H	110	THR
1	H	119	THR
1	H	127	LEU
1	H	131	ASP
1	H	132	LYS
1	H	133	ASN
1	H	135	ASP
1	H	137	VAL
1	H	144	LEU
1	H	145	PHE
1	H	151	TYR
1	H	152	ILE
1	H	160	VAL
1	H	161	GLU
1	H	163	ILE

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Mol	Chain	Res	Type
1	H	166	THR
1	H	167	VAL
1	H	175	ARG
1	H	177	ARG
1	H	183	PHE
1	H	191	VAL
1	H	192	THR
1	H	196	TRP
1	H	197	LEU
1	H	199	ARG
1	H	205	LEU
1	H	213	LEU
1	H	221	LEU
1	H	222	THR
1	H	225	THR
1	H	230	ARG
1	H	237	ASP
1	H	238	LEU
1	H	241	VAL
1	H	242	LEU
1	H	249	TRP
1	H	250	LEU
1	H	253	VAL
1	H	257	GLU
1	H	266	GLU
1	H	268	LEU
1	H	271	VAL
1	H	276	LEU
1	H	281	TYR
1	H	284	ILE
1	H	286	ASP
1	H	296	LEU
1	H	303	LYS
1	H	305	GLU
1	H	308	PHE
1	H	310	LEU
1	H	320	ILE
1	H	322	ASP
1	H	335	LYS
1	H	341	GLU
1	H	358	LEU
1	H	359	ILE

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Mol	Chain	Res	Type
1	H	360	ARG
1	H	363	LEU
1	H	373	VAL
1	H	380	ILE
1	H	383	ASP
1	H	384	GLN
1	H	385	ASN
1	H	395	THR
1	H	407	MET
1	H	417	LYS
1	H	418	GLU
1	H	421	SER
1	H	424	GLU
1	H	474	ARG
1	H	479	ARG
1	H	484	PRO
1	H	486	LEU
1	H	487	VAL
1	H	490	ASP
1	H	496	THR
1	H	501	SER
1	H	516	LEU
1	H	517	LEU
1	H	518	LEU
1	H	522	PHE
1	H	523	PHE
1	H	527	ILE
1	H	528	THR
1	H	533	ASP
1	H	536	ARG
1	H	539	LEU
1	H	549	LEU
1	H	580	ARG
1	H	585	SER
1	H	587	THR
1	H	595	SER
1	H	621	LYS
1	H	625	GLN
1	H	648	GLN
1	H	649	ARG
1	H	654	LEU
1	H	666	THR

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Mol	Chain	Res	Type
1	H	683	GLU
1	H	698	GLU
1	H	706	LEU
1	H	721	ASN
1	H	729	ARG
1	H	742	LEU
1	H	755	THR
1	H	770	LEU
1	H	778	GLU
1	H	779	LEU
1	H	785	GLN
1	H	793	LYS
1	H	794	LYS
1	H	810	LEU
1	I	1	MET
1	I	3	THR
1	I	18	VAL
1	I	36	ILE
1	I	38	GLN
1	I	50	MET
1	I	52	THR
1	I	57	HIS
1	I	60	ILE
1	I	61	VAL
1	I	70	GLN
1	I	74	LEU
1	I	75	PHE
1	I	80	GLN
1	I	83	LEU
1	I	84	ARG
1	I	106	GLU
1	I	110	THR
1	I	114	VAL
1	I	115	VAL
1	I	119	THR
1	I	123	LEU
1	I	127	LEU
1	I	131	ASP
1	I	132	LYS
1	I	135	ASP
1	I	137	VAL
1	I	145	PHE

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Mol	Chain	Res	Type
1	I	151	TYR
1	I	152	ILE
1	I	160	VAL
1	I	161	GLU
1	I	163	ILE
1	I	167	VAL
1	I	169	LYS
1	I	175	ARG
1	I	177	ARG
1	I	183	PHE
1	I	192	THR
1	I	197	LEU
1	I	199	ARG
1	I	201	VAL
1	I	205	LEU
1	I	213	LEU
1	I	216	VAL
1	I	221	LEU
1	I	222	THR
1	I	225	THR
1	I	230	ARG
1	I	234	ASN
1	I	236	ARG
1	I	238	LEU
1	I	242	LEU
1	I	249	TRP
1	I	250	LEU
1	I	253	VAL
1	I	254	GLN
1	I	257	GLU
1	I	266	GLU
1	I	267	VAL
1	I	268	LEU
1	I	271	VAL
1	I	276	LEU
1	I	281	TYR
1	I	284	ILE
1	I	286	ASP
1	I	294	ASN
1	I	296	LEU
1	I	301	VAL
1	I	308	PHE

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Mol	Chain	Res	Type
1	I	310	LEU
1	I	322	ASP
1	I	330	GLN
1	I	332	LEU
1	I	334	LEU
1	I	335	LYS
1	I	341	GLU
1	I	342	GLU
1	I	358	LEU
1	I	359	ILE
1	I	363	LEU
1	I	383	ASP
1	I	384	GLN
1	I	385	ASN
1	I	407	MET
1	I	418	GLU
1	I	474	ARG
1	I	479	ARG
1	I	486	LEU
1	I	487	VAL
1	I	490	ASP
1	I	495	PHE
1	I	496	THR
1	I	516	LEU
1	I	517	LEU
1	I	518	LEU
1	I	523	PHE
1	I	527	ILE
1	I	533	ASP
1	I	536	ARG
1	I	539	LEU
1	I	549	LEU
1	I	561	LEU
1	I	580	ARG
1	I	587	THR
1	I	621	LYS
1	I	648	GLN
1	I	654	LEU
1	I	666	THR
1	I	668	SER
1	I	691	GLN
1	I	698	GLU

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Mol	Chain	Res	Type
1	I	709	LEU
1	I	742	LEU
1	I	747	LYS
1	I	755	THR
1	I	766	ARG
1	I	770	LEU
1	I	778	GLU
1	I	780	GLU
1	I	790	VAL
1	I	793	LYS
1	I	802	LEU
1	I	806	THR
1	I	809	ASP
1	I	810	LEU
1	J	1	MET
1	J	3	THR
1	J	18	VAL
1	J	35	TYR
1	J	36	ILE
1	J	38	GLN
1	J	41	GLU
1	J	42	ARG
1	J	50	MET
1	J	60	ILE
1	J	61	VAL
1	J	63	ASN
1	J	70	GLN
1	J	74	LEU
1	J	75	PHE
1	J	83	LEU
1	J	84	ARG
1	J	106	GLU
1	J	114	VAL
1	J	119	THR
1	J	122	HIS
1	J	127	LEU
1	J	130	GLU
1	J	131	ASP
1	J	133	ASN
1	J	135	ASP
1	J	137	VAL
1	J	138	MET

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Mol	Chain	Res	Type
1	J	144	LEU
1	J	151	TYR
1	J	152	ILE
1	J	160	VAL
1	J	161	GLU
1	J	163	ILE
1	J	169	LYS
1	J	175	ARG
1	J	177	ARG
1	J	183	PHE
1	J	192	THR
1	J	197	LEU
1	J	199	ARG
1	J	201	VAL
1	J	205	LEU
1	J	213	LEU
1	J	217	ASP
1	J	221	LEU
1	J	222	THR
1	J	225	THR
1	J	230	ARG
1	J	238	LEU
1	J	242	LEU
1	J	249	TRP
1	J	250	LEU
1	J	253	VAL
1	J	257	GLU
1	J	266	GLU
1	J	268	LEU
1	J	271	VAL
1	J	276	LEU
1	J	281	TYR
1	J	284	ILE
1	J	286	ASP
1	J	293	LYS
1	J	296	LEU
1	J	298	GLN
1	J	300	ARG
1	J	301	VAL
1	J	302	VAL
1	J	308	PHE
1	J	310	LEU

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Mol	Chain	Res	Type
1	J	318	ARG
1	J	320	ILE
1	J	321	GLN
1	J	322	ASP
1	J	328	GLU
1	J	334	LEU
1	J	335	LYS
1	J	341	GLU
1	J	342	GLU
1	J	356	CYS
1	J	358	LEU
1	J	363	LEU
1	J	373	VAL
1	J	380	ILE
1	J	383	ASP
1	J	384	GLN
1	J	385	ASN
1	J	388	ILE
1	J	395	THR
1	J	407	MET
1	J	417	LYS
1	J	418	GLU
1	J	421	SER
1	J	474	ARG
1	J	479	ARG
1	J	486	LEU
1	J	487	VAL
1	J	490	ASP
1	J	496	THR
1	J	497	VAL
1	J	501	SER
1	J	504	ARG
1	J	516	LEU
1	J	517	LEU
1	J	518	LEU
1	J	522	PHE
1	J	527	ILE
1	J	533	ASP
1	J	536	ARG
1	J	539	LEU
1	J	549	LEU
1	J	561	LEU

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Mol	Chain	Res	Type
1	J	580	ARG
1	J	587	THR
1	J	595	SER
1	J	621	LYS
1	J	648	GLN
1	J	654	LEU
1	J	666	THR
1	J	668	SER
1	J	689	GLU
1	J	747	LYS
1	J	755	THR
1	J	761	ARG
1	J	769	GLU
1	J	770	LEU
1	J	771	ILE
1	J	793	LYS
1	J	794	LYS
1	J	802	LEU
1	J	808	ARG
1	K	1	MET
1	K	3	THR
1	K	13	TYR
1	K	18	VAL
1	K	35	TYR
1	K	36	ILE
1	K	38	GLN
1	K	50	MET
1	K	52	THR
1	K	60	ILE
1	K	61	VAL
1	K	63	ASN
1	K	65	VAL
1	K	70	GLN
1	K	74	LEU
1	K	75	PHE
1	K	82	ARG
1	K	83	LEU
1	K	84	ARG
1	K	104	VAL
1	K	108	ASP
1	K	110	THR
1	K	114	VAL

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Mol	Chain	Res	Type
1	K	119	THR
1	K	124	LYS
1	K	127	LEU
1	K	131	ASP
1	K	133	ASN
1	K	135	ASP
1	K	137	VAL
1	K	138	MET
1	K	141	ASP
1	K	144	LEU
1	K	148	PRO
1	K	151	TYR
1	K	152	ILE
1	K	155	LYS
1	K	156	GLU
1	K	160	VAL
1	K	161	GLU
1	K	163	ILE
1	K	166	THR
1	K	170	GLN
1	K	175	ARG
1	K	177	ARG
1	K	183	PHE
1	K	188	LYS
1	K	192	THR
1	K	196	TRP
1	K	197	LEU
1	K	199	ARG
1	K	204	TYR
1	K	205	LEU
1	K	208	VAL
1	K	213	LEU
1	K	220	ILE
1	K	221	LEU
1	K	222	THR
1	K	225	THR
1	K	227	LEU
1	K	230	ARG
1	K	234	ASN
1	K	238	LEU
1	K	242	LEU
1	K	249	TRP

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Mol	Chain	Res	Type
1	K	252	THR
1	K	253	VAL
1	K	257	GLU
1	K	266	GLU
1	K	268	LEU
1	K	271	VAL
1	K	276	LEU
1	K	284	ILE
1	K	286	ASP
1	K	293	LYS
1	K	294	ASN
1	K	295	GLN
1	K	296	LEU
1	K	301	VAL
1	K	308	PHE
1	K	318	ARG
1	K	320	ILE
1	K	322	ASP
1	K	327	SER
1	K	328	GLU
1	K	332	LEU
1	K	334	LEU
1	K	335	LYS
1	K	341	GLU
1	K	342	GLU
1	K	358	LEU
1	K	363	LEU
1	K	373	VAL
1	K	383	ASP
1	K	384	GLN
1	K	385	ASN
1	K	388	ILE
1	K	395	THR
1	K	407	MET
1	K	418	GLU
1	K	421	SER
1	K	424	GLU
1	K	474	ARG
1	K	479	ARG
1	K	486	LEU
1	K	487	VAL
1	K	512	ARG

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Mol	Chain	Res	Type
1	K	516	LEU
1	K	517	LEU
1	K	522	PHE
1	K	527	ILE
1	K	528	THR
1	K	533	ASP
1	K	536	ARG
1	K	539	LEU
1	K	549	LEU
1	K	551	ASN
1	K	561	LEU
1	K	580	ARG
1	K	587	THR
1	K	598	ILE
1	K	601	MET
1	K	621	LYS
1	K	625	GLN
1	K	633	LEU
1	K	648	GLN
1	K	666	THR
1	K	668	SER
1	K	690	ARG
1	K	692	LYS
1	K	706	LEU
1	K	718	SER
1	K	721	ASN
1	K	742	LEU
1	K	755	THR
1	K	769	GLU
1	K	771	ILE
1	K	779	LEU
1	K	790	VAL
1	K	793	LYS
1	K	802	LEU
1	K	806	THR
1	K	809	ASP
1	K	810	LEU
1	L	1	MET
1	L	3	THR
1	L	18	VAL
1	L	35	TYR
1	L	36	ILE

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Mol	Chain	Res	Type
1	L	38	GLN
1	L	41	GLU
1	L	50	MET
1	L	60	ILE
1	L	61	VAL
1	L	70	GLN
1	L	74	LEU
1	L	75	PHE
1	L	80	GLN
1	L	83	LEU
1	L	84	ARG
1	L	104	VAL
1	L	106	GLU
1	L	107	LYS
1	L	110	THR
1	L	114	VAL
1	L	115	VAL
1	L	119	THR
1	L	127	LEU
1	L	131	ASP
1	L	132	LYS
1	L	135	ASP
1	L	137	VAL
1	L	141	ASP
1	L	144	LEU
1	L	151	TYR
1	L	152	ILE
1	L	155	LYS
1	L	156	GLU
1	L	160	VAL
1	L	161	GLU
1	L	167	VAL
1	L	175	ARG
1	L	177	ARG
1	L	183	PHE
1	L	192	THR
1	L	198	VAL
1	L	199	ARG
1	L	201	VAL
1	L	205	LEU
1	L	213	LEU
1	L	221	LEU

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Mol	Chain	Res	Type
1	L	222	THR
1	L	225	THR
1	L	227	LEU
1	L	230	ARG
1	L	232	LEU
1	L	236	ARG
1	L	238	LEU
1	L	242	LEU
1	L	249	TRP
1	L	253	VAL
1	L	257	GLU
1	L	266	GLU
1	L	268	LEU
1	L	271	VAL
1	L	276	LEU
1	L	284	ILE
1	L	286	ASP
1	L	295	GLN
1	L	296	LEU
1	L	301	VAL
1	L	307	SER
1	L	308	PHE
1	L	320	ILE
1	L	322	ASP
1	L	327	SER
1	L	332	LEU
1	L	334	LEU
1	L	335	LYS
1	L	337	LEU
1	L	341	GLU
1	L	342	GLU
1	L	345	SER
1	L	356	CYS
1	L	358	LEU
1	L	363	LEU
1	L	373	VAL
1	L	380	ILE
1	L	383	ASP
1	L	384	GLN
1	L	385	ASN
1	L	395	THR
1	L	407	MET

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Mol	Chain	Res	Type
1	L	418	GLU
1	L	425	GLU
1	L	474	ARG
1	L	479	ARG
1	L	486	LEU
1	L	487	VAL
1	L	490	ASP
1	L	497	VAL
1	L	516	LEU
1	L	517	LEU
1	L	518	LEU
1	L	524	THR
1	L	536	ARG
1	L	539	LEU
1	L	549	LEU
1	L	561	LEU
1	L	580	ARG
1	L	587	THR
1	L	595	SER
1	L	598	ILE
1	L	601	MET
1	L	621	LYS
1	L	648	GLN
1	L	649	ARG
1	L	654	LEU
1	L	666	THR
1	L	668	SER
1	L	683	GLU
1	L	713	SER
1	L	721	ASN
1	L	742	LEU
1	L	747	LYS
1	L	755	THR
1	L	766	ARG
1	L	778	GLU
1	L	779	LEU
1	L	793	LYS
1	L	802	LEU
1	M	1	MET
1	M	3	THR
1	M	18	VAL
1	M	23	SER

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Mol	Chain	Res	Type
1	M	33	LYS
1	M	36	ILE
1	M	38	GLN
1	M	50	MET
1	M	52	THR
1	M	57	HIS
1	M	60	ILE
1	M	61	VAL
1	M	63	ASN
1	M	65	VAL
1	M	70	GLN
1	M	74	LEU
1	M	82	ARG
1	M	83	LEU
1	M	84	ARG
1	M	90	ILE
1	M	104	VAL
1	M	106	GLU
1	M	110	THR
1	M	114	VAL
1	M	115	VAL
1	M	119	THR
1	M	127	LEU
1	M	131	ASP
1	M	132	LYS
1	M	133	ASN
1	M	135	ASP
1	M	137	VAL
1	M	144	LEU
1	M	145	PHE
1	M	151	TYR
1	M	152	ILE
1	M	155	LYS
1	M	156	GLU
1	M	160	VAL
1	M	161	GLU
1	M	163	ILE
1	M	169	LYS
1	M	175	ARG
1	M	177	ARG
1	M	183	PHE
1	M	192	THR

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Mol	Chain	Res	Type
1	M	197	LEU
1	M	199	ARG
1	M	204	TYR
1	M	205	LEU
1	M	213	LEU
1	M	221	LEU
1	M	222	THR
1	M	225	THR
1	M	230	ARG
1	M	234	ASN
1	M	238	LEU
1	M	242	LEU
1	M	249	TRP
1	M	250	LEU
1	M	257	GLU
1	M	266	GLU
1	M	268	LEU
1	M	271	VAL
1	M	276	LEU
1	M	284	ILE
1	M	286	ASP
1	M	296	LEU
1	M	301	VAL
1	M	307	SER
1	M	308	PHE
1	M	318	ARG
1	M	320	ILE
1	M	322	ASP
1	M	334	LEU
1	M	335	LYS
1	M	340	LEU
1	M	341	GLU
1	M	342	GLU
1	M	356	CYS
1	M	358	LEU
1	M	363	LEU
1	M	373	VAL
1	M	380	ILE
1	M	383	ASP
1	M	384	GLN
1	M	385	ASN
1	M	388	ILE

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Mol	Chain	Res	Type
1	M	395	THR
1	M	407	MET
1	M	418	GLU
1	M	474	ARG
1	M	479	ARG
1	M	486	LEU
1	M	487	VAL
1	M	490	ASP
1	M	496	THR
1	M	516	LEU
1	M	517	LEU
1	M	518	LEU
1	M	523	PHE
1	M	527	ILE
1	M	533	ASP
1	M	536	ARG
1	M	539	LEU
1	M	549	LEU
1	M	580	ARG
1	M	586	VAL
1	M	587	THR
1	M	595	SER
1	M	621	LYS
1	M	648	GLN
1	M	654	LEU
1	M	666	THR
1	M	683	GLU
1	M	692	LYS
1	M	706	LEU
1	M	718	SER
1	M	734	ARG
1	M	747	LYS
1	M	755	THR
1	M	770	LEU
1	M	779	LEU
1	M	793	LYS
1	M	799	THR
1	M	806	THR
1	N	1	MET
1	N	3	THR
1	N	18	VAL
1	N	22	ASN

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Mol	Chain	Res	Type
1	N	23	SER
1	N	36	ILE
1	N	38	GLN
1	N	50	MET
1	N	52	THR
1	N	60	ILE
1	N	61	VAL
1	N	63	ASN
1	N	65	VAL
1	N	70	GLN
1	N	74	LEU
1	N	82	ARG
1	N	83	LEU
1	N	84	ARG
1	N	104	VAL
1	N	108	ASP
1	N	114	VAL
1	N	119	THR
1	N	127	LEU
1	N	131	ASP
1	N	135	ASP
1	N	144	LEU
1	N	145	PHE
1	N	152	ILE
1	N	155	LYS
1	N	156	GLU
1	N	160	VAL
1	N	161	GLU
1	N	163	ILE
1	N	175	ARG
1	N	177	ARG
1	N	179	ARG
1	N	183	PHE
1	N	191	VAL
1	N	192	THR
1	N	196	TRP
1	N	197	LEU
1	N	199	ARG
1	N	204	TYR
1	N	205	LEU
1	N	213	LEU
1	N	221	LEU

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Mol	Chain	Res	Type
1	N	222	THR
1	N	230	ARG
1	N	234	ASN
1	N	238	LEU
1	N	242	LEU
1	N	249	TRP
1	N	250	LEU
1	N	254	GLN
1	N	257	GLU
1	N	259	HIS
1	N	266	GLU
1	N	267	VAL
1	N	268	LEU
1	N	271	VAL
1	N	276	LEU
1	N	281	TYR
1	N	284	ILE
1	N	286	ASP
1	N	296	LEU
1	N	301	VAL
1	N	307	SER
1	N	308	PHE
1	N	318	ARG
1	N	320	ILE
1	N	321	GLN
1	N	322	ASP
1	N	334	LEU
1	N	335	LYS
1	N	337	LEU
1	N	340	LEU
1	N	341	GLU
1	N	342	GLU
1	N	358	LEU
1	N	363	LEU
1	N	370	LYS
1	N	373	VAL
1	N	380	ILE
1	N	383	ASP
1	N	384	GLN
1	N	385	ASN
1	N	388	ILE
1	N	395	THR

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Mol	Chain	Res	Type
1	N	407	MET
1	N	417	LYS
1	N	418	GLU
1	N	474	ARG
1	N	476	LYS
1	N	479	ARG
1	N	486	LEU
1	N	487	VAL
1	N	490	ASP
1	N	497	VAL
1	N	516	LEU
1	N	517	LEU
1	N	533	ASP
1	N	536	ARG
1	N	539	LEU
1	N	549	LEU
1	N	551	ASN
1	N	552	ARG
1	N	580	ARG
1	N	587	THR
1	N	621	LYS
1	N	624	ASP
1	N	633	LEU
1	N	648	GLN
1	N	654	LEU
1	N	666	THR
1	N	668	SER
1	N	683	GLU
1	N	734	ARG
1	N	742	LEU
1	N	755	THR
1	N	761	ARG
1	N	769	GLU
1	N	770	LEU
1	N	778	GLU
1	N	790	VAL
1	N	793	LYS
1	N	794	LYS
1	N	802	LEU
1	N	806	THR
1	O	1	MET
1	O	3	THR

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Mol	Chain	Res	Type
1	O	13	TYR
1	O	18	VAL
1	O	33	LYS
1	O	35	TYR
1	O	36	ILE
1	O	38	GLN
1	O	50	MET
1	O	57	HIS
1	O	60	ILE
1	O	61	VAL
1	O	63	ASN
1	O	65	VAL
1	O	70	GLN
1	O	74	LEU
1	O	75	PHE
1	O	83	LEU
1	O	95	ASP
1	O	104	VAL
1	O	106	GLU
1	O	110	THR
1	O	114	VAL
1	O	119	THR
1	O	127	LEU
1	O	131	ASP
1	O	132	LYS
1	O	133	ASN
1	O	135	ASP
1	O	137	VAL
1	O	144	LEU
1	O	151	TYR
1	O	152	ILE
1	O	155	LYS
1	O	156	GLU
1	O	158	GLU
1	O	160	VAL
1	O	161	GLU
1	O	162	ILE
1	O	175	ARG
1	O	177	ARG
1	O	179	ARG
1	O	191	VAL
1	O	192	THR

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Mol	Chain	Res	Type
1	O	197	LEU
1	O	199	ARG
1	O	201	VAL
1	O	204	TYR
1	O	205	LEU
1	O	213	LEU
1	O	221	LEU
1	O	222	THR
1	O	225	THR
1	O	230	ARG
1	O	235	PHE
1	O	238	LEU
1	O	242	LEU
1	O	249	TRP
1	O	250	LEU
1	O	253	VAL
1	O	257	GLU
1	O	259	HIS
1	O	266	GLU
1	O	267	VAL
1	O	268	LEU
1	O	271	VAL
1	O	276	LEU
1	O	281	TYR
1	O	284	ILE
1	O	286	ASP
1	O	296	LEU
1	O	301	VAL
1	O	302	VAL
1	O	307	SER
1	O	308	PHE
1	O	310	LEU
1	O	320	ILE
1	O	322	ASP
1	O	328	GLU
1	O	332	LEU
1	O	334	LEU
1	O	335	LYS
1	O	337	LEU
1	O	341	GLU
1	O	342	GLU
1	O	358	LEU

