



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 10:27 AM UTC

PDB ID : 5XJO / pdb_00005xjo
Title : Plant receptor ERL1-TMM in complex with peptide EPF1
Authors : Chai, J.; Lin, G.; Zhang, L.; Han, Z.; Shpak, E.D.; Yang, X.
Deposited on : 2017-05-03
Resolution : 2.63 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	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

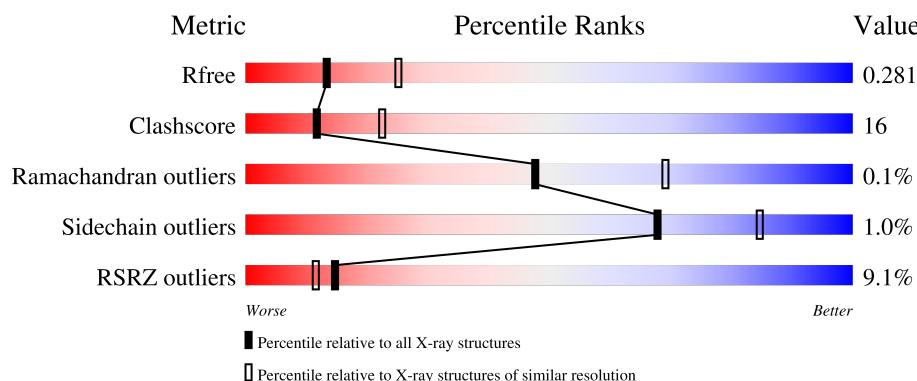
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.63 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}	180053	4951 (2.64-2.60)
Clashscore	190562	5303 (2.64-2.60)
Ramachandran