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Mol	Chain	Res	Type
1	O	363	LEU
1	O	373	VAL
1	O	380	ILE
1	O	384	GLN
1	O	385	ASN
1	O	393	VAL
1	O	407	MET
1	O	417	LYS
1	O	421	SER
1	O	424	GLU
1	O	474	ARG
1	O	479	ARG
1	O	486	LEU
1	O	487	VAL
1	O	490	ASP
1	O	496	THR
1	O	501	SER
1	O	504	ARG
1	O	512	ARG
1	O	516	LEU
1	O	517	LEU
1	O	518	LEU
1	O	523	PHE
1	O	527	ILE
1	O	539	LEU
1	O	549	LEU
1	O	580	ARG
1	O	587	THR
1	O	595	SER
1	O	598	ILE
1	O	621	LYS
1	O	633	LEU
1	O	648	GLN
1	O	654	LEU
1	O	666	THR
1	O	668	SER
1	O	692	LYS
1	O	698	GLU
1	O	706	LEU
1	O	721	ASN
1	O	747	LYS
1	O	764	LYS

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Mol	Chain	Res	Type
1	O	770	LEU
1	O	778	GLU
1	O	779	LEU
1	O	787	LEU
1	O	790	VAL
1	O	793	LYS
1	O	809	ASP
1	P	1	MET
1	P	3	THR
1	P	18	VAL
1	P	35	TYR
1	P	36	ILE
1	P	38	GLN
1	P	41	GLU
1	P	50	MET
1	P	57	HIS
1	P	60	ILE
1	P	61	VAL
1	P	63	ASN
1	P	65	VAL
1	P	70	GLN
1	P	74	LEU
1	P	75	PHE
1	P	83	LEU
1	P	84	ARG
1	P	95	ASP
1	P	104	VAL
1	P	105	LEU
1	P	106	GLU
1	P	114	VAL
1	P	119	THR
1	P	127	LEU
1	P	131	ASP
1	P	132	LYS
1	P	133	ASN
1	P	135	ASP
1	P	137	VAL
1	P	142	GLU
1	P	144	LEU
1	P	145	PHE
1	P	152	ILE
1	P	156	GLU

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Mol	Chain	Res	Type
1	P	160	VAL
1	P	161	GLU
1	P	169	LYS
1	P	175	ARG
1	P	177	ARG
1	P	183	PHE
1	P	192	THR
1	P	196	TRP
1	P	197	LEU
1	P	199	ARG
1	P	200	SER
1	P	205	LEU
1	P	213	LEU
1	P	221	LEU
1	P	222	THR
1	P	225	THR
1	P	227	LEU
1	P	230	ARG
1	P	234	ASN
1	P	236	ARG
1	P	238	LEU
1	P	241	VAL
1	P	242	LEU
1	P	244	ARG
1	P	249	TRP
1	P	250	LEU
1	P	253	VAL
1	P	257	GLU
1	P	266	GLU
1	P	267	VAL
1	P	268	LEU
1	P	271	VAL
1	P	276	LEU
1	P	281	TYR
1	P	284	ILE
1	P	286	ASP
1	P	296	LEU
1	P	308	PHE
1	P	310	LEU
1	P	318	ARG
1	P	320	ILE
1	P	322	ASP

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Mol	Chain	Res	Type
1	P	334	LEU
1	P	335	LYS
1	P	337	LEU
1	P	341	GLU
1	P	342	GLU
1	P	345	SER
1	P	356	CYS
1	P	358	LEU
1	P	360	ARG
1	P	363	LEU
1	P	373	VAL
1	P	380	ILE
1	P	383	ASP
1	P	384	GLN
1	P	385	ASN
1	P	388	ILE
1	P	395	THR
1	P	405	THR
1	P	407	MET
1	P	417	LYS
1	P	452	ARG
1	P	474	ARG
1	P	479	ARG
1	P	486	LEU
1	P	487	VAL
1	P	496	THR
1	P	507	ARG
1	P	512	ARG
1	P	516	LEU
1	P	517	LEU
1	P	518	LEU
1	P	522	PHE
1	P	523	PHE
1	P	527	ILE
1	P	533	ASP
1	P	536	ARG
1	P	539	LEU
1	P	549	LEU
1	P	575	ILE
1	P	580	ARG
1	P	585	SER
1	P	587	THR

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Mol	Chain	Res	Type
1	P	601	MET
1	P	621	LYS
1	P	648	GLN
1	P	654	LEU
1	P	666	THR
1	P	668	SER
1	P	683	GLU
1	P	706	LEU
1	P	734	ARG
1	P	755	THR
1	P	770	LEU
1	P	771	ILE
1	P	778	GLU
1	P	787	LEU
1	P	790	VAL
1	P	793	LYS
1	P	802	LEU
1	Q	1	MET
1	Q	3	THR
1	Q	18	VAL
1	Q	33	LYS
1	Q	35	TYR
1	Q	36	ILE
1	Q	38	GLN
1	Q	50	MET
1	Q	60	ILE
1	Q	61	VAL
1	Q	65	VAL
1	Q	66	SER
1	Q	68	ASP
1	Q	70	GLN
1	Q	71	SER
1	Q	74	LEU
1	Q	75	PHE
1	Q	82	ARG
1	Q	83	LEU
1	Q	108	ASP
1	Q	110	THR
1	Q	114	VAL
1	Q	119	THR
1	Q	124	LYS
1	Q	127	LEU

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Mol	Chain	Res	Type
1	Q	131	ASP
1	Q	135	ASP
1	Q	138	MET
1	Q	141	ASP
1	Q	144	LEU
1	Q	151	TYR
1	Q	152	ILE
1	Q	155	LYS
1	Q	156	GLU
1	Q	158	GLU
1	Q	160	VAL
1	Q	161	GLU
1	Q	163	ILE
1	Q	168	ILE
1	Q	174	LEU
1	Q	175	ARG
1	Q	177	ARG
1	Q	183	PHE
1	Q	191	VAL
1	Q	192	THR
1	Q	196	TRP
1	Q	197	LEU
1	Q	199	ARG
1	Q	204	TYR
1	Q	205	LEU
1	Q	213	LEU
1	Q	221	LEU
1	Q	222	THR
1	Q	225	THR
1	Q	227	LEU
1	Q	230	ARG
1	Q	234	ASN
1	Q	236	ARG
1	Q	238	LEU
1	Q	242	LEU
1	Q	249	TRP
1	Q	250	LEU
1	Q	257	GLU
1	Q	259	HIS
1	Q	266	GLU
1	Q	268	LEU
1	Q	271	VAL

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Mol	Chain	Res	Type
1	Q	276	LEU
1	Q	284	ILE
1	Q	286	ASP
1	Q	293	LYS
1	Q	296	LEU
1	Q	299	LYS
1	Q	301	VAL
1	Q	308	PHE
1	Q	310	LEU
1	Q	314	GLU
1	Q	318	ARG
1	Q	320	ILE
1	Q	322	ASP
1	Q	334	LEU
1	Q	335	LYS
1	Q	337	LEU
1	Q	341	GLU
1	Q	342	GLU
1	Q	345	SER
1	Q	358	LEU
1	Q	363	LEU
1	Q	373	VAL
1	Q	380	ILE
1	Q	383	ASP
1	Q	384	GLN
1	Q	385	ASN
1	Q	388	ILE
1	Q	395	THR
1	Q	407	MET
1	Q	417	LYS
1	Q	421	SER
1	Q	468	VAL
1	Q	474	ARG
1	Q	479	ARG
1	Q	486	LEU
1	Q	487	VAL
1	Q	496	THR
1	Q	501	SER
1	Q	516	LEU
1	Q	517	LEU
1	Q	518	LEU
1	Q	527	ILE

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Mol	Chain	Res	Type
1	Q	533	ASP
1	Q	536	ARG
1	Q	549	LEU
1	Q	580	ARG
1	Q	587	THR
1	Q	595	SER
1	Q	601	MET
1	Q	621	LYS
1	Q	633	LEU
1	Q	648	GLN
1	Q	654	LEU
1	Q	666	THR
1	Q	668	SER
1	Q	683	GLU
1	Q	721	ASN
1	Q	734	ARG
1	Q	742	LEU
1	Q	747	LYS
1	Q	755	THR
1	Q	760	GLU
1	Q	770	LEU
1	Q	778	GLU
1	Q	779	LEU
1	Q	793	LYS
1	Q	794	LYS
1	Q	806	THR
1	R	1	MET
1	R	3	THR
1	R	13	TYR
1	R	18	VAL
1	R	33	LYS
1	R	35	TYR
1	R	36	ILE
1	R	38	GLN
1	R	41	GLU
1	R	42	ARG
1	R	50	MET
1	R	60	ILE
1	R	61	VAL
1	R	66	SER
1	R	70	GLN
1	R	74	LEU

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Mol	Chain	Res	Type
1	R	82	ARG
1	R	83	LEU
1	R	106	GLU
1	R	110	THR
1	R	114	VAL
1	R	115	VAL
1	R	119	THR
1	R	123	LEU
1	R	127	LEU
1	R	131	ASP
1	R	133	ASN
1	R	135	ASP
1	R	137	VAL
1	R	138	MET
1	R	144	LEU
1	R	146	GLU
1	R	151	TYR
1	R	152	ILE
1	R	155	LYS
1	R	156	GLU
1	R	158	GLU
1	R	161	GLU
1	R	163	ILE
1	R	175	ARG
1	R	183	PHE
1	R	191	VAL
1	R	192	THR
1	R	196	TRP
1	R	197	LEU
1	R	200	SER
1	R	201	VAL
1	R	204	TYR
1	R	205	LEU
1	R	208	VAL
1	R	213	LEU
1	R	217	ASP
1	R	221	LEU
1	R	222	THR
1	R	225	THR
1	R	227	LEU
1	R	230	ARG
1	R	234	ASN

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Mol	Chain	Res	Type
1	R	236	ARG
1	R	238	LEU
1	R	242	LEU
1	R	249	TRP
1	R	252	THR
1	R	253	VAL
1	R	254	GLN
1	R	257	GLU
1	R	259	HIS
1	R	268	LEU
1	R	271	VAL
1	R	276	LEU
1	R	284	ILE
1	R	286	ASP
1	R	293	LYS
1	R	296	LEU
1	R	301	VAL
1	R	302	VAL
1	R	308	PHE
1	R	320	ILE
1	R	322	ASP
1	R	328	GLU
1	R	330	GLN
1	R	332	LEU
1	R	335	LYS
1	R	337	LEU
1	R	340	LEU
1	R	341	GLU
1	R	342	GLU
1	R	358	LEU
1	R	363	LEU
1	R	373	VAL
1	R	380	ILE
1	R	383	ASP
1	R	384	GLN
1	R	385	ASN
1	R	388	ILE
1	R	395	THR
1	R	407	MET
1	R	408	LEU
1	R	417	LYS
1	R	456	ARG

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Mol	Chain	Res	Type
1	R	474	ARG
1	R	486	LEU
1	R	487	VAL
1	R	490	ASP
1	R	496	THR
1	R	501	SER
1	R	516	LEU
1	R	517	LEU
1	R	518	LEU
1	R	522	PHE
1	R	527	ILE
1	R	533	ASP
1	R	536	ARG
1	R	549	LEU
1	R	575	ILE
1	R	580	ARG
1	R	585	SER
1	R	587	THR
1	R	601	MET
1	R	621	LYS
1	R	633	LEU
1	R	648	GLN
1	R	651	ARG
1	R	654	LEU
1	R	666	THR
1	R	668	SER
1	R	685	ARG
1	R	690	ARG
1	R	706	LEU
1	R	734	ARG
1	R	747	LYS
1	R	755	THR
1	R	769	GLU
1	R	770	LEU
1	R	778	GLU
1	R	779	LEU
1	R	785	GLN
1	R	787	LEU
1	R	790	VAL
1	R	793	LYS
1	R	794	LYS
1	R	806	THR

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Mol	Chain	Res	Type
1	S	1	MET
1	S	3	THR
1	S	13	TYR
1	S	18	VAL
1	S	23	SER
1	S	33	LYS
1	S	35	TYR
1	S	36	ILE
1	S	38	GLN
1	S	41	GLU
1	S	50	MET
1	S	52	THR
1	S	60	ILE
1	S	61	VAL
1	S	63	ASN
1	S	66	SER
1	S	70	GLN
1	S	74	LEU
1	S	75	PHE
1	S	83	LEU
1	S	84	ARG
1	S	95	ASP
1	S	104	VAL
1	S	106	GLU
1	S	110	THR
1	S	114	VAL
1	S	115	VAL
1	S	119	THR
1	S	127	LEU
1	S	130	GLU
1	S	131	ASP
1	S	133	ASN
1	S	135	ASP
1	S	137	VAL
1	S	144	LEU
1	S	152	ILE
1	S	156	GLU
1	S	160	VAL
1	S	161	GLU
1	S	163	ILE
1	S	174	LEU
1	S	175	ARG

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Mol	Chain	Res	Type
1	S	177	ARG
1	S	183	PHE
1	S	192	THR
1	S	196	TRP
1	S	197	LEU
1	S	199	ARG
1	S	201	VAL
1	S	205	LEU
1	S	213	LEU
1	S	221	LEU
1	S	222	THR
1	S	225	THR
1	S	230	ARG
1	S	236	ARG
1	S	238	LEU
1	S	242	LEU
1	S	249	TRP
1	S	253	VAL
1	S	257	GLU
1	S	259	HIS
1	S	266	GLU
1	S	268	LEU
1	S	271	VAL
1	S	276	LEU
1	S	284	ILE
1	S	286	ASP
1	S	296	LEU
1	S	305	GLU
1	S	308	PHE
1	S	309	PHE
1	S	322	ASP
1	S	332	LEU
1	S	334	LEU
1	S	335	LYS
1	S	341	GLU
1	S	342	GLU
1	S	358	LEU
1	S	363	LEU
1	S	373	VAL
1	S	380	ILE
1	S	383	ASP
1	S	384	GLN

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Mol	Chain	Res	Type
1	S	385	ASN
1	S	388	ILE
1	S	402	ILE
1	S	407	MET
1	S	417	LYS
1	S	474	ARG
1	S	479	ARG
1	S	486	LEU
1	S	487	VAL
1	S	496	THR
1	S	501	SER
1	S	516	LEU
1	S	517	LEU
1	S	518	LEU
1	S	522	PHE
1	S	529	ILE
1	S	533	ASP
1	S	536	ARG
1	S	549	LEU
1	S	580	ARG
1	S	587	THR
1	S	595	SER
1	S	621	LYS
1	S	633	LEU
1	S	648	GLN
1	S	654	LEU
1	S	666	THR
1	S	668	SER
1	S	698	GLU
1	S	706	LEU
1	S	734	ARG
1	S	742	LEU
1	S	747	LYS
1	S	755	THR
1	S	770	LEU
1	S	771	ILE
1	S	778	GLU
1	S	779	LEU
1	S	802	LEU
1	S	806	THR
1	T	1	MET
1	T	3	THR

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Mol	Chain	Res	Type
1	T	18	VAL
1	T	23	SER
1	T	33	LYS
1	T	35	TYR
1	T	36	ILE
1	T	38	GLN
1	T	41	GLU
1	T	50	MET
1	T	60	ILE
1	T	63	ASN
1	T	65	VAL
1	T	70	GLN
1	T	74	LEU
1	T	83	LEU
1	T	84	ARG
1	T	90	ILE
1	T	95	ASP
1	T	106	GLU
1	T	114	VAL
1	T	115	VAL
1	T	119	THR
1	T	127	LEU
1	T	131	ASP
1	T	132	LYS
1	T	135	ASP
1	T	137	VAL
1	T	138	MET
1	T	144	LEU
1	T	145	PHE
1	T	148	PRO
1	T	151	TYR
1	T	160	VAL
1	T	161	GLU
1	T	166	THR
1	T	169	LYS
1	T	175	ARG
1	T	177	ARG
1	T	183	PHE
1	T	191	VAL
1	T	196	TRP
1	T	197	LEU
1	T	199	ARG

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Mol	Chain	Res	Type
1	T	205	LEU
1	T	213	LEU
1	T	222	THR
1	T	225	THR
1	T	227	LEU
1	T	230	ARG
1	T	236	ARG
1	T	238	LEU
1	T	242	LEU
1	T	249	TRP
1	T	253	VAL
1	T	257	GLU
1	T	259	HIS
1	T	266	GLU
1	T	268	LEU
1	T	271	VAL
1	T	276	LEU
1	T	281	TYR
1	T	284	ILE
1	T	286	ASP
1	T	296	LEU
1	T	302	VAL
1	T	306	LYS
1	T	308	PHE
1	T	310	LEU
1	T	318	ARG
1	T	320	ILE
1	T	321	GLN
1	T	322	ASP
1	T	328	GLU
1	T	335	LYS
1	T	341	GLU
1	T	342	GLU
1	T	358	LEU
1	T	360	ARG
1	T	363	LEU
1	T	373	VAL
1	T	383	ASP
1	T	384	GLN
1	T	385	ASN
1	T	388	ILE
1	T	407	MET

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Mol	Chain	Res	Type
1	T	474	ARG
1	T	479	ARG
1	T	486	LEU
1	T	487	VAL
1	T	490	ASP
1	T	495	PHE
1	T	496	THR
1	T	501	SER
1	T	512	ARG
1	T	517	LEU
1	T	518	LEU
1	T	522	PHE
1	T	523	PHE
1	T	527	ILE
1	T	536	ARG
1	T	549	LEU
1	T	580	ARG
1	T	585	SER
1	T	587	THR
1	T	621	LYS
1	T	648	GLN
1	T	654	LEU
1	T	666	THR
1	T	668	SER
1	T	683	GLU
1	T	693	ILE
1	T	706	LEU
1	T	713	SER
1	T	734	ARG
1	T	755	THR
1	T	769	GLU
1	T	770	LEU
1	T	778	GLU
1	T	779	LEU
1	T	793	LYS
1	T	802	LEU
1	T	806	THR
1	U	1	MET
1	U	3	THR
1	U	18	VAL
1	U	33	LYS
1	U	35	TYR

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Mol	Chain	Res	Type
1	U	36	ILE
1	U	38	GLN
1	U	41	GLU
1	U	50	MET
1	U	60	ILE
1	U	61	VAL
1	U	65	VAL
1	U	70	GLN
1	U	74	LEU
1	U	75	PHE
1	U	83	LEU
1	U	84	ARG
1	U	95	ASP
1	U	106	GLU
1	U	110	THR
1	U	119	THR
1	U	127	LEU
1	U	131	ASP
1	U	132	LYS
1	U	133	ASN
1	U	135	ASP
1	U	137	VAL
1	U	144	LEU
1	U	151	TYR
1	U	152	ILE
1	U	160	VAL
1	U	161	GLU
1	U	163	ILE
1	U	174	LEU
1	U	175	ARG
1	U	177	ARG
1	U	183	PHE
1	U	191	VAL
1	U	192	THR
1	U	196	TRP
1	U	197	LEU
1	U	199	ARG
1	U	204	TYR
1	U	205	LEU
1	U	213	LEU
1	U	221	LEU
1	U	222	THR

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Mol	Chain	Res	Type
1	U	225	THR
1	U	227	LEU
1	U	230	ARG
1	U	234	ASN
1	U	236	ARG
1	U	238	LEU
1	U	242	LEU
1	U	249	TRP
1	U	250	LEU
1	U	253	VAL
1	U	257	GLU
1	U	259	HIS
1	U	266	GLU
1	U	267	VAL
1	U	268	LEU
1	U	271	VAL
1	U	276	LEU
1	U	281	TYR
1	U	284	ILE
1	U	286	ASP
1	U	296	LEU
1	U	301	VAL
1	U	308	PHE
1	U	318	ARG
1	U	320	ILE
1	U	321	GLN
1	U	322	ASP
1	U	330	GLN
1	U	335	LYS
1	U	337	LEU
1	U	340	LEU
1	U	341	GLU
1	U	342	GLU
1	U	358	LEU
1	U	360	ARG
1	U	363	LEU
1	U	373	VAL
1	U	383	ASP
1	U	384	GLN
1	U	385	ASN
1	U	388	ILE
1	U	395	THR

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Mol	Chain	Res	Type
1	U	407	MET
1	U	408	LEU
1	U	417	LYS
1	U	421	SER
1	U	474	ARG
1	U	476	LYS
1	U	479	ARG
1	U	486	LEU
1	U	487	VAL
1	U	490	ASP
1	U	496	THR
1	U	501	SER
1	U	516	LEU
1	U	517	LEU
1	U	518	LEU
1	U	523	PHE
1	U	527	ILE
1	U	533	ASP
1	U	536	ARG
1	U	549	LEU
1	U	561	LEU
1	U	580	ARG
1	U	587	THR
1	U	621	LYS
1	U	624	ASP
1	U	648	GLN
1	U	666	THR
1	U	683	GLU
1	U	690	ARG
1	U	693	ILE
1	U	706	LEU
1	U	734	ARG
1	U	742	LEU
1	U	747	LYS
1	U	755	THR
1	U	761	ARG
1	U	770	LEU
1	U	778	GLU
1	U	779	LEU
1	U	794	LYS
1	U	802	LEU
1	U	806	THR

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Mol	Chain	Res	Type
1	V	1	MET
1	V	3	THR
1	V	8	ILE
1	V	13	TYR
1	V	18	VAL
1	V	33	LYS
1	V	35	TYR
1	V	36	ILE
1	V	38	GLN
1	V	41	GLU
1	V	50	MET
1	V	52	THR
1	V	57	HIS
1	V	60	ILE
1	V	61	VAL
1	V	63	ASN
1	V	70	GLN
1	V	74	LEU
1	V	82	ARG
1	V	83	LEU
1	V	106	GLU
1	V	110	THR
1	V	115	VAL
1	V	119	THR
1	V	123	LEU
1	V	127	LEU
1	V	131	ASP
1	V	133	ASN
1	V	135	ASP
1	V	137	VAL
1	V	144	LEU
1	V	145	PHE
1	V	151	TYR
1	V	152	ILE
1	V	155	LYS
1	V	158	GLU
1	V	160	VAL
1	V	161	GLU
1	V	163	ILE
1	V	167	VAL
1	V	175	ARG
1	V	177	ARG

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Mol	Chain	Res	Type
1	V	183	PHE
1	V	188	LYS
1	V	192	THR
1	V	197	LEU
1	V	199	ARG
1	V	201	VAL
1	V	205	LEU
1	V	208	VAL
1	V	213	LEU
1	V	221	LEU
1	V	222	THR
1	V	225	THR
1	V	227	LEU
1	V	230	ARG
1	V	234	ASN
1	V	236	ARG
1	V	238	LEU
1	V	242	LEU
1	V	243	HIS
1	V	249	TRP
1	V	253	VAL
1	V	257	GLU
1	V	259	HIS
1	V	266	GLU
1	V	268	LEU
1	V	271	VAL
1	V	276	LEU
1	V	281	TYR
1	V	286	ASP
1	V	296	LEU
1	V	301	VAL
1	V	302	VAL
1	V	308	PHE
1	V	320	ILE
1	V	321	GLN
1	V	322	ASP
1	V	330	GLN
1	V	335	LYS
1	V	340	LEU
1	V	341	GLU
1	V	342	GLU
1	V	345	SER

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Mol	Chain	Res	Type
1	V	358	LEU
1	V	363	LEU
1	V	373	VAL
1	V	380	ILE
1	V	383	ASP
1	V	384	GLN
1	V	385	ASN
1	V	388	ILE
1	V	395	THR
1	V	407	MET
1	V	417	LYS
1	V	474	ARG
1	V	479	ARG
1	V	486	LEU
1	V	487	VAL
1	V	490	ASP
1	V	496	THR
1	V	507	ARG
1	V	512	ARG
1	V	516	LEU
1	V	517	LEU
1	V	518	LEU
1	V	522	PHE
1	V	523	PHE
1	V	527	ILE
1	V	533	ASP
1	V	536	ARG
1	V	549	LEU
1	V	561	LEU
1	V	580	ARG
1	V	587	THR
1	V	621	LYS
1	V	648	GLN
1	V	666	THR
1	V	683	GLU
1	V	693	ILE
1	V	698	GLU
1	V	706	LEU
1	V	734	ARG
1	V	742	LEU
1	V	755	THR
1	V	765	VAL

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Mol	Chain	Res	Type
1	V	769	GLU
1	V	770	LEU
1	V	771	ILE
1	V	778	GLU
1	V	793	LYS
1	V	794	LYS
1	V	802	LEU
1	W	1	MET
1	W	3	THR
1	W	18	VAL
1	W	23	SER
1	W	33	LYS
1	W	36	ILE
1	W	38	GLN
1	W	50	MET
1	W	52	THR
1	W	60	ILE
1	W	61	VAL
1	W	64	PRO
1	W	70	GLN
1	W	74	LEU
1	W	75	PHE
1	W	83	LEU
1	W	84	ARG
1	W	95	ASP
1	W	104	VAL
1	W	106	GLU
1	W	114	VAL
1	W	119	THR
1	W	123	LEU
1	W	127	LEU
1	W	131	ASP
1	W	133	ASN
1	W	137	VAL
1	W	144	LEU
1	W	145	PHE
1	W	151	TYR
1	W	152	ILE
1	W	160	VAL
1	W	161	GLU
1	W	167	VAL
1	W	174	LEU

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Mol	Chain	Res	Type
1	W	175	ARG
1	W	177	ARG
1	W	183	PHE
1	W	191	VAL
1	W	197	LEU
1	W	199	ARG
1	W	205	LEU
1	W	208	VAL
1	W	213	LEU
1	W	222	THR
1	W	227	LEU
1	W	230	ARG
1	W	238	LEU
1	W	242	LEU
1	W	249	TRP
1	W	253	VAL
1	W	257	GLU
1	W	259	HIS
1	W	266	GLU
1	W	268	LEU
1	W	271	VAL
1	W	276	LEU
1	W	281	TYR
1	W	284	ILE
1	W	286	ASP
1	W	295	GLN
1	W	296	LEU
1	W	308	PHE
1	W	322	ASP
1	W	334	LEU
1	W	335	LYS
1	W	341	GLU
1	W	342	GLU
1	W	358	LEU
1	W	363	LEU
1	W	373	VAL
1	W	380	ILE
1	W	383	ASP
1	W	384	GLN
1	W	385	ASN
1	W	388	ILE
1	W	395	THR

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Mol	Chain	Res	Type
1	W	407	MET
1	W	474	ARG
1	W	479	ARG
1	W	486	LEU
1	W	490	ASP
1	W	496	THR
1	W	501	SER
1	W	516	LEU
1	W	517	LEU
1	W	522	PHE
1	W	523	PHE
1	W	528	THR
1	W	533	ASP
1	W	536	ARG
1	W	549	LEU
1	W	561	LEU
1	W	575	ILE
1	W	580	ARG
1	W	587	THR
1	W	595	SER
1	W	621	LYS
1	W	648	GLN
1	W	651	ARG
1	W	668	SER
1	W	683	GLU
1	W	685	ARG
1	W	690	ARG
1	W	742	LEU
1	W	755	THR
1	W	756	GLU
1	W	766	ARG
1	W	769	GLU
1	W	770	LEU
1	W	776	GLN
1	W	779	LEU
1	W	787	LEU
1	W	793	LYS
1	W	794	LYS
1	W	798	MET
1	W	802	LEU
1	W	810	LEU
1	X	1	MET

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Mol	Chain	Res	Type
1	X	3	THR
1	X	13	TYR
1	X	18	VAL
1	X	23	SER
1	X	33	LYS
1	X	35	TYR
1	X	36	ILE
1	X	38	GLN
1	X	41	GLU
1	X	50	MET
1	X	52	THR
1	X	57	HIS
1	X	60	ILE
1	X	61	VAL
1	X	70	GLN
1	X	74	LEU
1	X	78	THR
1	X	82	ARG
1	X	83	LEU
1	X	84	ARG
1	X	106	GLU
1	X	114	VAL
1	X	115	VAL
1	X	119	THR
1	X	127	LEU
1	X	129	PHE
1	X	131	ASP
1	X	133	ASN
1	X	135	ASP
1	X	137	VAL
1	X	138	MET
1	X	144	LEU
1	X	152	ILE
1	X	160	VAL
1	X	161	GLU
1	X	166	THR
1	X	167	VAL
1	X	169	LYS
1	X	174	LEU
1	X	175	ARG
1	X	177	ARG
1	X	183	PHE

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Mol	Chain	Res	Type
1	X	192	THR
1	X	196	TRP
1	X	197	LEU
1	X	199	ARG
1	X	205	LEU
1	X	208	VAL
1	X	213	LEU
1	X	221	LEU
1	X	222	THR
1	X	225	THR
1	X	227	LEU
1	X	230	ARG
1	X	238	LEU
1	X	242	LEU
1	X	249	TRP
1	X	254	GLN
1	X	255	ASP
1	X	257	GLU
1	X	259	HIS
1	X	266	GLU
1	X	268	LEU
1	X	271	VAL
1	X	276	LEU
1	X	281	TYR
1	X	284	ILE
1	X	286	ASP
1	X	296	LEU
1	X	302	VAL
1	X	308	PHE
1	X	320	ILE
1	X	322	ASP
1	X	332	LEU
1	X	335	LYS
1	X	340	LEU
1	X	341	GLU
1	X	342	GLU
1	X	358	LEU
1	X	363	LEU
1	X	373	VAL
1	X	380	ILE
1	X	383	ASP
1	X	384	GLN

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Mol	Chain	Res	Type
1	X	385	ASN
1	X	388	ILE
1	X	407	MET
1	X	417	LYS
1	X	474	ARG
1	X	479	ARG
1	X	486	LEU
1	X	487	VAL
1	X	490	ASP
1	X	496	THR
1	X	501	SER
1	X	512	ARG
1	X	516	LEU
1	X	517	LEU
1	X	522	PHE
1	X	523	PHE
1	X	528	THR
1	X	533	ASP
1	X	536	ARG
1	X	549	LEU
1	X	580	ARG
1	X	587	THR
1	X	595	SER
1	X	621	LYS
1	X	648	GLN
1	X	649	ARG
1	X	651	ARG
1	X	666	THR
1	X	668	SER
1	X	693	ILE
1	X	706	LEU
1	X	734	ARG
1	X	742	LEU
1	X	747	LYS
1	X	755	THR
1	X	756	GLU
1	X	766	ARG
1	X	769	GLU
1	X	770	LEU
1	X	779	LEU
1	X	793	LYS
1	X	794	LYS

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Mol	Chain	Res	Type
1	X	802	LEU
1	X	810	LEU
1	Y	1	MET
1	Y	3	THR
1	Y	18	VAL
1	Y	23	SER
1	Y	35	TYR
1	Y	36	ILE
1	Y	38	GLN
1	Y	50	MET
1	Y	60	ILE
1	Y	61	VAL
1	Y	70	GLN
1	Y	74	LEU
1	Y	78	THR
1	Y	83	LEU
1	Y	106	GLU
1	Y	114	VAL
1	Y	118	ASN
1	Y	119	THR
1	Y	127	LEU
1	Y	131	ASP
1	Y	132	LYS
1	Y	133	ASN
1	Y	135	ASP
1	Y	137	VAL
1	Y	138	MET
1	Y	144	LEU
1	Y	151	TYR
1	Y	152	ILE
1	Y	155	LYS
1	Y	160	VAL
1	Y	161	GLU
1	Y	163	ILE
1	Y	168	ILE
1	Y	174	LEU
1	Y	175	ARG
1	Y	177	ARG
1	Y	183	PHE
1	Y	188	LYS
1	Y	192	THR
1	Y	197	LEU

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Mol	Chain	Res	Type
1	Y	199	ARG
1	Y	201	VAL
1	Y	205	LEU
1	Y	208	VAL
1	Y	213	LEU
1	Y	220	ILE
1	Y	221	LEU
1	Y	222	THR
1	Y	225	THR
1	Y	230	ARG
1	Y	238	LEU
1	Y	242	LEU
1	Y	249	TRP
1	Y	250	LEU
1	Y	254	GLN
1	Y	257	GLU
1	Y	259	HIS
1	Y	266	GLU
1	Y	268	LEU
1	Y	271	VAL
1	Y	276	LEU
1	Y	281	TYR
1	Y	284	ILE
1	Y	286	ASP
1	Y	294	ASN
1	Y	295	GLN
1	Y	296	LEU
1	Y	301	VAL
1	Y	302	VAL
1	Y	308	PHE
1	Y	320	ILE
1	Y	322	ASP
1	Y	341	GLU
1	Y	342	GLU
1	Y	356	CYS
1	Y	358	LEU
1	Y	363	LEU
1	Y	373	VAL
1	Y	383	ASP
1	Y	384	GLN
1	Y	385	ASN
1	Y	407	MET

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Mol	Chain	Res	Type
1	Y	417	LYS
1	Y	474	ARG
1	Y	477	ARG
1	Y	479	ARG
1	Y	486	LEU
1	Y	490	ASP
1	Y	496	THR
1	Y	497	VAL
1	Y	501	SER
1	Y	516	LEU
1	Y	517	LEU
1	Y	522	PHE
1	Y	523	PHE
1	Y	533	ASP
1	Y	536	ARG
1	Y	549	LEU
1	Y	580	ARG
1	Y	587	THR
1	Y	595	SER
1	Y	621	LYS
1	Y	625	GLN
1	Y	648	GLN
1	Y	654	LEU
1	Y	668	SER
1	Y	691	GLN
1	Y	742	LEU
1	Y	755	THR
1	Y	756	GLU
1	Y	766	ARG
1	Y	778	GLU
1	Y	779	LEU
1	Y	793	LYS
1	Y	794	LYS
1	Y	802	LEU
1	Z	1	MET
1	Z	3	THR
1	Z	18	VAL
1	Z	23	SER
1	Z	33	LYS
1	Z	35	TYR
1	Z	36	ILE
1	Z	38	GLN

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Mol	Chain	Res	Type
1	Z	41	GLU
1	Z	50	MET
1	Z	60	ILE
1	Z	61	VAL
1	Z	63	ASN
1	Z	66	SER
1	Z	68	ASP
1	Z	70	GLN
1	Z	74	LEU
1	Z	75	PHE
1	Z	83	LEU
1	Z	90	ILE
1	Z	95	ASP
1	Z	106	GLU
1	Z	110	THR
1	Z	114	VAL
1	Z	119	THR
1	Z	127	LEU
1	Z	131	ASP
1	Z	132	LYS
1	Z	133	ASN
1	Z	135	ASP
1	Z	144	LEU
1	Z	145	PHE
1	Z	151	TYR
1	Z	152	ILE
1	Z	158	GLU
1	Z	160	VAL
1	Z	161	GLU
1	Z	169	LYS
1	Z	175	ARG
1	Z	177	ARG
1	Z	191	VAL
1	Z	192	THR
1	Z	197	LEU
1	Z	199	ARG
1	Z	201	VAL
1	Z	205	LEU
1	Z	209	PHE
1	Z	213	LEU
1	Z	221	LEU
1	Z	222	THR

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Mol	Chain	Res	Type
1	Z	225	THR
1	Z	227	LEU
1	Z	230	ARG
1	Z	236	ARG
1	Z	238	LEU
1	Z	242	LEU
1	Z	249	TRP
1	Z	250	LEU
1	Z	253	VAL
1	Z	254	GLN
1	Z	257	GLU
1	Z	259	HIS
1	Z	266	GLU
1	Z	267	VAL
1	Z	268	LEU
1	Z	270	VAL
1	Z	271	VAL
1	Z	276	LEU
1	Z	284	ILE
1	Z	286	ASP
1	Z	293	LYS
1	Z	296	LEU
1	Z	301	VAL
1	Z	308	PHE
1	Z	320	ILE
1	Z	322	ASP
1	Z	327	SER
1	Z	332	LEU
1	Z	334	LEU
1	Z	335	LYS
1	Z	341	GLU
1	Z	342	GLU
1	Z	358	LEU
1	Z	363	LEU
1	Z	373	VAL
1	Z	383	ASP
1	Z	384	GLN
1	Z	385	ASN
1	Z	388	ILE
1	Z	395	THR
1	Z	407	MET
1	Z	417	LYS

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Mol	Chain	Res	Type
1	Z	418	GLU
1	Z	474	ARG
1	Z	479	ARG
1	Z	486	LEU
1	Z	487	VAL
1	Z	490	ASP
1	Z	496	THR
1	Z	501	SER
1	Z	516	LEU
1	Z	517	LEU
1	Z	518	LEU
1	Z	523	PHE
1	Z	528	THR
1	Z	533	ASP
1	Z	536	ARG
1	Z	549	LEU
1	Z	580	ARG
1	Z	587	THR
1	Z	595	SER
1	Z	621	LYS
1	Z	648	GLN
1	Z	654	LEU
1	Z	666	THR
1	Z	668	SER
1	Z	706	LEU
1	Z	721	ASN
1	Z	734	ARG
1	Z	742	LEU
1	Z	747	LYS
1	Z	755	THR
1	Z	766	ARG
1	Z	770	LEU
1	Z	779	LEU
1	Z	793	LYS
1	Z	806	THR
1	Z	808	ARG
1	a	1	MET
1	a	3	THR
1	a	13	TYR
1	a	18	VAL
1	a	33	LYS
1	a	35	TYR

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Mol	Chain	Res	Type
1	a	36	ILE
1	a	38	GLN
1	a	50	MET
1	a	52	THR
1	a	58	TYR
1	a	63	ASN
1	a	65	VAL
1	a	70	GLN
1	a	74	LEU
1	a	83	LEU
1	a	84	ARG
1	a	90	ILE
1	a	106	GLU
1	a	114	VAL
1	a	118	ASN
1	a	119	THR
1	a	123	LEU
1	a	127	LEU
1	a	129	PHE
1	a	131	ASP
1	a	135	ASP
1	a	137	VAL
1	a	138	MET
1	a	144	LEU
1	a	145	PHE
1	a	152	ILE
1	a	156	GLU
1	a	160	VAL
1	a	161	GLU
1	a	164	GLN
1	a	175	ARG
1	a	177	ARG
1	a	183	PHE
1	a	192	THR
1	a	196	TRP
1	a	197	LEU
1	a	199	ARG
1	a	205	LEU
1	a	209	PHE
1	a	213	LEU
1	a	221	LEU
1	a	222	THR

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Mol	Chain	Res	Type
1	a	227	LEU
1	a	230	ARG
1	a	234	ASN
1	a	236	ARG
1	a	238	LEU
1	a	242	LEU
1	a	249	TRP
1	a	253	VAL
1	a	254	GLN
1	a	266	GLU
1	a	267	VAL
1	a	268	LEU
1	a	271	VAL
1	a	276	LEU
1	a	284	ILE
1	a	286	ASP
1	a	293	LYS
1	a	295	GLN
1	a	296	LEU
1	a	299	LYS
1	a	301	VAL
1	a	308	PHE
1	a	321	GLN
1	a	322	ASP
1	a	332	LEU
1	a	335	LYS
1	a	340	LEU
1	a	341	GLU
1	a	342	GLU
1	a	345	SER
1	a	358	LEU
1	a	363	LEU
1	a	373	VAL
1	a	380	ILE
1	a	383	ASP
1	a	384	GLN
1	a	385	ASN
1	a	388	ILE
1	a	395	THR
1	a	407	MET
1	a	417	LYS
1	a	424	GLU

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Mol	Chain	Res	Type
1	a	474	ARG
1	a	479	ARG
1	a	486	LEU
1	a	487	VAL
1	a	490	ASP
1	a	496	THR
1	a	497	VAL
1	a	501	SER
1	a	516	LEU
1	a	517	LEU
1	a	523	PHE
1	a	528	THR
1	a	533	ASP
1	a	536	ARG
1	a	549	LEU
1	a	580	ARG
1	a	587	THR
1	a	595	SER
1	a	621	LYS
1	a	654	LEU
1	a	666	THR
1	a	668	SER
1	a	690	ARG
1	a	692	LYS
1	a	693	ILE
1	a	706	LEU
1	a	721	ASN
1	a	742	LEU
1	a	769	GLU
1	a	770	LEU
1	a	779	LEU
1	a	787	LEU
1	a	793	LYS
1	a	802	LEU
1	a	810	LEU
1	b	1	MET
1	b	3	THR
1	b	18	VAL
1	b	33	LYS
1	b	36	ILE
1	b	38	GLN
1	b	41	GLU

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Mol	Chain	Res	Type
1	b	50	MET
1	b	52	THR
1	b	58	TYR
1	b	60	ILE
1	b	61	VAL
1	b	65	VAL
1	b	70	GLN
1	b	74	LEU
1	b	75	PHE
1	b	82	ARG
1	b	83	LEU
1	b	84	ARG
1	b	90	ILE
1	b	106	GLU
1	b	114	VAL
1	b	115	VAL
1	b	119	THR
1	b	122	HIS
1	b	127	LEU
1	b	131	ASP
1	b	135	ASP
1	b	144	LEU
1	b	145	PHE
1	b	152	ILE
1	b	160	VAL
1	b	161	GLU
1	b	163	ILE
1	b	164	GLN
1	b	169	LYS
1	b	174	LEU
1	b	175	ARG
1	b	177	ARG
1	b	183	PHE
1	b	196	TRP
1	b	197	LEU
1	b	199	ARG
1	b	201	VAL
1	b	204	TYR
1	b	205	LEU
1	b	213	LEU
1	b	217	ASP
1	b	221	LEU

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Mol	Chain	Res	Type
1	b	222	THR
1	b	227	LEU
1	b	230	ARG
1	b	234	ASN
1	b	236	ARG
1	b	238	LEU
1	b	242	LEU
1	b	249	TRP
1	b	253	VAL
1	b	254	GLN
1	b	257	GLU
1	b	259	HIS
1	b	266	GLU
1	b	268	LEU
1	b	271	VAL
1	b	276	LEU
1	b	284	ILE
1	b	286	ASP
1	b	296	LEU
1	b	301	VAL
1	b	308	PHE
1	b	322	ASP
1	b	328	GLU
1	b	334	LEU
1	b	335	LYS
1	b	341	GLU
1	b	342	GLU
1	b	356	CYS
1	b	358	LEU
1	b	363	LEU
1	b	373	VAL
1	b	380	ILE
1	b	384	GLN
1	b	385	ASN
1	b	407	MET
1	b	417	LYS
1	b	424	GLU
1	b	452	ARG
1	b	474	ARG
1	b	477	ARG
1	b	479	ARG
1	b	486	LEU

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Mol	Chain	Res	Type
1	b	487	VAL
1	b	490	ASP
1	b	496	THR
1	b	501	SER
1	b	512	ARG
1	b	516	LEU
1	b	517	LEU
1	b	518	LEU
1	b	523	PHE
1	b	528	THR
1	b	533	ASP
1	b	536	ARG
1	b	549	LEU
1	b	552	ARG
1	b	580	ARG
1	b	585	SER
1	b	587	THR
1	b	595	SER
1	b	601	MET
1	b	621	LYS
1	b	642	SER
1	b	648	GLN
1	b	654	LEU
1	b	666	THR
1	b	668	SER
1	b	670	GLU
1	b	683	GLU
1	b	692	LYS
1	b	706	LEU
1	b	741	VAL
1	b	747	LYS
1	b	755	THR
1	b	770	LEU
1	b	778	GLU
1	b	779	LEU
1	b	790	VAL
1	b	793	LYS
1	b	806	THR
1	c	1	MET
1	c	3	THR
1	c	18	VAL
1	c	23	SER

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Mol	Chain	Res	Type
1	c	33	LYS
1	c	35	TYR
1	c	36	ILE
1	c	38	GLN
1	c	41	GLU
1	c	50	MET
1	c	60	ILE
1	c	63	ASN
1	c	65	VAL
1	c	70	GLN
1	c	74	LEU
1	c	75	PHE
1	c	83	LEU
1	c	84	ARG
1	c	95	ASP
1	c	104	VAL
1	c	106	GLU
1	c	110	THR
1	c	114	VAL
1	c	115	VAL
1	c	119	THR
1	c	127	LEU
1	c	131	ASP
1	c	132	LYS
1	c	133	ASN
1	c	135	ASP
1	c	137	VAL
1	c	144	LEU
1	c	151	TYR
1	c	160	VAL
1	c	161	GLU
1	c	163	ILE
1	c	164	GLN
1	c	175	ARG
1	c	177	ARG
1	c	179	ARG
1	c	183	PHE
1	c	188	LYS
1	c	191	VAL
1	c	192	THR
1	c	197	LEU
1	c	199	ARG

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Mol	Chain	Res	Type
1	c	205	LEU
1	c	213	LEU
1	c	219	VAL
1	c	221	LEU
1	c	222	THR
1	c	227	LEU
1	c	230	ARG
1	c	234	ASN
1	c	238	LEU
1	c	242	LEU
1	c	249	TRP
1	c	253	VAL
1	c	257	GLU
1	c	266	GLU
1	c	267	VAL
1	c	268	LEU
1	c	271	VAL
1	c	276	LEU
1	c	284	ILE
1	c	286	ASP
1	c	296	LEU
1	c	299	LYS
1	c	301	VAL
1	c	308	PHE
1	c	310	LEU
1	c	320	ILE
1	c	322	ASP
1	c	334	LEU
1	c	335	LYS
1	c	341	GLU
1	c	342	GLU
1	c	345	SER
1	c	356	CYS
1	c	358	LEU
1	c	373	VAL
1	c	380	ILE
1	c	383	ASP
1	c	384	GLN
1	c	385	ASN
1	c	388	ILE
1	c	395	THR
1	c	407	MET

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Mol	Chain	Res	Type
1	c	417	LYS
1	c	418	GLU
1	c	456	ARG
1	c	474	ARG
1	c	479	ARG
1	c	486	LEU
1	c	487	VAL
1	c	490	ASP
1	c	496	THR
1	c	516	LEU
1	c	517	LEU
1	c	518	LEU
1	c	523	PHE
1	c	524	THR
1	c	528	THR
1	c	533	ASP
1	c	536	ARG
1	c	549	LEU
1	c	552	ARG
1	c	580	ARG
1	c	587	THR
1	c	595	SER
1	c	621	LYS
1	c	642	SER
1	c	648	GLN
1	c	654	LEU
1	c	666	THR
1	c	668	SER
1	c	683	GLU
1	c	690	ARG
1	c	692	LYS
1	c	706	LEU
1	c	721	ASN
1	c	729	ARG
1	c	747	LYS
1	c	755	THR
1	c	770	LEU
1	c	778	GLU
1	c	779	LEU
1	c	787	LEU
1	c	793	LYS
1	c	806	THR

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Mol	Chain	Res	Type
1	c	808	ARG
1	c	809	ASP
1	d	1	MET
1	d	3	THR
1	d	18	VAL
1	d	33	LYS
1	d	35	TYR
1	d	36	ILE
1	d	38	GLN
1	d	41	GLU
1	d	50	MET
1	d	57	HIS
1	d	60	ILE
1	d	63	ASN
1	d	65	VAL
1	d	70	GLN
1	d	74	LEU
1	d	75	PHE
1	d	82	ARG
1	d	83	LEU
1	d	84	ARG
1	d	106	GLU
1	d	108	ASP
1	d	114	VAL
1	d	115	VAL
1	d	118	ASN
1	d	119	THR
1	d	127	LEU
1	d	131	ASP
1	d	132	LYS
1	d	133	ASN
1	d	144	LEU
1	d	151	TYR
1	d	152	ILE
1	d	156	GLU
1	d	158	GLU
1	d	160	VAL
1	d	161	GLU
1	d	167	VAL
1	d	175	ARG
1	d	177	ARG
1	d	183	PHE

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Mol	Chain	Res	Type
1	d	192	THR
1	d	197	LEU
1	d	199	ARG
1	d	201	VAL
1	d	205	LEU
1	d	213	LEU
1	d	221	LEU
1	d	222	THR
1	d	225	THR
1	d	227	LEU
1	d	230	ARG
1	d	236	ARG
1	d	238	LEU
1	d	242	LEU
1	d	245	THR
1	d	249	TRP
1	d	253	VAL
1	d	257	GLU
1	d	259	HIS
1	d	262	ASP
1	d	266	GLU
1	d	268	LEU
1	d	271	VAL
1	d	276	LEU
1	d	284	ILE
1	d	286	ASP
1	d	293	LYS
1	d	296	LEU
1	d	301	VAL
1	d	308	PHE
1	d	320	ILE
1	d	322	ASP
1	d	328	GLU
1	d	334	LEU
1	d	341	GLU
1	d	342	GLU
1	d	356	CYS
1	d	358	LEU
1	d	359	ILE
1	d	363	LEU
1	d	373	VAL
1	d	383	ASP

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Mol	Chain	Res	Type
1	d	384	GLN
1	d	385	ASN
1	d	407	MET
1	d	417	LYS
1	d	418	GLU
1	d	474	ARG
1	d	479	ARG
1	d	486	LEU
1	d	487	VAL
1	d	490	ASP
1	d	496	THR
1	d	497	VAL
1	d	504	ARG
1	d	507	ARG
1	d	516	LEU
1	d	517	LEU
1	d	518	LEU
1	d	523	PHE
1	d	529	ILE
1	d	533	ASP
1	d	536	ARG
1	d	549	LEU
1	d	580	ARG
1	d	587	THR
1	d	595	SER
1	d	604	PHE
1	d	621	LYS
1	d	648	GLN
1	d	666	THR
1	d	668	SER
1	d	683	GLU
1	d	693	ILE
1	d	706	LEU
1	d	755	THR
1	d	770	LEU
1	d	779	LEU
1	d	785	GLN
1	d	793	LYS
1	d	806	THR
1	e	1	MET
1	e	3	THR
1	e	18	VAL

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Mol	Chain	Res	Type
1	e	35	TYR
1	e	36	ILE
1	e	38	GLN
1	e	41	GLU
1	e	50	MET
1	e	52	THR
1	e	56	ARG
1	e	60	ILE
1	e	61	VAL
1	e	65	VAL
1	e	70	GLN
1	e	74	LEU
1	e	75	PHE
1	e	83	LEU
1	e	84	ARG
1	e	90	ILE
1	e	95	ASP
1	e	106	GLU
1	e	108	ASP
1	e	110	THR
1	e	114	VAL
1	e	119	THR
1	e	124	LYS
1	e	127	LEU
1	e	131	ASP
1	e	132	LYS
1	e	133	ASN
1	e	135	ASP
1	e	144	LEU
1	e	151	TYR
1	e	156	GLU
1	e	160	VAL
1	e	161	GLU
1	e	163	ILE
1	e	169	LYS
1	e	175	ARG
1	e	177	ARG
1	e	183	PHE
1	e	192	THR
1	e	197	LEU
1	e	199	ARG
1	e	201	VAL

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Mol	Chain	Res	Type
1	e	205	LEU
1	e	208	VAL
1	e	213	LEU
1	e	221	LEU
1	e	222	THR
1	e	225	THR
1	e	227	LEU
1	e	230	ARG
1	e	242	LEU
1	e	245	THR
1	e	249	TRP
1	e	250	LEU
1	e	253	VAL
1	e	257	GLU
1	e	259	HIS
1	e	266	GLU
1	e	268	LEU
1	e	271	VAL
1	e	276	LEU
1	e	281	TYR
1	e	284	ILE
1	e	286	ASP
1	e	295	GLN
1	e	296	LEU
1	e	301	VAL
1	e	308	PHE
1	e	320	ILE
1	e	322	ASP
1	e	335	LYS
1	e	341	GLU
1	e	342	GLU
1	e	345	SER
1	e	347	GLU
1	e	356	CYS
1	e	358	LEU
1	e	359	ILE
1	e	363	LEU
1	e	373	VAL
1	e	383	ASP
1	e	384	GLN
1	e	385	ASN
1	e	407	MET

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Mol	Chain	Res	Type
1	e	417	LYS
1	e	418	GLU
1	e	420	PRO
1	e	421	SER
1	e	452	ARG
1	e	474	ARG
1	e	479	ARG
1	e	486	LEU
1	e	487	VAL
1	e	490	ASP
1	e	516	LEU
1	e	517	LEU
1	e	518	LEU
1	e	523	PHE
1	e	528	THR
1	e	533	ASP
1	e	549	LEU
1	e	580	ARG
1	e	587	THR
1	e	599	ILE
1	e	601	MET
1	e	621	LYS
1	e	654	LEU
1	e	666	THR
1	e	683	GLU
1	e	689	GLU
1	e	692	LYS
1	e	693	ILE
1	e	721	ASN
1	e	742	LEU
1	e	755	THR
1	e	756	GLU
1	e	770	LEU
1	e	778	GLU
1	e	779	LEU
1	e	787	LEU
1	e	793	LYS
1	e	802	LEU
1	e	806	THR
1	e	807	ILE
1	e	809	ASP
1	e	810	LEU

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Mol	Chain	Res	Type
1	f	1	MET
1	f	3	THR
1	f	18	VAL
1	f	23	SER
1	f	33	LYS
1	f	35	TYR
1	f	36	ILE
1	f	38	GLN
1	f	50	MET
1	f	57	HIS
1	f	60	ILE
1	f	61	VAL
1	f	65	VAL
1	f	70	GLN
1	f	74	LEU
1	f	83	LEU
1	f	84	ARG
1	f	90	ILE
1	f	106	GLU
1	f	108	ASP
1	f	114	VAL
1	f	115	VAL
1	f	119	THR
1	f	127	LEU
1	f	131	ASP
1	f	132	LYS
1	f	133	ASN
1	f	135	ASP
1	f	137	VAL
1	f	138	MET
1	f	144	LEU
1	f	145	PHE
1	f	151	TYR
1	f	152	ILE
1	f	155	LYS
1	f	156	GLU
1	f	158	GLU
1	f	160	VAL
1	f	161	GLU
1	f	163	ILE
1	f	175	ARG
1	f	177	ARG

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Mol	Chain	Res	Type
1	f	192	THR
1	f	197	LEU
1	f	199	ARG
1	f	205	LEU
1	f	213	LEU
1	f	217	ASP
1	f	221	LEU
1	f	222	THR
1	f	225	THR
1	f	230	ARG
1	f	234	ASN
1	f	236	ARG
1	f	238	LEU
1	f	242	LEU
1	f	249	TRP
1	f	253	VAL
1	f	254	GLN
1	f	257	GLU
1	f	266	GLU
1	f	268	LEU
1	f	271	VAL
1	f	276	LEU
1	f	284	ILE
1	f	286	ASP
1	f	296	LEU
1	f	301	VAL
1	f	308	PHE
1	f	310	LEU
1	f	318	ARG
1	f	321	GLN
1	f	322	ASP
1	f	327	SER
1	f	334	LEU
1	f	335	LYS
1	f	337	LEU
1	f	340	LEU
1	f	341	GLU
1	f	342	GLU
1	f	347	GLU
1	f	358	LEU
1	f	359	ILE
1	f	363	LEU

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Mol	Chain	Res	Type
1	f	373	VAL
1	f	380	ILE
1	f	383	ASP
1	f	384	GLN
1	f	385	ASN
1	f	388	ILE
1	f	407	MET
1	f	417	LYS
1	f	418	GLU
1	f	452	ARG
1	f	456	ARG
1	f	474	ARG
1	f	479	ARG
1	f	486	LEU
1	f	487	VAL
1	f	490	ASP
1	f	496	THR
1	f	501	SER
1	f	516	LEU
1	f	517	LEU
1	f	518	LEU
1	f	539	LEU
1	f	549	LEU
1	f	580	ARG
1	f	587	THR
1	f	595	SER
1	f	621	LYS
1	f	642	SER
1	f	658	VAL
1	f	666	THR
1	f	683	GLU
1	f	692	LYS
1	f	698	GLU
1	f	706	LEU
1	f	742	LEU
1	f	755	THR
1	f	770	LEU
1	f	779	LEU
1	f	790	VAL
1	f	793	LYS
1	f	799	THR
1	f	802	LEU

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Mol	Chain	Res	Type
1	f	806	THR
1	g	1	MET
1	g	3	THR
1	g	13	TYR
1	g	18	VAL
1	g	33	LYS
1	g	36	ILE
1	g	38	GLN
1	g	50	MET
1	g	52	THR
1	g	57	HIS
1	g	60	ILE
1	g	63	ASN
1	g	65	VAL
1	g	70	GLN
1	g	74	LEU
1	g	75	PHE
1	g	83	LEU
1	g	84	ARG
1	g	90	ILE
1	g	95	ASP
1	g	106	GLU
1	g	108	ASP
1	g	114	VAL
1	g	119	THR
1	g	127	LEU
1	g	131	ASP
1	g	135	ASP
1	g	137	VAL
1	g	144	LEU
1	g	145	PHE
1	g	151	TYR
1	g	152	ILE
1	g	156	GLU
1	g	160	VAL
1	g	161	GLU
1	g	166	THR
1	g	174	LEU
1	g	175	ARG
1	g	177	ARG
1	g	183	PHE
1	g	191	VAL

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Mol	Chain	Res	Type
1	g	192	THR
1	g	197	LEU
1	g	199	ARG
1	g	204	TYR
1	g	205	LEU
1	g	213	LEU
1	g	221	LEU
1	g	222	THR
1	g	225	THR
1	g	227	LEU
1	g	230	ARG
1	g	234	ASN
1	g	236	ARG
1	g	238	LEU
1	g	242	LEU
1	g	249	TRP
1	g	253	VAL
1	g	257	GLU
1	g	259	HIS
1	g	262	ASP
1	g	266	GLU
1	g	268	LEU
1	g	271	VAL
1	g	275	THR
1	g	276	LEU
1	g	281	TYR
1	g	284	ILE
1	g	286	ASP
1	g	293	LYS
1	g	296	LEU
1	g	299	LYS
1	g	301	VAL
1	g	308	PHE
1	g	318	ARG
1	g	320	ILE
1	g	321	GLN
1	g	322	ASP
1	g	335	LYS
1	g	340	LEU
1	g	341	GLU
1	g	342	GLU
1	g	358	LEU

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Mol	Chain	Res	Type
1	g	359	ILE
1	g	363	LEU
1	g	373	VAL
1	g	380	ILE
1	g	383	ASP
1	g	385	ASN
1	g	388	ILE
1	g	395	THR
1	g	407	MET
1	g	417	LYS
1	g	474	ARG
1	g	476	LYS
1	g	479	ARG
1	g	486	LEU
1	g	487	VAL
1	g	490	ASP
1	g	496	THR
1	g	516	LEU
1	g	517	LEU
1	g	518	LEU
1	g	522	PHE
1	g	523	PHE
1	g	533	ASP
1	g	536	ARG
1	g	539	LEU
1	g	549	LEU
1	g	580	ARG
1	g	587	THR
1	g	595	SER
1	g	621	LYS
1	g	625	GLN
1	g	648	GLN
1	g	654	LEU
1	g	658	VAL
1	g	666	THR
1	g	668	SER
1	g	683	GLU
1	g	690	ARG
1	g	693	ILE
1	g	742	LEU
1	g	760	GLU
1	g	770	LEU

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Mol	Chain	Res	Type
1	g	779	LEU
1	g	790	VAL
1	g	793	LYS
1	g	799	THR
1	g	802	LEU
1	h	1	MET
1	h	3	THR
1	h	18	VAL
1	h	33	LYS
1	h	35	TYR
1	h	36	ILE
1	h	38	GLN
1	h	42	ARG
1	h	50	MET
1	h	52	THR
1	h	60	ILE
1	h	61	VAL
1	h	63	ASN
1	h	65	VAL
1	h	70	GLN
1	h	74	LEU
1	h	82	ARG
1	h	83	LEU
1	h	90	ILE
1	h	95	ASP
1	h	106	GLU
1	h	114	VAL
1	h	119	THR
1	h	127	LEU
1	h	131	ASP
1	h	132	LYS
1	h	133	ASN
1	h	135	ASP
1	h	138	MET
1	h	144	LEU
1	h	145	PHE
1	h	151	TYR
1	h	152	ILE
1	h	158	GLU
1	h	160	VAL
1	h	161	GLU
1	h	163	ILE

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Mol	Chain	Res	Type
1	h	166	THR
1	h	175	ARG
1	h	177	ARG
1	h	183	PHE
1	h	191	VAL
1	h	192	THR
1	h	197	LEU
1	h	199	ARG
1	h	204	TYR
1	h	205	LEU
1	h	213	LEU
1	h	221	LEU
1	h	222	THR
1	h	225	THR
1	h	227	LEU
1	h	230	ARG
1	h	234	ASN
1	h	236	ARG
1	h	238	LEU
1	h	242	LEU
1	h	249	TRP
1	h	250	LEU
1	h	253	VAL
1	h	257	GLU
1	h	266	GLU
1	h	268	LEU
1	h	276	LEU
1	h	281	TYR
1	h	284	ILE
1	h	286	ASP
1	h	296	LEU
1	h	301	VAL
1	h	306	LYS
1	h	308	PHE
1	h	310	LEU
1	h	320	ILE
1	h	322	ASP
1	h	330	GLN
1	h	334	LEU
1	h	335	LYS
1	h	341	GLU
1	h	342	GLU

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Mol	Chain	Res	Type
1	h	345	SER
1	h	347	GLU
1	h	358	LEU
1	h	359	ILE
1	h	360	ARG
1	h	363	LEU
1	h	373	VAL
1	h	380	ILE
1	h	384	GLN
1	h	385	ASN
1	h	407	MET
1	h	417	LYS
1	h	474	ARG
1	h	479	ARG
1	h	486	LEU
1	h	487	VAL
1	h	490	ASP
1	h	496	THR
1	h	507	ARG
1	h	516	LEU
1	h	517	LEU
1	h	518	LEU
1	h	522	PHE
1	h	523	PHE
1	h	536	ARG
1	h	549	LEU
1	h	580	ARG
1	h	585	SER
1	h	587	THR
1	h	595	SER
1	h	621	LYS
1	h	625	GLN
1	h	648	GLN
1	h	662	ILE
1	h	666	THR
1	h	668	SER
1	h	683	GLU
1	h	688	LEU
1	h	690	ARG
1	h	706	LEU
1	h	747	LYS
1	h	755	THR

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Mol	Chain	Res	Type
1	h	760	GLU
1	h	769	GLU
1	h	770	LEU
1	h	779	LEU
1	h	793	LYS
1	h	794	LYS
1	h	802	LEU
1	i	1	MET
1	i	3	THR
1	i	18	VAL
1	i	36	ILE
1	i	38	GLN
1	i	50	MET
1	i	60	ILE
1	i	61	VAL
1	i	63	ASN
1	i	65	VAL
1	i	70	GLN
1	i	74	LEU
1	i	80	GLN
1	i	83	LEU
1	i	84	ARG
1	i	95	ASP
1	i	106	GLU
1	i	108	ASP
1	i	110	THR
1	i	119	THR
1	i	127	LEU
1	i	131	ASP
1	i	132	LYS
1	i	133	ASN
1	i	137	VAL
1	i	144	LEU
1	i	145	PHE
1	i	151	TYR
1	i	152	ILE
1	i	156	GLU
1	i	158	GLU
1	i	160	VAL
1	i	161	GLU
1	i	163	ILE
1	i	167	VAL

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Mol	Chain	Res	Type
1	i	174	LEU
1	i	175	ARG
1	i	177	ARG
1	i	183	PHE
1	i	192	THR
1	i	196	TRP
1	i	197	LEU
1	i	199	ARG
1	i	201	VAL
1	i	205	LEU
1	i	213	LEU
1	i	221	LEU
1	i	222	THR
1	i	225	THR
1	i	227	LEU
1	i	230	ARG
1	i	234	ASN
1	i	236	ARG
1	i	238	LEU
1	i	242	LEU
1	i	249	TRP
1	i	253	VAL
1	i	257	GLU
1	i	259	HIS
1	i	266	GLU
1	i	268	LEU
1	i	271	VAL
1	i	276	LEU
1	i	281	TYR
1	i	284	ILE
1	i	286	ASP
1	i	295	GLN
1	i	296	LEU
1	i	301	VAL
1	i	308	PHE
1	i	310	LEU
1	i	318	ARG
1	i	320	ILE
1	i	322	ASP
1	i	330	GLN
1	i	332	LEU
1	i	335	LYS

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Mol	Chain	Res	Type
1	i	340	LEU
1	i	341	GLU
1	i	342	GLU
1	i	345	SER
1	i	347	GLU
1	i	356	CYS
1	i	358	LEU
1	i	359	ILE
1	i	363	LEU
1	i	380	ILE
1	i	383	ASP
1	i	384	GLN
1	i	385	ASN
1	i	388	ILE
1	i	393	VAL
1	i	407	MET
1	i	417	LYS
1	i	474	ARG
1	i	479	ARG
1	i	486	LEU
1	i	487	VAL
1	i	496	THR
1	i	516	LEU
1	i	517	LEU
1	i	518	LEU
1	i	533	ASP
1	i	536	ARG
1	i	539	LEU
1	i	543	TYR
1	i	549	LEU
1	i	580	ARG
1	i	587	THR
1	i	595	SER
1	i	621	LYS
1	i	625	GLN
1	i	633	LEU
1	i	648	GLN
1	i	654	LEU
1	i	666	THR
1	i	668	SER
1	i	683	GLU
1	i	698	GLU

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Mol	Chain	Res	Type
1	i	706	LEU
1	i	721	ASN
1	i	755	THR
1	i	761	ARG
1	i	766	ARG
1	i	770	LEU
1	i	779	LEU
1	i	790	VAL
1	i	793	LYS
1	i	794	LYS
1	i	802	LEU
1	j	1	MET
1	j	3	THR
1	j	8	ILE
1	j	18	VAL
1	j	33	LYS
1	j	35	TYR
1	j	36	ILE
1	j	38	GLN
1	j	50	MET
1	j	52	THR
1	j	60	ILE
1	j	65	VAL
1	j	70	GLN
1	j	74	LEU
1	j	75	PHE
1	j	83	LEU
1	j	84	ARG
1	j	104	VAL
1	j	106	GLU
1	j	107	LYS
1	j	108	ASP
1	j	114	VAL
1	j	119	THR
1	j	127	LEU
1	j	131	ASP
1	j	133	ASN
1	j	137	VAL
1	j	144	LEU
1	j	145	PHE
1	j	151	TYR
1	j	152	ILE

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Mol	Chain	Res	Type
1	j	158	GLU
1	j	160	VAL
1	j	161	GLU
1	j	163	ILE
1	j	167	VAL
1	j	174	LEU
1	j	175	ARG
1	j	177	ARG
1	j	179	ARG
1	j	183	PHE
1	j	192	THR
1	j	196	TRP
1	j	197	LEU
1	j	199	ARG
1	j	201	VAL
1	j	204	TYR
1	j	205	LEU
1	j	209	PHE
1	j	213	LEU
1	j	222	THR
1	j	225	THR
1	j	227	LEU
1	j	230	ARG
1	j	234	ASN
1	j	238	LEU
1	j	242	LEU
1	j	253	VAL
1	j	257	GLU
1	j	259	HIS
1	j	266	GLU
1	j	267	VAL
1	j	268	LEU
1	j	271	VAL
1	j	276	LEU
1	j	286	ASP
1	j	296	LEU
1	j	301	VAL
1	j	302	VAL
1	j	307	SER
1	j	308	PHE
1	j	310	LEU
1	j	315	ARG

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Mol	Chain	Res	Type
1	j	320	ILE
1	j	322	ASP
1	j	335	LYS
1	j	341	GLU
1	j	342	GLU
1	j	358	LEU
1	j	359	ILE
1	j	363	LEU
1	j	380	ILE
1	j	383	ASP
1	j	384	GLN
1	j	385	ASN
1	j	395	THR
1	j	407	MET
1	j	417	LYS
1	j	474	ARG
1	j	479	ARG
1	j	486	LEU
1	j	487	VAL
1	j	496	THR
1	j	516	LEU
1	j	517	LEU
1	j	533	ASP
1	j	536	ARG
1	j	549	LEU
1	j	561	LEU
1	j	580	ARG
1	j	587	THR
1	j	595	SER
1	j	621	LYS
1	j	625	GLN
1	j	648	GLN
1	j	666	THR
1	j	668	SER
1	j	685	ARG
1	j	688	LEU
1	j	690	ARG
1	j	692	LYS
1	j	698	GLU
1	j	706	LEU
1	j	742	LEU
1	j	747	LYS

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Mol	Chain	Res	Type
1	j	755	THR
1	j	768	MET
1	j	770	LEU
1	j	778	GLU
1	j	779	LEU
1	j	793	LYS
1	j	794	LYS
1	j	802	LEU
1	k	1	MET
1	k	3	THR
1	k	7	ILE
1	k	8	ILE
1	k	18	VAL
1	k	35	TYR
1	k	36	ILE
1	k	38	GLN
1	k	50	MET
1	k	58	TYR
1	k	60	ILE
1	k	61	VAL
1	k	65	VAL
1	k	70	GLN
1	k	74	LEU
1	k	75	PHE
1	k	83	LEU
1	k	90	ILE
1	k	104	VAL
1	k	108	ASP
1	k	110	THR
1	k	114	VAL
1	k	118	ASN
1	k	119	THR
1	k	124	LYS
1	k	127	LEU
1	k	131	ASP
1	k	132	LYS
1	k	133	ASN
1	k	135	ASP
1	k	138	MET
1	k	144	LEU
1	k	145	PHE
1	k	151	TYR

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Mol	Chain	Res	Type
1	k	152	ILE
1	k	156	GLU
1	k	158	GLU
1	k	160	VAL
1	k	161	GLU
1	k	163	ILE
1	k	167	VAL
1	k	174	LEU
1	k	175	ARG
1	k	177	ARG
1	k	192	THR
1	k	197	LEU
1	k	199	ARG
1	k	201	VAL
1	k	205	LEU
1	k	213	LEU
1	k	221	LEU
1	k	222	THR
1	k	225	THR
1	k	227	LEU
1	k	230	ARG
1	k	238	LEU
1	k	242	LEU
1	k	249	TRP
1	k	250	LEU
1	k	253	VAL
1	k	257	GLU
1	k	259	HIS
1	k	262	ASP
1	k	266	GLU
1	k	267	VAL
1	k	268	LEU
1	k	271	VAL
1	k	276	LEU
1	k	286	ASP
1	k	295	GLN
1	k	296	LEU
1	k	299	LYS
1	k	301	VAL
1	k	307	SER
1	k	308	PHE
1	k	320	ILE

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Mol	Chain	Res	Type
1	k	322	ASP
1	k	328	GLU
1	k	335	LYS
1	k	340	LEU
1	k	341	GLU
1	k	342	GLU
1	k	356	CYS
1	k	358	LEU
1	k	363	LEU
1	k	373	VAL
1	k	380	ILE
1	k	383	ASP
1	k	384	GLN
1	k	385	ASN
1	k	402	ILE
1	k	407	MET
1	k	417	LYS
1	k	424	GLU
1	k	449	SER
1	k	474	ARG
1	k	479	ARG
1	k	486	LEU
1	k	487	VAL
1	k	490	ASP
1	k	495	PHE
1	k	496	THR
1	k	501	SER
1	k	516	LEU
1	k	517	LEU
1	k	518	LEU
1	k	533	ASP
1	k	536	ARG
1	k	549	LEU
1	k	580	ARG
1	k	587	THR
1	k	595	SER
1	k	621	LYS
1	k	625	GLN
1	k	648	GLN
1	k	654	LEU
1	k	666	THR
1	k	668	SER

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Mol	Chain	Res	Type
1	k	679	ARG
1	k	692	LYS
1	k	706	LEU
1	k	729	ARG
1	k	747	LYS
1	k	755	THR
1	k	765	VAL
1	k	770	LEU
1	k	779	LEU
1	k	787	LEU
1	k	793	LYS
1	k	794	LYS
1	k	802	LEU
1	k	810	LEU
1	l	1	MET
1	l	3	THR
1	l	8	ILE
1	l	18	VAL
1	l	35	TYR
1	l	36	ILE
1	l	38	GLN
1	l	41	GLU
1	l	50	MET
1	l	57	HIS
1	l	60	ILE
1	l	61	VAL
1	l	70	GLN
1	l	74	LEU
1	l	75	PHE
1	l	83	LEU
1	l	84	ARG
1	l	104	VAL
1	l	110	THR
1	l	114	VAL
1	l	119	THR
1	l	127	LEU
1	l	131	ASP
1	l	133	ASN
1	l	135	ASP
1	l	137	VAL
1	l	138	MET
1	l	141	ASP

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Mol	Chain	Res	Type
1	1	144	LEU
1	1	152	ILE
1	1	160	VAL
1	1	161	GLU
1	1	163	ILE
1	1	168	ILE
1	1	174	LEU
1	1	175	ARG
1	1	177	ARG
1	1	183	PHE
1	1	191	VAL
1	1	197	LEU
1	1	199	ARG
1	1	201	VAL
1	1	205	LEU
1	1	208	VAL
1	1	213	LEU
1	1	221	LEU
1	1	222	THR
1	1	227	LEU
1	1	230	ARG
1	1	238	LEU
1	1	242	LEU
1	1	249	TRP
1	1	250	LEU
1	1	253	VAL
1	1	254	GLN
1	1	257	GLU
1	1	266	GLU
1	1	268	LEU
1	1	271	VAL
1	1	276	LEU
1	1	286	ASP
1	1	295	GLN
1	1	296	LEU
1	1	301	VAL
1	1	308	PHE
1	1	320	ILE
1	1	322	ASP
1	1	328	GLU
1	1	334	LEU
1	1	335	LYS

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Mol	Chain	Res	Type
1	1	341	GLU
1	1	342	GLU
1	1	347	GLU
1	1	356	CYS
1	1	358	LEU
1	1	359	ILE
1	1	363	LEU
1	1	380	ILE
1	1	383	ASP
1	1	384	GLN
1	1	385	ASN
1	1	395	THR
1	1	407	MET
1	1	424	GLU
1	1	425	GLU
1	1	474	ARG
1	1	479	ARG
1	1	486	LEU
1	1	487	VAL
1	1	496	THR
1	1	516	LEU
1	1	517	LEU
1	1	523	PHE
1	1	533	ASP
1	1	536	ARG
1	1	549	LEU
1	1	580	ARG
1	1	587	THR
1	1	595	SER
1	1	621	LYS
1	1	633	LEU
1	1	648	GLN
1	1	651	ARG
1	1	654	LEU
1	1	666	THR
1	1	668	SER
1	1	683	GLU
1	1	698	GLU
1	1	706	LEU
1	1	742	LEU
1	1	747	LYS
1	1	755	THR

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Mol	Chain	Res	Type
1	l	765	VAL
1	l	766	ARG
1	l	770	LEU
1	l	779	LEU
1	l	793	LYS
1	l	794	LYS
1	l	798	MET
1	l	802	LEU
1	l	808	ARG
1	l	809	ASP
1	m	1	MET
1	m	3	THR
1	m	8	ILE
1	m	18	VAL
1	m	23	SER
1	m	33	LYS
1	m	35	TYR
1	m	36	ILE
1	m	38	GLN
1	m	50	MET
1	m	57	HIS
1	m	60	ILE
1	m	61	VAL
1	m	63	ASN
1	m	70	GLN
1	m	74	LEU
1	m	75	PHE
1	m	83	LEU
1	m	90	ILE
1	m	95	ASP
1	m	110	THR
1	m	114	VAL
1	m	119	THR
1	m	127	LEU
1	m	131	ASP
1	m	133	ASN
1	m	135	ASP
1	m	137	VAL
1	m	144	LEU
1	m	151	TYR
1	m	152	ILE
1	m	160	VAL

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Mol	Chain	Res	Type
1	m	161	GLU
1	m	163	ILE
1	m	166	THR
1	m	174	LEU
1	m	175	ARG
1	m	177	ARG
1	m	183	PHE
1	m	196	TRP
1	m	197	LEU
1	m	205	LEU
1	m	213	LEU
1	m	217	ASP
1	m	219	VAL
1	m	222	THR
1	m	230	ARG
1	m	234	ASN
1	m	238	LEU
1	m	242	LEU
1	m	249	TRP
1	m	250	LEU
1	m	253	VAL
1	m	254	GLN
1	m	257	GLU
1	m	266	GLU
1	m	267	VAL
1	m	268	LEU
1	m	271	VAL
1	m	274	THR
1	m	276	LEU
1	m	286	ASP
1	m	296	LEU
1	m	302	VAL
1	m	308	PHE
1	m	320	ILE
1	m	322	ASP
1	m	328	GLU
1	m	334	LEU
1	m	341	GLU
1	m	342	GLU
1	m	347	GLU
1	m	356	CYS
1	m	358	LEU

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Mol	Chain	Res	Type
1	m	359	ILE
1	m	363	LEU
1	m	384	GLN
1	m	385	ASN
1	m	388	ILE
1	m	402	ILE
1	m	407	MET
1	m	417	LYS
1	m	420	PRO
1	m	456	ARG
1	m	474	ARG
1	m	479	ARG
1	m	481	VAL
1	m	486	LEU
1	m	487	VAL
1	m	490	ASP
1	m	496	THR
1	m	501	SER
1	m	512	ARG
1	m	516	LEU
1	m	517	LEU
1	m	518	LEU
1	m	523	PHE
1	m	533	ASP
1	m	536	ARG
1	m	549	LEU
1	m	580	ARG
1	m	585	SER
1	m	587	THR
1	m	621	LYS
1	m	625	GLN
1	m	648	GLN
1	m	651	ARG
1	m	666	THR
1	m	668	SER
1	m	683	GLU
1	m	706	LEU
1	m	747	LYS
1	m	755	THR
1	m	769	GLU
1	m	770	LEU
1	m	778	GLU

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Mol	Chain	Res	Type
1	m	779	LEU
1	m	782	SER
1	m	793	LYS
1	m	794	LYS
1	m	806	THR
1	m	810	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (645) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	22	ASN
1	A	24	ASN
1	A	40	ASN
1	A	70	GLN
1	A	118	ASN
1	A	122	HIS
1	A	164	GLN
1	A	234	ASN
1	A	254	GLN
1	A	280	HIS
1	A	509	HIS
1	A	534	HIS
1	A	648	GLN
1	A	696	GLN
1	A	776	GLN
1	B	17	HIS
1	B	22	ASN
1	B	24	ASN
1	B	40	ASN
1	B	70	GLN
1	B	118	ASN
1	B	234	ASN
1	B	254	GLN
1	B	329	GLN
1	B	384	GLN
1	B	385	ASN
1	B	494	GLN
1	B	509	HIS
1	B	534	HIS
1	B	538	GLN
1	B	648	GLN
1	B	691	GLN

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Mol	Chain	Res	Type
1	B	696	GLN
1	B	776	GLN
1	C	17	HIS
1	C	22	ASN
1	C	24	ASN
1	C	40	ASN
1	C	118	ASN
1	C	234	ASN
1	C	254	GLN
1	C	280	HIS
1	C	385	ASN
1	C	494	GLN
1	C	509	HIS
1	C	534	HIS
1	C	630	GLN
1	C	691	GLN
1	D	22	ASN
1	D	24	ASN
1	D	40	ASN
1	D	118	ASN
1	D	254	GLN
1	D	280	HIS
1	D	294	ASN
1	D	298	GLN
1	D	385	ASN
1	D	509	HIS
1	D	630	GLN
1	D	648	GLN
1	D	691	GLN
1	D	696	GLN
1	E	17	HIS
1	E	21	GLN
1	E	22	ASN
1	E	24	ASN
1	E	40	ASN
1	E	118	ASN
1	E	133	ASN
1	E	234	ASN
1	E	254	GLN
1	E	298	GLN
1	E	329	GLN
1	E	378	GLN

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Mol	Chain	Res	Type
1	E	385	ASN
1	E	494	GLN
1	E	509	HIS
1	E	648	GLN
1	F	17	HIS
1	F	21	GLN
1	F	22	ASN
1	F	24	ASN
1	F	40	ASN
1	F	70	GLN
1	F	118	ASN
1	F	234	ASN
1	F	254	GLN
1	F	294	ASN
1	F	298	GLN
1	F	311	GLN
1	F	494	GLN
1	F	509	HIS
1	F	630	GLN
1	F	696	GLN
1	G	17	HIS
1	G	21	GLN
1	G	22	ASN
1	G	40	ASN
1	G	70	GLN
1	G	118	ASN
1	G	234	ASN
1	G	254	GLN
1	G	294	ASN
1	G	494	GLN
1	G	509	HIS
1	G	538	GLN
1	G	648	GLN
1	G	691	GLN
1	G	696	GLN
1	H	17	HIS
1	H	22	ASN
1	H	24	ASN
1	H	40	ASN
1	H	118	ASN
1	H	234	ASN
1	H	254	GLN

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Mol	Chain	Res	Type
1	H	294	ASN
1	H	311	GLN
1	H	465	ASN
1	H	494	GLN
1	H	534	HIS
1	H	648	GLN
1	H	675	HIS
1	H	696	GLN
1	H	785	GLN
1	H	789	ASN
1	I	17	HIS
1	I	22	ASN
1	I	24	ASN
1	I	40	ASN
1	I	70	GLN
1	I	118	ASN
1	I	164	GLN
1	I	234	ASN
1	I	254	GLN
1	I	294	ASN
1	I	311	GLN
1	I	378	GLN
1	I	494	GLN
1	I	534	HIS
1	I	592	HIS
1	I	648	GLN
1	I	696	GLN
1	J	17	HIS
1	J	22	ASN
1	J	24	ASN
1	J	40	ASN
1	J	63	ASN
1	J	70	GLN
1	J	118	ASN
1	J	234	ASN
1	J	254	GLN
1	J	280	HIS
1	J	294	ASN
1	J	298	GLN
1	J	494	GLN
1	J	641	GLN
1	J	696	GLN

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Mol	Chain	Res	Type
1	K	22	ASN
1	K	24	ASN
1	K	40	ASN
1	K	118	ASN
1	K	170	GLN
1	K	234	ASN
1	K	254	GLN
1	K	280	HIS
1	K	321	GLN
1	K	352	GLN
1	K	494	GLN
1	K	509	HIS
1	K	534	HIS
1	K	659	GLN
1	K	696	GLN
1	K	785	GLN
1	L	17	HIS
1	L	21	GLN
1	L	22	ASN
1	L	24	ASN
1	L	40	ASN
1	L	85	HIS
1	L	118	ASN
1	L	122	HIS
1	L	234	ASN
1	L	254	GLN
1	L	294	ASN
1	L	378	GLN
1	L	385	ASN
1	L	494	GLN
1	L	534	HIS
1	L	641	GLN
1	L	696	GLN
1	L	776	GLN
1	L	785	GLN
1	M	17	HIS
1	M	21	GLN
1	M	22	ASN
1	M	24	ASN
1	M	40	ASN
1	M	70	GLN
1	M	118	ASN

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Mol	Chain	Res	Type
1	M	122	HIS
1	M	164	GLN
1	M	234	ASN
1	M	254	GLN
1	M	280	HIS
1	M	294	ASN
1	M	311	GLN
1	M	384	GLN
1	M	385	ASN
1	M	494	GLN
1	M	509	HIS
1	M	696	GLN
1	N	17	HIS
1	N	22	ASN
1	N	24	ASN
1	N	40	ASN
1	N	63	ASN
1	N	70	GLN
1	N	118	ASN
1	N	164	GLN
1	N	234	ASN
1	N	254	GLN
1	N	280	HIS
1	N	294	ASN
1	N	329	GLN
1	N	384	GLN
1	N	385	ASN
1	N	494	GLN
1	N	648	GLN
1	N	696	GLN
1	O	22	ASN
1	O	24	ASN
1	O	40	ASN
1	O	63	ASN
1	O	118	ASN
1	O	133	ASN
1	O	234	ASN
1	O	254	GLN
1	O	280	HIS
1	O	385	ASN
1	O	494	GLN
1	O	509	HIS

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Mol	Chain	Res	Type
1	O	659	GLN
1	O	691	GLN
1	P	22	ASN
1	P	40	ASN
1	P	70	GLN
1	P	118	ASN
1	P	133	ASN
1	P	234	ASN
1	P	254	GLN
1	P	280	HIS
1	P	294	ASN
1	P	384	GLN
1	P	494	GLN
1	P	509	HIS
1	P	630	GLN
1	P	631	ASN
1	P	641	GLN
1	P	648	GLN
1	P	696	GLN
1	Q	17	HIS
1	Q	21	GLN
1	Q	22	ASN
1	Q	24	ASN
1	Q	40	ASN
1	Q	70	GLN
1	Q	118	ASN
1	Q	122	HIS
1	Q	133	ASN
1	Q	234	ASN
1	Q	254	GLN
1	Q	280	HIS
1	Q	294	ASN
1	Q	385	ASN
1	Q	464	HIS
1	Q	494	GLN
1	Q	509	HIS
1	Q	691	GLN
1	Q	696	GLN
1	Q	789	ASN
1	R	21	GLN
1	R	22	ASN
1	R	24	ASN

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Mol	Chain	Res	Type
1	R	40	ASN
1	R	63	ASN
1	R	118	ASN
1	R	133	ASN
1	R	234	ASN
1	R	254	GLN
1	R	294	ASN
1	R	378	GLN
1	R	385	ASN
1	R	494	GLN
1	R	509	HIS
1	R	630	GLN
1	R	648	GLN
1	R	696	GLN
1	R	749	GLN
1	R	776	GLN
1	S	22	ASN
1	S	40	ASN
1	S	70	GLN
1	S	118	ASN
1	S	164	GLN
1	S	234	ASN
1	S	254	GLN
1	S	294	ASN
1	S	311	GLN
1	S	384	GLN
1	S	385	ASN
1	S	494	GLN
1	S	509	HIS
1	S	648	GLN
1	S	696	GLN
1	S	789	ASN
1	T	17	HIS
1	T	22	ASN
1	T	24	ASN
1	T	40	ASN
1	T	70	GLN
1	T	118	ASN
1	T	254	GLN
1	T	294	ASN
1	T	321	GLN
1	T	378	GLN

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Mol	Chain	Res	Type
1	T	384	GLN
1	T	494	GLN
1	T	509	HIS
1	T	534	HIS
1	T	691	GLN
1	T	696	GLN
1	U	17	HIS
1	U	22	ASN
1	U	24	ASN
1	U	38	GLN
1	U	40	ASN
1	U	118	ASN
1	U	234	ASN
1	U	254	GLN
1	U	280	HIS
1	U	494	GLN
1	U	509	HIS
1	U	648	GLN
1	U	696	GLN
1	U	789	ASN
1	V	17	HIS
1	V	22	ASN
1	V	24	ASN
1	V	40	ASN
1	V	70	GLN
1	V	118	ASN
1	V	122	HIS
1	V	234	ASN
1	V	254	GLN
1	V	280	HIS
1	V	294	ASN
1	V	311	GLN
1	V	321	GLN
1	V	385	ASN
1	V	494	GLN
1	V	509	HIS
1	V	691	GLN
1	V	696	GLN
1	W	17	HIS
1	W	22	ASN
1	W	24	ASN
1	W	40	ASN

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Mol	Chain	Res	Type
1	W	70	GLN
1	W	118	ASN
1	W	122	HIS
1	W	234	ASN
1	W	254	GLN
1	W	294	ASN
1	W	321	GLN
1	W	384	GLN
1	W	494	GLN
1	W	509	HIS
1	W	648	GLN
1	W	691	GLN
1	W	696	GLN
1	W	789	ASN
1	X	17	HIS
1	X	21	GLN
1	X	22	ASN
1	X	24	ASN
1	X	40	ASN
1	X	118	ASN
1	X	234	ASN
1	X	254	GLN
1	X	280	HIS
1	X	298	GLN
1	X	385	ASN
1	X	494	GLN
1	X	509	HIS
1	X	691	GLN
1	X	696	GLN
1	Y	17	HIS
1	Y	21	GLN
1	Y	22	ASN
1	Y	40	ASN
1	Y	70	GLN
1	Y	118	ASN
1	Y	133	ASN
1	Y	234	ASN
1	Y	254	GLN
1	Y	280	HIS
1	Y	298	GLN
1	Y	384	GLN
1	Y	385	ASN

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Mol	Chain	Res	Type
1	Y	494	GLN
1	Y	509	HIS
1	Y	659	GLN
1	Y	696	GLN
1	Y	749	GLN
1	Z	17	HIS
1	Z	21	GLN
1	Z	22	ASN
1	Z	24	ASN
1	Z	40	ASN
1	Z	70	GLN
1	Z	118	ASN
1	Z	122	HIS
1	Z	164	GLN
1	Z	234	ASN
1	Z	254	GLN
1	Z	280	HIS
1	Z	294	ASN
1	Z	321	GLN
1	Z	494	GLN
1	Z	648	GLN
1	a	21	GLN
1	a	22	ASN
1	a	70	GLN
1	a	118	ASN
1	a	122	HIS
1	a	164	GLN
1	a	234	ASN
1	a	254	GLN
1	a	294	ASN
1	a	321	GLN
1	a	329	GLN
1	a	338	GLN
1	a	385	ASN
1	a	494	GLN
1	a	509	HIS
1	a	696	GLN
1	b	22	ASN
1	b	40	ASN
1	b	118	ASN
1	b	122	HIS
1	b	133	ASN

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Mol	Chain	Res	Type
1	b	164	GLN
1	b	234	ASN
1	b	254	GLN
1	b	280	HIS
1	b	321	GLN
1	b	329	GLN
1	b	494	GLN
1	b	630	GLN
1	b	648	GLN
1	b	696	GLN
1	b	789	ASN
1	c	17	HIS
1	c	21	GLN
1	c	22	ASN
1	c	24	ASN
1	c	40	ASN
1	c	70	GLN
1	c	118	ASN
1	c	122	HIS
1	c	164	GLN
1	c	234	ASN
1	c	254	GLN
1	c	280	HIS
1	c	298	GLN
1	c	378	GLN
1	c	385	ASN
1	c	494	GLN
1	c	509	HIS
1	c	648	GLN
1	c	659	GLN
1	c	696	GLN
1	d	21	GLN
1	d	22	ASN
1	d	24	ASN
1	d	40	ASN
1	d	118	ASN
1	d	133	ASN
1	d	164	GLN
1	d	234	ASN
1	d	254	GLN
1	d	294	ASN
1	d	311	GLN

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Mol	Chain	Res	Type
1	d	378	GLN
1	d	384	GLN
1	d	385	ASN
1	d	494	GLN
1	d	509	HIS
1	d	648	GLN
1	d	696	GLN
1	e	22	ASN
1	e	24	ASN
1	e	40	ASN
1	e	118	ASN
1	e	234	ASN
1	e	254	GLN
1	e	294	ASN
1	e	298	GLN
1	e	329	GLN
1	e	385	ASN
1	e	509	HIS
1	e	648	GLN
1	e	691	GLN
1	e	696	GLN
1	e	749	GLN
1	f	17	HIS
1	f	22	ASN
1	f	24	ASN
1	f	40	ASN
1	f	70	GLN
1	f	118	ASN
1	f	234	ASN
1	f	254	GLN
1	f	280	HIS
1	f	294	ASN
1	f	321	GLN
1	f	378	GLN
1	f	385	ASN
1	f	494	GLN
1	f	509	HIS
1	f	534	HIS
1	f	691	GLN
1	f	696	GLN
1	g	17	HIS
1	g	22	ASN

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Mol	Chain	Res	Type
1	g	24	ASN
1	g	40	ASN
1	g	63	ASN
1	g	118	ASN
1	g	122	HIS
1	g	234	ASN
1	g	254	GLN
1	g	280	HIS
1	g	329	GLN
1	g	378	GLN
1	g	385	ASN
1	g	494	GLN
1	g	630	GLN
1	g	648	GLN
1	h	17	HIS
1	h	22	ASN
1	h	40	ASN
1	h	70	GLN
1	h	118	ASN
1	h	122	HIS
1	h	234	ASN
1	h	254	GLN
1	h	280	HIS
1	h	294	ASN
1	h	378	GLN
1	h	385	ASN
1	h	494	GLN
1	h	534	HIS
1	h	648	GLN
1	h	691	GLN
1	h	696	GLN
1	i	17	HIS
1	i	22	ASN
1	i	24	ASN
1	i	40	ASN
1	i	63	ASN
1	i	70	GLN
1	i	118	ASN
1	i	234	ASN
1	i	254	GLN
1	i	294	ASN
1	i	385	ASN

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Mol	Chain	Res	Type
1	i	494	GLN
1	i	509	HIS
1	i	534	HIS
1	i	696	GLN
1	i	749	GLN
1	j	17	HIS
1	j	22	ASN
1	j	24	ASN
1	j	40	ASN
1	j	70	GLN
1	j	118	ASN
1	j	234	ASN
1	j	254	GLN
1	j	280	HIS
1	j	294	ASN
1	j	494	GLN
1	j	691	GLN
1	j	696	GLN
1	j	776	GLN
1	j	789	ASN
1	k	22	ASN
1	k	24	ASN
1	k	40	ASN
1	k	70	GLN
1	k	118	ASN
1	k	133	ASN
1	k	234	ASN
1	k	254	GLN
1	k	385	ASN
1	k	464	HIS
1	k	494	GLN
1	k	551	ASN
1	k	641	GLN
1	k	696	GLN
1	k	785	GLN
1	k	789	ASN
1	l	22	ASN
1	l	24	ASN
1	l	40	ASN
1	l	118	ASN
1	l	122	HIS
1	l	234	ASN

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Mol	Chain	Res	Type
1	l	254	GLN
1	l	321	GLN
1	l	329	GLN
1	l	385	ASN
1	l	494	GLN
1	l	648	GLN
1	l	696	GLN
1	m	17	HIS
1	m	22	ASN
1	m	24	ASN
1	m	40	ASN
1	m	118	ASN
1	m	122	HIS
1	m	234	ASN
1	m	254	GLN
1	m	280	HIS
1	m	294	ASN
1	m	384	GLN
1	m	385	ASN
1	m	494	GLN
1	m	509	HIS
1	m	648	GLN
1	m	691	GLN
1	m	696	GLN
1	m	785	GLN

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 monosaccharides 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	812/861 (94%)	0.13	41 (5%) 28 25	46, 106, 218, 285	0
1	B	812/861 (94%)	0.14	44 (5%) 25 23	30, 112, 219, 284	0
1	C	812/861 (94%)	0.17	44 (5%) 25 23	54, 113, 221, 291	0
1	D	812/861 (94%)	0.20	49 (6%) 21 19	43, 113, 218, 277	0
1	E	812/861 (94%)	0.36	68 (8%) 11 11	53, 112, 222, 283	0
1	F	812/861 (94%)	0.26	63 (7%) 13 13	46, 114, 223, 278	0
1	G	812/861 (94%)	0.16	49 (6%) 21 19	55, 113, 223, 258	0
1	H	812/861 (94%)	0.06	39 (4%) 30 27	50, 112, 221, 281	0
1	I	812/861 (94%)	0.16	53 (6%) 18 17	56, 108, 215, 266	0
1	J	812/861 (94%)	0.27	57 (7%) 16 16	44, 105, 215, 277	0
1	K	812/861 (94%)	0.33	56 (6%) 16 16	32, 98, 207, 278	0
1	L	812/861 (94%)	0.24	55 (6%) 17 16	33, 99, 210, 277	0
1	M	812/861 (94%)	0.04	41 (5%) 28 25	45, 103, 207, 293	0
1	N	812/861 (94%)	-0.02	36 (4%) 34 30	40, 104, 210, 249	0
1	O	812/861 (94%)	-0.02	38 (4%) 31 28	33, 103, 214, 272	0
1	P	812/861 (94%)	0.08	44 (5%) 25 23	35, 103, 211, 294	0
1	Q	812/861 (94%)	0.29	59 (7%) 15 15	35, 101, 215, 277	0
1	R	812/861 (94%)	0.28	58 (7%) 16 15	37, 101, 217, 298	0
1	S	812/861 (94%)	0.17	53 (6%) 18 17	48, 106, 212, 284	0
1	T	812/861 (94%)	0.11	55 (6%) 17 16	52, 114, 220, 288	0
1	U	812/861 (94%)	0.01	42 (5%) 27 24	53, 113, 221, 282	0
1	V	812/861 (94%)	0.11	50 (6%) 20 18	57, 114, 220, 287	0
1	W	812/861 (94%)	0.28	66 (8%) 12 12	48, 116, 223, 288	0
1	X	812/861 (94%)	0.25	63 (7%) 13 13	47, 117, 220, 300	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	Y	812/861 (94%)	0.16	53 (6%) 18 17	43, 117, 218, 278	0
1	Z	812/861 (94%)	0.14	56 (6%) 16 16	51, 114, 219, 263	0
1	a	812/861 (94%)	0.10	50 (6%) 20 18	50, 113, 216, 300	0
1	b	812/861 (94%)	0.10	43 (5%) 26 24	28, 110, 217, 281	0
1	c	812/861 (94%)	0.15	57 (7%) 16 16	26, 109, 218, 277	0
1	d	812/861 (94%)	0.11	48 (5%) 22 20	49, 106, 213, 274	0
1	e	812/861 (94%)	0.12	52 (6%) 19 18	47, 105, 210, 284	0
1	f	812/861 (94%)	0.14	53 (6%) 18 17	43, 106, 214, 266	0
1	g	812/861 (94%)	0.05	42 (5%) 27 24	50, 109, 213, 285	0
1	h	812/861 (94%)	-0.00	40 (4%) 29 26	54, 110, 210, 277	0
1	i	812/861 (94%)	0.08	47 (5%) 23 20	48, 108, 215, 271	0
1	j	812/861 (94%)	0.16	57 (7%) 16 16	50, 105, 216, 267	0
1	k	812/861 (94%)	0.16	51 (6%) 20 18	41, 104, 210, 261	0
1	l	812/861 (94%)	0.14	52 (6%) 19 18	46, 105, 213, 300	0
1	m	812/861 (94%)	0.18	49 (6%) 21 19	40, 106, 219, 276	0
All	All	31668/33579 (94%)	0.15	1973 (6%) 20 18	26, 108, 217, 300	0

All (1973) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	R	26	SER	26.5
1	Q	26	SER	21.2
1	X	26	SER	15.5
1	K	26	SER	15.2
1	Q	25	VAL	15.1
1	F	838	PRO	14.4
1	Y	27	ARG	14.3
1	W	27	ARG	13.1
1	e	26	SER	12.6
1	Q	27	ARG	11.8
1	F	837	SER	11.8
1	K	82	ARG	11.5
1	K	837	SER	11.5
1	I	845	ALA	11.5
1	J	98	PRO	11.4
1	l	27	ARG	11.4
1	Z	26	SER	11.3

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Mol	Chain	Res	Type	RSRZ
1	f	26	SER	11.3
1	k	26	SER	11.0
1	S	79	GLY	10.9
1	X	80	GLN	10.9
1	J	26	SER	10.8
1	J	837	SER	10.6
1	P	27	ARG	10.5
1	Q	82	ARG	10.3
1	d	82	ARG	10.3
1	F	844	THR	10.2
1	S	80	GLN	10.1
1	K	844	THR	10.1
1	E	27	ARG	10.1
1	S	27	ARG	10.0
1	J	25	VAL	10.0
1	a	26	SER	9.7
1	M	844	THR	9.6
1	A	837	SER	9.6
1	K	83	LEU	9.5
1	S	98	PRO	9.5
1	W	80	GLN	9.5
1	j	26	SER	9.4
1	W	26	SER	9.4
1	S	26	SER	9.3
1	D	840	ASN	9.2
1	J	840	ASN	9.2
1	Q	22	ASN	9.2
1	H	840	ASN	9.2
1	c	26	SER	9.2
1	f	27	ARG	9.2
1	E	840	ASN	9.2
1	E	837	SER	9.1
1	W	22	ASN	9.1
1	B	837	SER	9.1
1	G	833	THR	9.1
1	E	26	SER	9.0
1	M	836	SER	9.0
1	F	834	ASP	9.0
1	G	840	ASN	8.9
1	E	834	ASP	8.9
1	R	27	ARG	8.8
1	j	25	VAL	8.8

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Mol	Chain	Res	Type	RSRZ
1	D	844	THR	8.8
1	k	78	THR	8.8
1	X	25	VAL	8.7
1	K	840	ASN	8.7
1	H	834	ASP	8.6
1	C	833	THR	8.6
1	L	837	SER	8.6
1	I	837	SER	8.6
1	L	833	THR	8.5
1	L	26	SER	8.5
1	R	25	VAL	8.4
1	g	26	SER	8.4
1	l	26	SER	8.3
1	E	844	THR	8.3
1	E	838	PRO	8.3
1	I	844	THR	8.2
1	M	837	SER	8.2
1	T	79	GLY	8.2
1	K	25	VAL	8.2
1	R	22	ASN	8.1
1	J	838	PRO	8.1
1	O	837	SER	8.1
1	H	837	SER	8.1
1	K	22	ASN	8.1
1	Z	27	ARG	8.0
1	R	82	ARG	8.0
1	N	845	ALA	8.0
1	O	840	ASN	8.0
1	E	79	GLY	8.0
1	K	27	ARG	7.9
1	I	840	ASN	7.9
1	L	840	ASN	7.8
1	G	837	SER	7.7
1	P	844	THR	7.7
1	M	26	SER	7.7
1	j	27	ARG	7.7
1	L	838	PRO	7.6
1	K	836	SER	7.6
1	F	833	THR	7.6
1	G	844	THR	7.6
1	N	840	ASN	7.6
1	F	829	SER	7.6

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Mol	Chain	Res	Type	RSRZ
1	F	840	ASN	7.6
1	J	844	THR	7.5
1	E	82	ARG	7.5
1	L	27	ARG	7.5
1	O	844	THR	7.5
1	M	840	ASN	7.5
1	K	78	THR	7.4
1	F	845	ALA	7.4
1	f	836	SER	7.4
1	C	844	THR	7.4
1	e	833	THR	7.4
1	Q	837	SER	7.3
1	K	94	GLN	7.3
1	k	82	ARG	7.3
1	m	19	LEU	7.3
1	H	829	SER	7.3
1	U	836	SER	7.3
1	X	27	ARG	7.3
1	E	80	GLN	7.3
1	X	79	GLY	7.3
1	e	27	ARG	7.3
1	e	25	VAL	7.3
1	H	844	THR	7.2
1	K	834	ASP	7.2
1	W	833	THR	7.2
1	L	844	THR	7.2
1	m	26	SER	7.2
1	X	42	ARG	7.2
1	d	79	GLY	7.1
1	P	26	SER	7.1
1	M	845	ALA	7.1
1	H	838	PRO	7.0
1	M	838	PRO	7.0
1	Q	1	MET	7.0
1	D	837	SER	7.0
1	A	840	ASN	7.0
1	C	22	ASN	7.0
1	i	26	SER	6.9
1	B	844	THR	6.9
1	Q	844	THR	6.9
1	J	829	SER	6.9
1	P	837	SER	6.9

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Mol	Chain	Res	Type	RSRZ
1	Y	26	SER	6.9
1	m	829	SER	6.9
1	B	27	ARG	6.9
1	B	836	SER	6.9
1	E	829	SER	6.9
1	d	26	SER	6.9
1	E	81	VAL	6.9
1	H	835	GLY	6.9
1	Y	836	SER	6.9
1	Y	28	VAL	6.9
1	D	829	SER	6.9
1	G	829	SER	6.9
1	R	78	THR	6.8
1	C	829	SER	6.8
1	G	838	PRO	6.8
1	h	26	SER	6.8
1	R	28	VAL	6.8
1	c	836	SER	6.8
1	D	838	PRO	6.8
1	f	28	VAL	6.8
1	G	845	ALA	6.8
1	K	829	SER	6.8
1	d	836	SER	6.8
1	C	838	PRO	6.8
1	V	835	GLY	6.8
1	A	829	SER	6.8
1	E	845	ALA	6.8
1	i	27	ARG	6.7
1	N	837	SER	6.7
1	R	845	ALA	6.7
1	J	845	ALA	6.7
1	B	840	ASN	6.7
1	D	818	GLN	6.7
1	H	818	GLN	6.7
1	D	834	ASP	6.7
1	R	840	ASN	6.7
1	O	26	SER	6.7
1	c	25	VAL	6.7
1	I	838	PRO	6.7
1	C	834	ASP	6.7
1	I	80	GLN	6.7
1	R	837	SER	6.7

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Mol	Chain	Res	Type	RSRZ
1	I	829	SER	6.6
1	V	26	SER	6.6
1	B	829	SER	6.6
1	P	79	GLY	6.6
1	Q	98	PRO	6.5
1	K	845	ALA	6.5
1	E	818	GLN	6.5
1	C	840	ASN	6.5
1	g	836	SER	6.5
1	k	79	GLY	6.5
1	J	28	VAL	6.5
1	M	834	ASP	6.5
1	H	843	SER	6.5
1	K	838	PRO	6.5
1	G	843	SER	6.5
1	Z	836	SER	6.5
1	P	829	SER	6.5
1	h	829	SER	6.4
1	L	829	SER	6.4
1	F	26	SER	6.4
1	Q	840	ASN	6.4
1	Q	845	ALA	6.4
1	l	837	SER	6.4
1	A	844	THR	6.4
1	M	833	THR	6.4
1	N	829	SER	6.4
1	F	818	GLN	6.4
1	O	27	ARG	6.4
1	m	840	ASN	6.4
1	G	818	GLN	6.3
1	V	837	SER	6.3
1	R	83	LEU	6.3
1	d	835	GLY	6.3
1	N	844	THR	6.3
1	S	42	ARG	6.3
1	B	835	GLY	6.2
1	C	841	LEU	6.2
1	J	833	THR	6.2
1	L	818	GLN	6.2
1	C	837	SER	6.2
1	I	827	LEU	6.2
1	O	838	PRO	6.2

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Mol	Chain	Res	Type	RSRZ
1	J	82	ARG	6.2
1	m	837	SER	6.2
1	f	82	ARG	6.2
1	H	845	ALA	6.2
1	G	834	ASP	6.2
1	j	829	SER	6.2
1	N	834	ASP	6.2
1	T	837	SER	6.2
1	B	838	PRO	6.1
1	A	818	GLN	6.1
1	g	1	MET	6.1
1	E	346	GLU	6.1
1	V	834	ASP	6.1
1	j	835	GLY	6.1
1	S	837	SER	6.1
1	Q	838	PRO	6.1
1	k	829	SER	6.1
1	h	836	SER	6.0
1	D	27	ARG	6.0
1	L	845	ALA	6.0
1	E	22	ASN	6.0
1	k	83	LEU	6.0
1	L	841	LEU	6.0
1	e	22	ASN	6.0
1	O	845	ALA	6.0
1	L	843	SER	6.0
1	I	843	SER	6.0
1	e	835	GLY	6.0
1	e	829	SER	6.0
1	l	818	GLN	6.0
1	F	843	SER	6.0
1	L	834	ASP	5.9
1	k	836	SER	6.0
1	G	827	LEU	5.9
1	k	844	THR	5.9
1	V	829	SER	5.9
1	W	829	SER	5.9
1	e	836	SER	5.9
1	Z	28	VAL	5.9
1	C	818	GLN	5.9
1	K	843	SER	5.9
1	J	27	ARG	5.9

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Mol	Chain	Res	Type	RSRZ
1	h	835	GLY	5.9
1	l	840	ASN	5.9
1	P	840	ASN	5.9
1	l	829	SER	5.9
1	P	845	ALA	5.9
1	k	840	ASN	5.9
1	P	838	PRO	5.9
1	M	829	SER	5.8
1	C	845	ALA	5.8
1	O	834	ASP	5.8
1	b	835	GLY	5.8
1	R	829	SER	5.8
1	C	100	TYR	5.8
1	X	829	SER	5.8
1	L	839	ILE	5.8
1	k	835	GLY	5.8
1	k	837	SER	5.8
1	U	835	GLY	5.8
1	a	835	GLY	5.8
1	T	829	SER	5.8
1	R	838	PRO	5.8
1	S	840	ASN	5.8
1	S	845	ALA	5.8
1	T	844	THR	5.8
1	A	845	ALA	5.8
1	B	826	GLY	5.7
1	W	79	GLY	5.7
1	N	838	PRO	5.7
1	E	833	THR	5.7
1	b	836	SER	5.7
1	j	19	LEU	5.7
1	K	833	THR	5.7
1	S	844	THR	5.7
1	H	836	SER	5.7
1	J	843	SER	5.7
1	j	834	ASP	5.7
1	j	840	ASN	5.7
1	B	845	ALA	5.7
1	c	837	SER	5.7
1	i	835	GLY	5.7
1	A	824	SER	5.7
1	k	22	ASN	5.7

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Mol	Chain	Res	Type	RSRZ
1	L	79	GLY	5.7
1	i	829	SER	5.7
1	f	829	SER	5.6
1	m	844	THR	5.6
1	D	843	SER	5.6
1	U	838	PRO	5.6
1	I	818	GLN	5.6
1	c	78	THR	5.6
1	T	840	ASN	5.6
1	g	835	GLY	5.6
1	G	832	ILE	5.6
1	C	101	PRO	5.6
1	M	842	PHE	5.6
1	m	841	LEU	5.6
1	l	79	GLY	5.6
1	D	26	SER	5.6
1	N	833	THR	5.6
1	R	80	GLN	5.6
1	J	841	LEU	5.6
1	J	818	GLN	5.6
1	W	94	GLN	5.6
1	T	835	GLY	5.6
1	U	829	SER	5.6
1	c	835	GLY	5.6
1	N	841	LEU	5.6
1	Q	829	SER	5.6
1	Z	829	SER	5.6
1	g	829	SER	5.6
1	B	26	SER	5.6
1	J	826	GLY	5.6
1	c	829	SER	5.6
1	f	835	GLY	5.5
1	S	81	VAL	5.5
1	I	834	ASP	5.5
1	Z	83	LEU	5.5
1	A	833	THR	5.5
1	J	839	ILE	5.5
1	K	823	GLN	5.5
1	D	845	ALA	5.5
1	d	78	THR	5.5
1	S	829	SER	5.5
1	K	820	LYS	5.5

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Mol	Chain	Res	Type	RSRZ
1	B	818	GLN	5.5
1	K	818	GLN	5.5
1	b	829	SER	5.5
1	J	1	MET	5.5
1	Q	834	ASP	5.5
1	e	79	GLY	5.5
1	C	826	GLY	5.5
1	X	836	SER	5.5
1	a	843	SER	5.5
1	R	98	PRO	5.5
1	W	83	LEU	5.5
1	N	824	SER	5.5
1	a	836	SER	5.5
1	i	836	SER	5.5
1	j	844	THR	5.5
1	H	842	PHE	5.5
1	R	844	THR	5.5
1	i	840	ASN	5.4
1	U	26	SER	5.4
1	U	840	ASN	5.4
1	h	840	ASN	5.4
1	S	82	ARG	5.4
1	l	844	THR	5.4
1	b	843	SER	5.4
1	b	20	ASP	5.4
1	A	838	PRO	5.4
1	L	826	GLY	5.4
1	M	78	THR	5.4
1	N	820	LYS	5.4
1	I	820	LYS	5.4
1	W	837	SER	5.4
1	O	826	GLY	5.4
1	M	843	SER	5.4
1	V	833	THR	5.4
1	O	818	GLN	5.3
1	m	818	GLN	5.3
1	F	27	ARG	5.3
1	O	829	SER	5.3
1	D	833	THR	5.3
1	I	79	GLY	5.3
1	N	830	THR	5.3
1	N	843	SER	5.3

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Mol	Chain	Res	Type	RSRZ
1	m	834	ASP	5.3
1	m	826	GLY	5.3
1	i	837	SER	5.3
1	V	840	ASN	5.3
1	l	820	LYS	5.3
1	G	839	ILE	5.3
1	G	826	GLY	5.3
1	m	79	GLY	5.3
1	F	91	ARG	5.3
1	j	836	SER	5.3
1	F	830	THR	5.3
1	M	818	GLN	5.3
1	K	842	PHE	5.2
1	K	826	GLY	5.2
1	J	842	PHE	5.2
1	d	829	SER	5.2
1	X	844	THR	5.2
1	M	826	GLY	5.2
1	l	833	THR	5.2
1	I	824	SER	5.2
1	j	837	SER	5.2
1	Q	818	GLN	5.2
1	A	820	LYS	5.2
1	P	834	ASP	5.2
1	L	832	ILE	5.2
1	l	838	PRO	5.2
1	M	830	THR	5.2
1	B	820	LYS	5.2
1	R	841	LEU	5.2
1	i	838	PRO	5.2
1	i	25	VAL	5.1
1	V	838	PRO	5.1
1	U	837	SER	5.1
1	Y	837	SER	5.1
1	g	837	SER	5.1
1	U	833	THR	5.1
1	P	83	LEU	5.1
1	j	824	SER	5.1
1	A	826	GLY	5.1
1	C	820	LYS	5.1
1	I	819	VAL	5.1
1	H	841	LEU	5.1

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Mol	Chain	Res	Type	RSRZ
1	E	826	GLY	5.1
1	I	826	GLY	5.1
1	J	830	THR	5.1
1	Y	829	SER	5.1
1	I	830	THR	5.1
1	V	844	THR	5.1
1	W	835	GLY	5.1
1	A	830	THR	5.1
1	L	94	GLN	5.1
1	Q	824	SER	5.1
1	i	844	THR	5.1
1	I	842	PHE	5.1
1	V	25	VAL	5.1
1	h	818	GLN	5.1
1	m	100	TYR	5.1
1	D	826	GLY	5.1
1	E	843	SER	5.1
1	G	824	SER	5.1
1	h	824	SER	5.1
1	H	833	THR	5.1
1	P	826	GLY	5.1
1	e	78	THR	5.1
1	F	822	LEU	5.0
1	R	19	LEU	5.0
1	U	826	GLY	5.0
1	c	98	PRO	5.0
1	B	833	THR	5.0
1	X	837	SER	5.0
1	i	820	LYS	5.0
1	f	837	SER	5.0
1	f	25	VAL	5.0
1	F	826	GLY	5.0
1	k	818	GLN	5.0
1	K	839	ILE	5.0
1	a	829	SER	5.0
1	H	826	GLY	5.0
1	R	1	MET	5.0
1	U	844	THR	5.0
1	c	81	VAL	5.0
1	E	36	ILE	5.0
1	T	832	ILE	5.0
1	T	845	ALA	5.0

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Mol	Chain	Res	Type	RSRZ
1	m	824	SER	5.0
1	L	830	THR	5.0
1	J	83	LEU	5.0
1	D	830	THR	5.0
1	Y	838	PRO	5.0
1	R	834	ASP	5.0
1	d	838	PRO	5.0
1	k	824	SER	5.0
1	D	819	VAL	5.0
1	O	824	SER	5.0
1	O	830	THR	5.0
1	Q	826	GLY	5.0
1	F	827	LEU	4.9
1	Z	835	GLY	4.9
1	d	49	ARG	4.9
1	d	844	THR	4.9
1	f	838	PRO	4.9
1	Z	36	ILE	4.9
1	Q	836	SER	4.9
1	V	836	SER	4.9
1	G	819	VAL	4.9
1	D	841	LEU	4.9
1	l	826	GLY	4.9
1	P	1	MET	4.9
1	B	830	THR	4.9
1	g	818	GLN	4.9
1	C	830	THR	4.9
1	E	221	LEU	4.9
1	M	824	SER	4.9
1	P	830	THR	4.9
1	R	818	GLN	4.9
1	R	42	ARG	4.9
1	Y	840	ASN	4.9
1	J	100	TYR	4.9
1	l	824	SER	4.9
1	f	834	ASP	4.9
1	k	55	PRO	4.9
1	B	839	ILE	4.9
1	F	42	ARG	4.9
1	R	832	ILE	4.9
1	A	841	LEU	4.9
1	O	4	GLU	4.9

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Mol	Chain	Res	Type	RSRZ
1	N	818	GLN	4.9
1	P	827	LEU	4.8
1	H	830	THR	4.8
1	N	839	ILE	4.8
1	W	840	ASN	4.8
1	l	845	ALA	4.8
1	e	42	ARG	4.8
1	G	830	THR	4.8
1	B	843	SER	4.8
1	d	837	SER	4.8
1	L	824	SER	4.8
1	J	19	LEU	4.8
1	l	78	THR	4.8
1	e	28	VAL	4.8
1	W	838	PRO	4.8
1	K	832	ILE	4.8
1	L	83	LEU	4.8
1	S	818	GLN	4.8
1	f	818	GLN	4.8
1	R	824	SER	4.8
1	R	830	THR	4.8
1	g	830	THR	4.8
1	E	827	LEU	4.8
1	e	838	PRO	4.8
1	i	826	GLY	4.8
1	L	819	VAL	4.8
1	C	835	GLY	4.8
1	F	832	ILE	4.8
1	K	830	THR	4.8
1	l	830	THR	4.8
1	P	818	GLN	4.8
1	S	834	ASP	4.8
1	i	834	ASP	4.8
1	g	824	SER	4.8
1	m	830	THR	4.8
1	h	820	LYS	4.8
1	m	836	SER	4.8
1	C	839	ILE	4.8
1	H	832	ILE	4.8
1	X	840	ASN	4.8
1	Y	41	GLU	4.8
1	D	824	SER	4.8

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Mol	Chain	Res	Type	RSRZ
1	l	83	LEU	4.8
1	f	55	PRO	4.8
1	E	830	THR	4.7
1	H	824	SER	4.7
1	m	14	HIS	4.7
1	H	827	LEU	4.7
1	O	827	LEU	4.7
1	S	830	THR	4.7
1	j	838	PRO	4.7
1	Z	840	ASN	4.7
1	U	843	SER	4.7
1	i	818	GLN	4.7
1	k	826	GLY	4.7
1	m	820	LYS	4.7
1	j	278	PRO	4.7
1	L	820	LYS	4.7
1	e	818	GLN	4.7
1	L	42	ARG	4.7
1	E	839	ILE	4.7
1	E	819	VAL	4.7
1	F	824	SER	4.7
1	c	832	ILE	4.7
1	M	839	ILE	4.7
1	d	25	VAL	4.7
1	Y	830	THR	4.7
1	m	845	ALA	4.7
1	j	80	GLN	4.7
1	Y	824	SER	4.7
1	e	82	ARG	4.7
1	C	843	SER	4.7
1	V	98	PRO	4.7
1	S	838	PRO	4.7
1	V	843	SER	4.7
1	k	838	PRO	4.7
1	c	830	THR	4.6
1	f	830	THR	4.6
1	N	826	GLY	4.6
1	j	820	LYS	4.6
1	D	839	ILE	4.6
1	X	830	THR	4.6
1	H	821	LEU	4.6
1	U	19	LEU	4.6

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Mol	Chain	Res	Type	RSRZ
1	m	1	MET	4.6
1	G	823	GLN	4.6
1	a	827	LEU	4.6
1	J	832	ILE	4.6
1	V	818	GLN	4.6
1	W	844	THR	4.6
1	W	845	ALA	4.6
1	N	842	PHE	4.6
1	B	100	TYR	4.6
1	m	819	VAL	4.6
1	K	841	LEU	4.6
1	W	830	THR	4.6
1	N	835	GLY	4.6
1	b	837	SER	4.6
1	m	823	GLN	4.6
1	g	833	THR	4.6
1	g	840	ASN	4.6
1	C	824	SER	4.6
1	m	843	SER	4.6
1	R	826	GLY	4.6
1	d	22	ASN	4.6
1	e	826	GLY	4.6
1	F	819	VAL	4.6
1	I	839	ILE	4.6
1	b	830	THR	4.6
1	g	25	VAL	4.6
1	G	821	LEU	4.6
1	H	26	SER	4.6
1	H	823	GLN	4.6
1	W	818	GLN	4.6
1	d	818	GLN	4.6
1	c	826	GLY	4.6
1	f	826	GLY	4.6
1	h	844	THR	4.6
1	V	42	ARG	4.6
1	L	821	LEU	4.6
1	j	830	THR	4.6
1	K	824	SER	4.6
1	C	842	PHE	4.6
1	E	842	PHE	4.6
1	Z	833	THR	4.6
1	B	824	SER	4.5

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Mol	Chain	Res	Type	RSRZ
1	i	824	SER	4.5
1	Q	820	LYS	4.5
1	T	830	THR	4.5
1	m	101	PRO	4.5
1	Q	830	THR	4.5
1	Q	832	ILE	4.5
1	S	824	SER	4.5
1	T	826	GLY	4.5
1	b	49	ARG	4.5
1	T	818	GLN	4.5
1	h	826	GLY	4.5
1	W	832	ILE	4.5
1	b	838	PRO	4.5
1	L	17	HIS	4.5
1	J	827	LEU	4.5
1	T	843	SER	4.5
1	H	819	VAL	4.5
1	b	840	ASN	4.5
1	M	819	VAL	4.5
1	Z	98	PRO	4.5
1	j	826	GLY	4.5
1	X	818	GLN	4.5
1	J	824	SER	4.5
1	P	824	SER	4.5
1	W	836	SER	4.5
1	g	844	THR	4.5
1	O	819	VAL	4.5
1	Q	833	THR	4.5
1	S	843	SER	4.5
1	i	830	THR	4.5
1	I	821	LEU	4.5
1	C	822	LEU	4.5
1	h	838	PRO	4.5
1	b	818	GLN	4.5
1	Y	844	THR	4.5
1	d	830	THR	4.5
1	f	844	THR	4.5
1	c	41	GLU	4.5
1	P	832	ILE	4.5
1	B	819	VAL	4.5
1	J	819	VAL	4.5
1	U	830	THR	4.5

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Mol	Chain	Res	Type	RSRZ
1	b	55	PRO	4.5
1	U	818	GLN	4.5
1	Z	818	GLN	4.5
1	g	826	GLY	4.5
1	P	843	SER	4.5
1	k	27	ARG	4.5
1	Q	55	PRO	4.4
1	X	41	GLU	4.4
1	E	832	ILE	4.4
1	W	824	SER	4.4
1	a	837	SER	4.4
1	m	838	PRO	4.4
1	k	822	LEU	4.4
1	e	837	SER	4.4
1	l	836	SER	4.4
1	e	830	THR	4.4
1	F	842	PHE	4.4
1	E	138	MET	4.4
1	Z	826	GLY	4.4
1	Z	838	PRO	4.4
1	c	838	PRO	4.4
1	I	19	LEU	4.4
1	V	845	ALA	4.4
1	Z	830	THR	4.4
1	Z	824	SER	4.4
1	a	826	GLY	4.4
1	O	823	GLN	4.4
1	h	833	THR	4.4
1	P	821	LEU	4.4
1	Q	839	ILE	4.4
1	R	843	SER	4.4
1	B	821	LEU	4.4
1	C	832	ILE	4.4
1	H	839	ILE	4.4
1	N	832	ILE	4.4
1	X	827	LEU	4.4
1	a	832	ILE	4.4
1	m	822	LEU	4.4
1	C	836	SER	4.4
1	c	833	THR	4.4
1	O	842	PHE	4.4
1	Z	101	PRO	4.4

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Mol	Chain	Res	Type	RSRZ
1	A	821	LEU	4.4
1	G	842	PHE	4.4
1	V	830	THR	4.4
1	a	830	THR	4.4
1	E	841	LEU	4.4
1	L	842	PHE	4.4
1	j	79	GLY	4.4
1	k	830	THR	4.4
1	S	823	GLN	4.4
1	F	821	LEU	4.4
1	M	832	ILE	4.4
1	N	4	GLU	4.4
1	W	42	ARG	4.4
1	F	92	LEU	4.4
1	T	824	SER	4.3
1	T	836	SER	4.3
1	f	840	ASN	4.3
1	J	831	LEU	4.3
1	O	843	SER	4.3
1	d	824	SER	4.3
1	j	22	ASN	4.3
1	j	818	GLN	4.3
1	U	845	ALA	4.3
1	b	832	ILE	4.3
1	D	827	LEU	4.3
1	N	827	LEU	4.3
1	k	817	MET	4.3
1	G	80	GLN	4.3
1	h	830	THR	4.3
1	R	836	SER	4.3
1	V	824	SER	4.3
1	Q	83	LEU	4.3
1	J	79	GLY	4.3
1	L	1	MET	4.3
1	S	94	GLN	4.3
1	e	840	ASN	4.3
1	K	821	LEU	4.3
1	A	819	VAL	4.3
1	P	839	ILE	4.3
1	A	843	SER	4.3
1	S	835	GLY	4.3
1	A	822	LEU	4.3

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Mol	Chain	Res	Type	RSRZ
1	J	823	GLN	4.3
1	T	838	PRO	4.3
1	k	819	VAL	4.3
1	L	835	GLY	4.3
1	Z	844	THR	4.3
1	C	825	LEU	4.3
1	X	824	SER	4.3
1	P	823	GLN	4.3
1	d	823	GLN	4.3
1	j	823	GLN	4.3
1	F	817	MET	4.3
1	A	834	ASP	4.3
1	M	823	GLN	4.3
1	U	832	ILE	4.3
1	Y	823	GLN	4.3
1	E	820	LYS	4.3
1	S	826	GLY	4.3
1	k	820	LYS	4.3
1	S	841	LEU	4.3
1	k	827	LEU	4.3
1	F	839	ILE	4.2
1	I	832	ILE	4.2
1	Y	826	GLY	4.2
1	l	19	LEU	4.2
1	C	41	GLU	4.2
1	O	839	ILE	4.2
1	b	824	SER	4.2
1	g	838	PRO	4.2
1	E	822	LEU	4.2
1	E	831	LEU	4.2
1	B	832	ILE	4.2
1	m	78	THR	4.2
1	d	840	ASN	4.2
1	J	821	LEU	4.2
1	c	818	GLN	4.2
1	E	41	GLU	4.2
1	E	817	MET	4.2
1	a	101	PRO	4.2
1	L	28	VAL	4.2
1	F	841	LEU	4.2
1	P	841	LEU	4.2
1	W	82	ARG	4.2

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Mol	Chain	Res	Type	RSRZ
1	B	823	GLN	4.2
1	M	820	LYS	4.2
1	D	842	PHE	4.2
1	X	826	GLY	4.2
1	X	833	THR	4.2
1	d	826	GLY	4.2
1	Y	818	GLN	4.2
1	i	823	GLN	4.2
1	F	820	LYS	4.2
1	E	824	SER	4.2
1	N	823	GLN	4.2
1	X	98	PRO	4.2
1	V	821	LEU	4.2
1	G	817	MET	4.2
1	a	27	ARG	4.2
1	M	27	ARG	4.2
1	Y	36	ILE	4.2
1	l	825	LEU	4.2
1	l	819	VAL	4.2
1	S	832	ILE	4.2
1	A	827	LEU	4.2
1	S	822	LEU	4.2
1	T	841	LEU	4.2
1	E	42	ARG	4.2
1	i	833	THR	4.2
1	I	822	LEU	4.2
1	I	828	LYS	4.2
1	Q	821	LEU	4.2
1	W	826	GLY	4.2
1	F	831	LEU	4.1
1	X	823	GLN	4.1
1	i	22	ASN	4.1
1	C	98	PRO	4.1
1	E	185	ARG	4.1
1	Y	15	TYR	4.1
1	W	822	LEU	4.1
1	l	831	LEU	4.1
1	B	831	LEU	4.1
1	K	831	LEU	4.1
1	W	843	SER	4.1
1	f	827	LEU	4.1
1	l	841	LEU	4.1

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Mol	Chain	Res	Type	RSRZ
1	R	833	THR	4.1
1	E	83	LEU	4.1
1	g	827	LEU	4.1
1	K	819	VAL	4.1
1	g	817	MET	4.1
1	l	843	SER	4.1
1	L	831	LEU	4.1
1	Q	823	GLN	4.1
1	I	4	GLU	4.1
1	Y	37	ARG	4.1
1	C	827	LEU	4.1
1	I	78	THR	4.1
1	m	835	GLY	4.1
1	F	825	LEU	4.1
1	W	823	GLN	4.1
1	a	844	THR	4.1
1	c	839	ILE	4.1
1	P	819	VAL	4.1
1	Q	819	VAL	4.1
1	A	817	MET	4.1
1	M	822	LEU	4.1
1	M	841	LEU	4.1
1	Q	827	LEU	4.1
1	T	821	LEU	4.1
1	j	832	ILE	4.1
1	R	842	PHE	4.1
1	X	838	PRO	4.1
1	L	822	LEU	4.1
1	M	831	LEU	4.1
1	C	819	VAL	4.1
1	D	832	ILE	4.1
1	E	821	LEU	4.1
1	Y	98	PRO	4.1
1	I	831	LEU	4.1
1	N	817	MET	4.1
1	T	823	GLN	4.1
1	N	819	VAL	4.1
1	m	839	ILE	4.1
1	D	821	LEU	4.1
1	F	278	PRO	4.1
1	G	822	LEU	4.1
1	K	822	LEU	4.1

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Mol	Chain	Res	Type	RSRZ
1	b	19	LEU	4.1
1	j	44	LEU	4.1
1	T	833	THR	4.1
1	F	823	GLN	4.1
1	j	841	LEU	4.1
1	V	826	GLY	4.1
1	k	833	THR	4.1
1	M	827	LEU	4.0
1	F	82	ARG	4.0
1	Q	80	GLN	4.0
1	a	840	ASN	4.0
1	V	827	LEU	4.0
1	j	105	LEU	4.0
1	I	823	GLN	4.0
1	L	823	GLN	4.0
1	Q	94	GLN	4.0
1	U	42	ARG	4.0
1	U	824	SER	4.0
1	f	833	THR	4.0
1	M	821	LEU	4.0
1	k	831	LEU	4.0
1	T	27	ARG	4.0
1	Z	278	PRO	4.0
1	E	78	THR	4.0
1	O	841	LEU	4.0
1	U	819	VAL	4.0
1	m	832	ILE	4.0
1	L	80	GLN	4.0
1	A	831	LEU	4.0
1	D	820	LYS	4.0
1	D	822	LEU	4.0
1	R	821	LEU	4.0
1	g	27	ARG	4.0
1	b	826	GLY	4.0
1	A	823	GLN	4.0
1	B	817	MET	4.0
1	a	818	GLN	4.0
1	i	841	LEU	4.0
1	j	843	SER	4.0
1	b	833	THR	4.0
1	S	839	ILE	4.0
1	A	835	GLY	4.0

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Mol	Chain	Res	Type	RSRZ
1	O	820	LYS	4.0
1	O	833	THR	4.0
1	e	819	VAL	4.0
1	k	843	SER	4.0
1	F	828	LYS	4.0
1	Y	835	GLY	4.0
1	h	822	LEU	4.0
1	j	821	LEU	4.0
1	Y	845	ALA	4.0
1	C	831	LEU	4.0
1	g	822	LEU	4.0
1	m	831	LEU	4.0
1	Z	837	SER	4.0
1	V	841	LEU	4.0
1	W	827	LEU	4.0
1	a	838	PRO	4.0
1	M	835	GLY	4.0
1	T	819	VAL	4.0
1	b	822	LEU	4.0
1	K	828	LYS	4.0
1	U	823	GLN	4.0
1	k	823	GLN	4.0
1	R	820	LYS	4.0
1	L	82	ARG	4.0
1	V	823	GLN	3.9
1	l	823	GLN	3.9
1	F	98	PRO	3.9
1	R	819	VAL	3.9
1	A	842	PHE	3.9
1	h	1	MET	3.9
1	k	834	ASP	3.9
1	g	819	VAL	3.9
1	g	832	ILE	3.9
1	B	822	LEU	3.9
1	O	822	LEU	3.9
1	R	823	GLN	3.9
1	A	839	ILE	3.9
1	S	820	LYS	3.9
1	X	820	LYS	3.9
1	C	27	ARG	3.9
1	j	845	ALA	3.9
1	H	822	LEU	3.9

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Mol	Chain	Res	Type	RSRZ
1	e	823	GLN	3.9
1	N	822	LEU	3.9
1	c	19	LEU	3.9
1	g	843	SER	3.9
1	h	832	ILE	3.9
1	f	822	LEU	3.9
1	k	821	LEU	3.9
1	l	822	LEU	3.9
1	a	839	ILE	3.9
1	f	817	MET	3.9
1	P	78	THR	3.9
1	f	824	SER	3.9
1	A	825	LEU	3.9
1	a	821	LEU	3.9
1	c	844	THR	3.9
1	j	78	THR	3.9
1	C	821	LEU	3.9
1	H	831	LEU	3.9
1	J	822	LEU	3.9
1	I	26	SER	3.9
1	j	822	LEU	3.9
1	B	842	PHE	3.9
1	R	835	GLY	3.9
1	T	822	LEU	3.9
1	Y	820	LYS	3.9
1	B	834	ASP	3.9
1	C	817	MET	3.9
1	J	817	MET	3.9
1	I	841	LEU	3.9
1	L	825	LEU	3.9
1	I	817	MET	3.9
1	S	819	VAL	3.8
1	i	819	VAL	3.8
1	P	817	MET	3.8
1	W	842	PHE	3.8
1	Y	42	ARG	3.8
1	L	4	GLU	3.8
1	D	835	GLY	3.8
1	h	823	GLN	3.8
1	i	831	LEU	3.8
1	M	42	ARG	3.8
1	m	821	LEU	3.8

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Mol	Chain	Res	Type	RSRZ
1	O	832	ILE	3.8
1	E	94	GLN	3.8
1	P	835	GLY	3.8
1	l	821	LEU	3.8
1	l	827	LEU	3.8
1	D	817	MET	3.8
1	B	827	LEU	3.8
1	I	825	LEU	3.8
1	J	99	LEU	3.8
1	K	28	VAL	3.8
1	P	822	LEU	3.8
1	S	821	LEU	3.8
1	f	820	LYS	3.8
1	P	842	PHE	3.8
1	j	49	ARG	3.8
1	D	831	LEU	3.8
1	f	819	VAL	3.8
1	X	82	ARG	3.8
1	m	817	MET	3.8
1	k	845	ALA	3.8
1	R	839	ILE	3.8
1	V	819	VAL	3.8
1	a	824	SER	3.8
1	J	820	LYS	3.8
1	b	27	ARG	3.8
1	i	42	ARG	3.8
1	j	82	ARG	3.8
1	Z	834	ASP	3.8
1	G	831	LEU	3.8
1	e	827	LEU	3.8
1	D	278	PRO	3.8
1	P	80	GLN	3.8
1	N	831	LEU	3.8
1	R	36	ILE	3.8
1	X	843	SER	3.8
1	c	824	SER	3.8
1	e	824	SER	3.8
1	a	833	THR	3.8
1	B	14	HIS	3.8
1	U	821	LEU	3.8
1	b	26	SER	3.8
1	F	94	GLN	3.8

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Mol	Chain	Res	Type	RSRZ
1	J	825	LEU	3.8
1	k	839	ILE	3.8
1	m	25	VAL	3.8
1	O	828	LYS	3.8
1	Q	835	GLY	3.8
1	Q	843	SER	3.8
1	K	1	MET	3.8
1	X	819	VAL	3.8
1	h	821	LEU	3.8
1	h	834	ASP	3.8
1	a	98	PRO	3.8
1	L	828	LYS	3.8
1	P	820	LYS	3.8
1	j	833	THR	3.7
1	Y	822	LEU	3.7
1	g	820	LYS	3.7
1	j	28	VAL	3.7
1	L	817	MET	3.7
1	h	837	SER	3.7
1	J	80	GLN	3.7
1	U	841	LEU	3.7
1	H	817	MET	3.7
1	l	835	GLY	3.7
1	V	820	LYS	3.7
1	V	19	LEU	3.7
1	g	823	GLN	3.7
1	i	822	LEU	3.7
1	m	833	THR	3.7
1	G	278	PRO	3.7
1	Q	822	LEU	3.7
1	g	821	LEU	3.7
1	M	817	MET	3.7
1	b	844	THR	3.7
1	V	822	LEU	3.7
1	W	105	LEU	3.7
1	c	821	LEU	3.7
1	c	827	LEU	3.7
1	l	82	ARG	3.7
1	E	823	GLN	3.7
1	H	825	LEU	3.7
1	O	825	LEU	3.7
1	i	821	LEU	3.7

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Mol	Chain	Res	Type	RSRZ
1	l	842	PHE	3.7
1	i	843	SER	3.7
1	h	817	MET	3.7
1	F	41	GLU	3.7
1	F	101	PRO	3.7
1	c	840	ASN	3.7
1	W	278	PRO	3.7
1	e	36	ILE	3.7
1	i	845	ALA	3.7
1	F	81	VAL	3.7
1	U	822	LEU	3.7
1	j	831	LEU	3.7
1	R	817	MET	3.7
1	f	843	SER	3.7
1	B	25	VAL	3.7
1	i	827	LEU	3.7
1	j	819	VAL	3.7
1	J	22	ASN	3.7
1	K	347	GLU	3.7
1	O	831	LEU	3.7
1	a	822	LEU	3.7
1	D	825	LEU	3.6
1	S	842	PHE	3.6
1	T	26	SER	3.6
1	Z	843	SER	3.6
1	B	825	LEU	3.6
1	Z	821	LEU	3.6
1	E	828	LYS	3.6
1	G	820	LYS	3.6
1	P	42	ARG	3.6
1	S	836	SER	3.6
1	R	827	LEU	3.6
1	W	820	LYS	3.6
1	Y	841	LEU	3.6
1	Z	820	LYS	3.6
1	e	817	MET	3.6
1	b	839	ILE	3.6
1	H	828	LYS	3.6
1	l	817	MET	3.6
1	I	833	THR	3.6
1	J	828	LYS	3.6
1	a	825	LEU	3.6

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Mol	Chain	Res	Type	RSRZ
1	e	844	THR	3.6
1	X	835	GLY	3.6
1	W	25	VAL	3.6
1	c	819	VAL	3.6
1	f	821	LEU	3.6
1	f	845	ALA	3.6
1	X	278	PRO	3.6
1	g	79	GLY	3.6
1	Z	823	GLN	3.6
1	m	842	PHE	3.6
1	i	817	MET	3.6
1	C	823	GLN	3.6
1	Q	842	PHE	3.6
1	d	831	LEU	3.6
1	A	26	SER	3.6
1	S	4	GLU	3.6
1	V	839	ILE	3.6
1	Z	82	ARG	3.6
1	a	823	GLN	3.6
1	c	841	LEU	3.6
1	T	93	ALA	3.6
1	F	34	THR	3.6
1	W	41	GLU	3.6
1	N	821	LEU	3.6
1	f	80	GLN	3.6
1	S	817	MET	3.6
1	X	94	GLN	3.6
1	Z	822	LEU	3.6
1	m	55	PRO	3.6
1	b	823	GLN	3.6
1	f	823	GLN	3.6
1	L	149	GLY	3.6
1	Z	25	VAL	3.6
1	d	827	LEU	3.6
1	h	79	GLY	3.6
1	h	819	VAL	3.6
1	P	831	LEU	3.6
1	Q	831	LEU	3.6
1	A	832	ILE	3.6
1	E	25	VAL	3.6
1	F	28	VAL	3.6
1	j	839	ILE	3.6

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Mol	Chain	Res	Type	RSRZ
1	O	821	LEU	3.6
1	g	831	LEU	3.6
1	U	820	LYS	3.5
1	Y	843	SER	3.5
1	E	825	LEU	3.5
1	P	19	LEU	3.5
1	W	821	LEU	3.5
1	j	827	LEU	3.5
1	m	825	LEU	3.5
1	G	825	LEU	3.5
1	c	259	HIS	3.5
1	d	821	LEU	3.5
1	S	833	THR	3.5
1	M	825	LEU	3.5
1	X	105	LEU	3.5
1	Y	821	LEU	3.5
1	P	836	SER	3.5
1	c	820	LYS	3.5
1	a	819	VAL	3.5
1	e	822	LEU	3.5
1	e	832	ILE	3.5
1	c	823	GLN	3.5
1	E	28	VAL	3.5
1	T	842	PHE	3.5
1	X	821	LEU	3.5
1	M	828	LYS	3.5
1	T	820	LYS	3.5
1	W	819	VAL	3.5
1	X	841	LEU	3.5
1	h	831	LEU	3.5
1	I	816	GLU	3.5
1	L	98	PRO	3.5
1	f	832	ILE	3.5
1	e	839	ILE	3.5
1	V	86	ALA	3.5
1	I	27	ARG	3.5
1	Q	841	LEU	3.5
1	D	823	GLN	3.5
1	i	41	GLU	3.5
1	c	83	LEU	3.5
1	c	822	LEU	3.5
1	d	833	THR	3.5

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Mol	Chain	Res	Type	RSRZ
1	L	816	GLU	3.5
1	G	36	ILE	3.5
1	T	839	ILE	3.5
1	Z	819	VAL	3.5
1	S	831	LEU	3.4
1	Y	831	LEU	3.4
1	l	839	ILE	3.4
1	G	346	GLU	3.4
1	K	346	GLU	3.4
1	X	822	LEU	3.4
1	d	822	LEU	3.4
1	B	278	PRO	3.4
1	J	834	ASP	3.4
1	j	55	PRO	3.4
1	X	832	ILE	3.4
1	g	834	ASP	3.4
1	E	19	LEU	3.4
1	W	15	TYR	3.4
1	B	841	LEU	3.4
1	K	98	PRO	3.4
1	F	37	ARG	3.4
1	a	841	LEU	3.4
1	E	171	ASN	3.4
1	F	816	GLU	3.4
1	V	105	LEU	3.4
1	k	841	LEU	3.4
1	k	832	ILE	3.4
1	Y	833	THR	3.4
1	i	842	PHE	3.4
1	R	822	LEU	3.4
1	f	831	LEU	3.4
1	I	835	GLY	3.4
1	S	221	LEU	3.4
1	V	817	MET	3.4
1	b	821	LEU	3.4
1	U	825	LEU	3.4
1	W	93	ALA	3.4
1	Y	825	LEU	3.4
1	K	835	GLY	3.4
1	E	199	ARG	3.4
1	E	88	GLN	3.4
1	X	259	HIS	3.4

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Mol	Chain	Res	Type	RSRZ
1	b	820	LYS	3.4
1	X	839	ILE	3.4
1	P	825	LEU	3.4
1	X	197	LEU	3.4
1	j	817	MET	3.4
1	A	836	SER	3.3
1	W	36	ILE	3.3
1	g	842	PHE	3.3
1	f	98	PRO	3.3
1	G	42	ARG	3.3
1	L	827	LEU	3.3
1	T	831	LEU	3.3
1	k	825	LEU	3.3
1	g	845	ALA	3.3
1	C	42	ARG	3.3
1	O	835	GLY	3.3
1	W	28	VAL	3.3
1	Z	79	GLY	3.3
1	K	825	LEU	3.3
1	e	831	LEU	3.3
1	g	839	ILE	3.3
1	l	36	ILE	3.3
1	f	100	TYR	3.3
1	i	28	VAL	3.3
1	R	831	LEU	3.3
1	g	80	GLN	3.3
1	k	80	GLN	3.3
1	h	843	SER	3.3
1	P	28	VAL	3.3
1	Y	819	VAL	3.3
1	Y	842	PHE	3.3
1	U	831	LEU	3.3
1	O	817	MET	3.3
1	T	817	MET	3.3
1	W	138	MET	3.3
1	X	831	LEU	3.3
1	h	827	LEU	3.3
1	Q	185	ARG	3.3
1	a	28	VAL	3.3
1	i	832	ILE	3.3
1	G	41	GLU	3.3
1	I	105	LEU	3.3

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Mol	Chain	Res	Type	RSRZ
1	W	825	LEU	3.3
1	W	841	LEU	3.3
1	V	842	PHE	3.3
1	F	105	LEU	3.3
1	f	83	LEU	3.3
1	C	259	HIS	3.3
1	N	44	LEU	3.3
1	C	816	GLU	3.3
1	D	828	LYS	3.3
1	Y	185	ARG	3.3
1	Q	28	VAL	3.3
1	Q	36	ILE	3.3
1	k	842	PHE	3.3
1	W	74	LEU	3.3
1	e	821	LEU	3.3
1	e	845	ALA	3.3
1	D	41	GLU	3.3
1	Q	817	MET	3.3
1	S	78	THR	3.3
1	f	842	PHE	3.3
1	V	831	LEU	3.3
1	K	817	MET	3.3
1	K	45	PHE	3.3
1	Y	839	ILE	3.3
1	W	831	LEU	3.2
1	g	841	LEU	3.2
1	d	820	LYS	3.2
1	h	54	PRO	3.2
1	b	819	VAL	3.2
1	P	833	THR	3.2
1	R	825	LEU	3.2
1	X	95	ASP	3.2
1	Y	817	MET	3.2
1	c	79	GLY	3.2
1	F	36	ILE	3.2
1	b	831	LEU	3.2
1	N	825	LEU	3.2
1	d	845	ALA	3.2
1	J	101	PRO	3.2
1	m	99	LEU	3.2
1	H	278	PRO	3.2
1	T	827	LEU	3.2

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Mol	Chain	Res	Type	RSRZ
1	U	827	LEU	3.2
1	W	834	ASP	3.2
1	d	819	VAL	3.2
1	Z	827	LEU	3.2
1	k	42	ARG	3.2
1	m	827	LEU	3.2
1	Q	131	ASP	3.2
1	a	820	LYS	3.2
1	Y	834	ASP	3.2
1	K	81	VAL	3.2
1	L	19	LEU	3.2
1	Q	42	ARG	3.2
1	h	825	LEU	3.2
1	H	816	GLU	3.2
1	Z	839	ILE	3.2
1	a	831	LEU	3.2
1	k	4	GLU	3.2
1	l	832	ILE	3.2
1	E	836	SER	3.2
1	j	842	PHE	3.2
1	Q	105	LEU	3.2
1	W	91	ARG	3.2
1	Y	832	ILE	3.2
1	E	278	PRO	3.2
1	X	834	ASP	3.2
1	E	835	GLY	3.2
1	K	42	ARG	3.2
1	Y	79	GLY	3.2
1	f	841	LEU	3.2
1	Q	346	GLU	3.2
1	c	80	GLN	3.1
1	J	105	LEU	3.1
1	E	816	GLU	3.1
1	W	817	MET	3.1
1	a	54	PRO	3.1
1	W	185	ARG	3.1
1	S	816	GLU	3.1
1	K	816	GLU	3.1
1	b	834	ASP	3.1
1	l	834	ASP	3.1
1	X	24	ASN	3.1
1	Z	832	ILE	3.1

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Mol	Chain	Res	Type	RSRZ
1	T	19	LEU	3.1
1	D	816	GLU	3.1
1	c	211	GLU	3.1
1	D	98	PRO	3.1
1	E	55	PRO	3.1
1	G	27	ARG	3.1
1	T	825	LEU	3.1
1	X	845	ALA	3.1
1	N	828	LYS	3.1
1	W	839	ILE	3.1
1	T	1	MET	3.1
1	c	817	MET	3.1
1	j	101	PRO	3.1
1	G	836	SER	3.1
1	U	839	ILE	3.1
1	S	211	GLU	3.1
1	G	14	HIS	3.1
1	c	831	LEU	3.1
1	I	103	GLU	3.1
1	m	103	GLU	3.1
1	G	828	LYS	3.1
1	e	843	SER	3.1
1	e	4	GLU	3.1
1	m	117	PRO	3.1
1	S	828	LYS	3.1
1	h	816	GLU	3.1
1	k	828	LYS	3.1
1	A	19	LEU	3.1
1	e	825	LEU	3.1
1	g	825	LEU	3.1
1	P	25	VAL	3.0
1	X	93	ALA	3.0
1	Y	828	LYS	3.0
1	S	19	LEU	3.0
1	K	80	GLN	3.0
1	F	1	MET	3.0
1	J	47	PRO	3.0
1	c	126	LEU	3.0
1	d	278	PRO	3.0
1	d	329	GLN	3.0
1	X	221	LEU	3.0
1	X	817	MET	3.0

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Mol	Chain	Res	Type	RSRZ
1	h	20	ASP	3.0
1	l	55	PRO	3.0
1	U	828	LYS	3.0
1	c	100	TYR	3.0
1	d	843	SER	3.0
1	e	820	LYS	3.0
1	K	79	GLY	3.0
1	f	825	LEU	3.0
1	U	817	MET	3.0
1	j	42	ARG	3.0
1	H	820	LYS	3.0
1	d	842	PHE	3.0
1	f	79	GLY	3.0
1	W	816	GLU	3.0
1	l	330	GLN	3.0
1	D	25	VAL	3.0
1	M	278	PRO	3.0
1	Q	24	ASN	3.0
1	d	839	ILE	3.0
1	Q	825	LEU	3.0
1	Y	827	LEU	3.0
1	a	845	ALA	3.0
1	j	825	LEU	3.0
1	B	816	GLU	3.0
1	Z	55	PRO	3.0
1	A	816	GLU	3.0
1	T	14	HIS	3.0
1	W	14	HIS	3.0
1	i	839	ILE	3.0
1	j	816	GLU	3.0
1	l	42	ARG	3.0
1	I	28	VAL	3.0
1	h	839	ILE	3.0
1	d	19	LEU	3.0
1	K	278	PRO	3.0
1	Z	845	ALA	3.0
1	a	79	GLY	3.0
1	S	41	GLU	3.0
1	b	825	LEU	3.0
1	l	828	LYS	3.0
1	c	843	SER	3.0
1	H	82	ARG	3.0

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Mol	Chain	Res	Type	RSRZ
1	R	18	VAL	2.9
1	V	48	VAL	2.9
1	e	841	LEU	2.9
1	V	22	ASN	2.9
1	f	42	ARG	2.9
1	l	80	GLN	2.9
1	f	839	ILE	2.9
1	O	19	LEU	2.9
1	Q	19	LEU	2.9
1	e	83	LEU	2.9
1	R	79	GLY	2.9
1	b	845	ALA	2.9
1	C	828	LYS	2.9
1	b	816	GLU	2.9
1	e	834	ASP	2.9
1	X	48	VAL	2.9
1	k	25	VAL	2.9
1	T	828	LYS	2.9
1	J	816	GLU	2.9
1	N	42	ARG	2.9
1	Q	816	GLU	2.9
1	S	185	ARG	2.9
1	V	346	GLU	2.9
1	V	825	LEU	2.9
1	i	825	LEU	2.9
1	j	1	MET	2.9
1	U	148	PRO	2.9
1	B	259	HIS	2.9
1	M	98	PRO	2.9
1	O	816	GLU	2.9
1	c	14	HIS	2.9
1	G	835	GLY	2.9
1	i	1	MET	2.9
1	F	259	HIS	2.9
1	Q	221	LEU	2.9
1	A	27	ARG	2.9
1	Z	100	TYR	2.9
1	c	27	ARG	2.9
1	d	817	MET	2.9
1	j	50	MET	2.9
1	g	42	ARG	2.9
1	K	4	GLU	2.9

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Mol	Chain	Res	Type	RSRZ
1	d	1	MET	2.9
1	a	278	PRO	2.9
1	k	98	PRO	2.9
1	V	41	GLU	2.9
1	F	185	ARG	2.9
1	K	19	LEU	2.9
1	V	832	ILE	2.9
1	h	841	LEU	2.9
1	I	101	PRO	2.9
1	H	1	MET	2.9
1	Z	29	GLU	2.9
1	R	828	LYS	2.8
1	E	101	PRO	2.8
1	e	55	PRO	2.8
1	b	842	PHE	2.8
1	R	49	ARG	2.8
1	A	14	HIS	2.8
1	V	278	PRO	2.8
1	Y	14	HIS	2.8
1	a	100	TYR	2.8
1	d	825	LEU	2.8
1	F	90	ILE	2.8
1	Q	347	GLU	2.8
1	a	828	LYS	2.8
1	c	28	VAL	2.8
1	f	94	GLN	2.8
1	Z	841	LEU	2.8
1	L	278	PRO	2.8
1	W	92	LEU	2.8
1	a	817	MET	2.8
1	c	834	ASP	2.8
1	W	81	VAL	2.8
1	f	539	LEU	2.8
1	Q	828	LYS	2.8
1	O	1	MET	2.8
1	V	36	ILE	2.8
1	Y	259	HIS	2.8
1	d	4	GLU	2.8
1	T	148	PRO	2.8
1	Z	828	LYS	2.8
1	l	98	PRO	2.8
1	h	842	PHE	2.8

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Mol	Chain	Res	Type	RSRZ
1	U	41	GLU	2.8
1	B	28	VAL	2.8
1	a	185	ARG	2.8
1	X	83	LEU	2.8
1	Z	831	LEU	2.8
1	Q	4	GLU	2.8
1	E	205	LEU	2.8
1	a	211	GLU	2.8
1	Z	171	ASN	2.8
1	F	74	LEU	2.8
1	B	101	PRO	2.8
1	Z	812	VAL	2.8
1	J	41	GLU	2.7
1	L	146	GLU	2.7
1	j	4	GLU	2.7
1	F	80	GLN	2.7
1	L	22	ASN	2.7
1	D	259	HIS	2.7
1	S	74	LEU	2.7
1	X	149	GLY	2.7
1	N	836	SER	2.7
1	T	17	HIS	2.7
1	J	185	ARG	2.7
1	d	834	ASP	2.7
1	G	816	GLU	2.7
1	U	842	PHE	2.7
1	X	825	LEU	2.7
1	b	827	LEU	2.7
1	f	19	LEU	2.7
1	R	131	ASP	2.7
1	U	816	GLU	2.7
1	F	45	PHE	2.7
1	b	15	TYR	2.7
1	d	27	ARG	2.7
1	m	828	LYS	2.7
1	Z	211	GLU	2.7
1	j	100	TYR	2.7
1	K	44	LEU	2.7
1	Z	842	PHE	2.7
1	V	816	GLU	2.7
1	Z	80	GLN	2.7
1	O	149	GLY	2.7

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Mol	Chain	Res	Type	RSRZ
1	J	78	THR	2.7
1	h	4	GLU	2.7
1	k	816	GLU	2.7
1	I	100	TYR	2.7
1	S	825	LEU	2.7
1	W	211	GLU	2.7
1	S	97	PHE	2.7
1	M	94	GLN	2.7
1	I	148	PRO	2.7
1	J	33	LYS	2.7
1	Z	825	LEU	2.7
1	c	99	LEU	2.7
1	h	828	LYS	2.7
1	I	25	VAL	2.7
1	R	94	GLN	2.7
1	a	259	HIS	2.7
1	d	17	HIS	2.7
1	P	828	LYS	2.7
1	N	816	GLU	2.7
1	l	81	VAL	2.7
1	f	36	ILE	2.7
1	F	221	LEU	2.6
1	S	827	LEU	2.6
1	Z	22	ASN	2.7
1	c	825	LEU	2.6
1	A	828	LYS	2.6
1	O	836	SER	2.6
1	E	259	HIS	2.6
1	X	151	TYR	2.6
1	Z	116	LEU	2.6
1	l	4	GLU	2.6
1	W	148	PRO	2.6
1	T	42	ARG	2.6
1	T	834	ASP	2.6
1	E	109	ILE	2.6
1	S	36	ILE	2.6
1	X	842	PHE	2.6
1	W	95	ASP	2.6
1	l	28	VAL	2.6
1	P	82	ARG	2.6
1	k	278	PRO	2.6
1	M	80	GLN	2.6

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Mol	Chain	Res	Type	RSRZ
1	D	836	SER	2.6
1	V	828	LYS	2.6
1	j	828	LYS	2.6
1	C	36	ILE	2.6
1	L	15	TYR	2.6
1	W	17	HIS	2.6
1	b	817	MET	2.6
1	K	827	LEU	2.6
1	N	26	SER	2.6
1	R	4	GLU	2.6
1	B	828	LYS	2.6
1	H	36	ILE	2.6
1	K	116	LEU	2.6
1	l	100	TYR	2.6
1	a	55	PRO	2.6
1	i	80	GLN	2.6
1	X	828	LYS	2.6
1	Q	45	PHE	2.6
1	H	812	VAL	2.6
1	O	42	ARG	2.6
1	a	57	HIS	2.6
1	D	36	ILE	2.6
1	V	94	GLN	2.6
1	g	828	LYS	2.6
1	c	116	LEU	2.6
1	Z	154	GLN	2.6
1	i	37	ARG	2.6
1	P	211	GLU	2.5
1	U	834	ASP	2.5
1	c	278	PRO	2.5
1	D	82	ARG	2.5
1	I	278	PRO	2.5
1	D	211	GLU	2.5
1	A	83	LEU	2.5
1	Y	119	THR	2.5
1	R	185	ARG	2.5
1	c	82	ARG	2.5
1	D	19	LEU	2.5
1	b	259	HIS	2.5
1	a	36	ILE	2.5
1	c	105	LEU	2.5
1	T	346	GLU	2.5

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Mol	Chain	Res	Type	RSRZ
1	Y	199	ARG	2.5
1	m	27	ARG	2.5
1	a	170	GLN	2.5
1	d	832	ILE	2.5
1	g	539	LEU	2.5
1	I	18	VAL	2.5
1	F	48	VAL	2.5
1	X	170	GLN	2.5
1	g	278	PRO	2.5
1	O	25	VAL	2.5
1	a	14	HIS	2.5
1	Z	817	MET	2.5
1	d	841	LEU	2.5
1	A	278	PRO	2.5
1	S	25	VAL	2.5
1	E	98	PRO	2.5
1	S	148	PRO	2.5
1	R	50	MET	2.5
1	i	79	GLY	2.5
1	T	78	THR	2.5
1	b	278	PRO	2.5
1	f	4	GLU	2.5
1	m	98	PRO	2.5
1	b	841	LEU	2.5
1	I	36	ILE	2.5
1	R	259	HIS	2.5
1	J	151	TYR	2.5
1	R	816	GLU	2.5
1	f	278	PRO	2.5
1	b	14	HIS	2.5
1	J	24	ASN	2.4
1	M	816	GLU	2.4
1	X	91	ARG	2.4
1	e	842	PHE	2.4
1	B	170	GLN	2.4
1	G	221	LEU	2.4
1	J	4	GLU	2.4
1	X	4	GLU	2.4
1	k	19	LEU	2.4
1	D	28	VAL	2.4
1	U	27	ARG	2.4
1	L	347	GLU	2.4

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Mol	Chain	Res	Type	RSRZ
1	Y	25	VAL	2.4
1	H	41	GLU	2.4
1	X	215	LEU	2.4
1	C	109	ILE	2.4
1	Y	278	PRO	2.4
1	j	20	ASP	2.4
1	W	24	ASN	2.4
1	h	42	ARG	2.4
1	G	12	PRO	2.4
1	N	98	PRO	2.4
1	S	164	GLN	2.4
1	T	55	PRO	2.4
1	k	36	ILE	2.4
1	e	49	ARG	2.4
1	i	83	LEU	2.4
1	d	346	GLU	2.4
1	G	15	TYR	2.4
1	H	211	GLU	2.4
1	L	133	ASN	2.4
1	g	22	ASN	2.4
1	I	17	HIS	2.4
1	T	259	HIS	2.4
1	I	836	SER	2.4
1	T	4	GLU	2.4
1	W	828	LYS	2.4
1	L	18	VAL	2.4
1	T	94	GLN	2.4
1	k	100	TYR	2.4
1	N	1	MET	2.4
1	F	93	ALA	2.4
1	b	828	LYS	2.4
1	c	845	ALA	2.4
1	Z	816	GLU	2.4
1	F	835	GLY	2.4
1	A	28	VAL	2.4
1	D	174	LEU	2.4
1	I	81	VAL	2.4
1	I	49	ARG	2.4
1	I	102	GLY	2.4
1	e	816	GLU	2.4
1	m	816	GLU	2.4
1	E	174	LEU	2.4

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Mol	Chain	Res	Type	RSRZ
1	R	539	LEU	2.4
1	X	185	ARG	2.4
1	a	842	PHE	2.4
1	U	25	VAL	2.4
1	d	83	LEU	2.4
1	E	1	MET	2.3
1	P	44	LEU	2.3
1	i	221	LEU	2.3
1	b	101	PRO	2.3
1	e	105	LEU	2.3
1	i	259	HIS	2.3
1	c	828	LYS	2.3
1	A	101	PRO	2.3
1	e	48	VAL	2.3
1	D	199	ARG	2.3
1	G	62	ALA	2.3
1	d	259	HIS	2.3
1	T	41	GLU	2.3
1	W	19	LEU	2.3
1	f	346	GLU	2.3
1	j	83	LEU	2.3
1	Q	148	PRO	2.3
1	m	54	PRO	2.3
1	i	816	GLU	2.3
1	Y	94	GLN	2.3
1	c	55	PRO	2.3
1	X	205	LEU	2.3
1	Z	41	GLU	2.3
1	G	841	LEU	2.3
1	K	812	VAL	2.3
1	P	816	GLU	2.3
1	c	346	GLU	2.3
1	J	77	ILE	2.3
1	T	80	GLN	2.3
1	H	221	LEU	2.3
1	U	259	HIS	2.3
1	D	22	ASN	2.3
1	c	103	GLU	2.3
1	b	330	GLN	2.3
1	C	199	ARG	2.3
1	l	185	ARG	2.3
1	L	33	LYS	2.3

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Mol	Chain	Res	Type	RSRZ
1	S	83	LEU	2.3
1	i	640	VAL	2.3
1	j	18	VAL	2.3
1	V	101	PRO	2.3
1	X	28	VAL	2.3
1	J	55	PRO	2.3
1	V	47	PRO	2.3
1	B	17	HIS	2.3
1	T	53	VAL	2.2
1	g	19	LEU	2.2
1	m	74	LEU	2.2
1	U	78	THR	2.2
1	J	156	GLU	2.2
1	f	41	GLU	2.2
1	i	330	GLN	2.2
1	l	329	GLN	2.2
1	l	816	GLU	2.2
1	c	101	PRO	2.2
1	j	98	PRO	2.2
1	L	126	LEU	2.2
1	Z	42	ARG	2.2
1	k	74	LEU	2.2
1	F	35	TYR	2.2
1	f	9	ARG	2.2
1	G	259	HIS	2.2
1	V	45	PHE	2.2
1	M	211	GLU	2.2
1	Y	539	LEU	2.2
1	T	49	ARG	2.2
1	h	27	ARG	2.2
1	Y	19	LEU	2.2
1	J	278	PRO	2.2
1	U	278	PRO	2.2
1	Y	221	LEU	2.2
1	h	518	LEU	2.2
1	h	259	HIS	2.2
1	D	342	GLU	2.2
1	Z	81	VAL	2.2
1	b	116	LEU	2.2
1	G	7	ILE	2.2
1	A	15	TYR	2.2
1	L	44	LEU	2.2

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Mol	Chain	Res	Type	RSRZ
1	a	337	LEU	2.2
1	e	17	HIS	2.2
1	i	211	GLU	2.2
1	U	185	ARG	2.2
1	E	142	GLU	2.2
1	Q	81	VAL	2.2
1	c	842	PHE	2.2
1	m	80	GLN	2.2
1	W	227	LEU	2.2
1	e	828	LYS	2.2
1	i	828	LYS	2.2
1	Z	93	ALA	2.2
1	R	15	TYR	2.2
1	A	185	ARG	2.2
1	E	177	ARG	2.2
1	G	92	LEU	2.2
1	g	4	GLU	2.2
1	V	49	ARG	2.2
1	k	44	LEU	2.2
1	G	156	GLU	2.2
1	f	816	GLU	2.2
1	A	42	ARG	2.2
1	Y	816	GLU	2.2
1	g	36	ILE	2.2
1	G	26	SER	2.1
1	a	78	THR	2.1
1	K	36	ILE	2.1
1	X	101	PRO	2.1
1	e	1	MET	2.1
1	Q	259	HIS	2.1
1	j	259	HIS	2.1
1	T	156	GLU	2.1
1	e	330	GLN	2.1
1	D	197	LEU	2.1
1	D	212	VAL	2.1
1	M	105	LEU	2.1
1	T	25	VAL	2.1
1	E	211	GLU	2.1
1	W	47	PRO	2.1
1	W	48	VAL	2.1
1	d	828	LYS	2.1
1	W	151	TYR	2.1

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Mol	Chain	Res	Type	RSRZ
1	T	816	GLU	2.1
1	V	798	MET	2.1
1	X	268	LEU	2.1
1	a	126	LEU	2.1
1	Y	344	GLU	2.1
1	C	14	HIS	2.1
1	j	94	GLN	2.1
1	E	54	PRO	2.1
1	k	45	PHE	2.1
1	d	80	GLN	2.1
1	e	18	VAL	2.1
1	F	95	ASP	2.1
1	T	101	PRO	2.1
1	c	127	LEU	2.1
1	c	539	LEU	2.1
1	e	539	LEU	2.1
1	E	100	TYR	2.1
1	B	117	PRO	2.1
1	Q	211	GLU	2.1
1	Q	116	LEU	2.1
1	a	329	GLN	2.1
1	d	330	GLN	2.1
1	l	259	HIS	2.1
1	X	211	GLU	2.1
1	a	834	ASP	2.1
1	m	346	GLU	2.1
1	W	259	HIS	2.1
1	F	25	VAL	2.1
1	J	18	VAL	2.1
1	K	149	GLY	2.1
1	L	25	VAL	2.1
1	e	19	LEU	2.1
1	X	22	ASN	2.1
1	D	33	LYS	2.1
1	V	82	ARG	2.1
1	T	18	VAL	2.1
1	B	19	LEU	2.1
1	l	1	MET	2.1
1	F	49	ARG	2.0
1	G	100	TYR	2.0
1	R	48	VAL	2.0
1	R	105	LEU	2.0

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Mol	Chain	Res	Type	RSRZ
1	I	5	GLU	2.0
1	f	347	GLU	2.0
1	G	34	THR	2.0
1	I	82	ARG	2.0
1	F	151	TYR	2.0
1	U	105	LEU	2.0
1	Z	259	HIS	2.0
1	h	539	LEU	2.0
1	l	44	LEU	2.0
1	E	91	ARG	2.0
1	W	798	MET	2.0
1	C	537	LEU	2.0
1	f	518	LEU	2.0
1	F	50	MET	2.0
1	X	162	ILE	2.0
1	F	19	LEU	2.0
1	M	259	HIS	2.0
1	R	84	ARG	2.0
1	T	59	CYS	2.0
1	Y	82	ARG	2.0
1	B	215	LEU	2.0
1	f	1	MET	2.0
1	k	221	LEU	2.0
1	C	185	ARG	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

There are no monosaccharides 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.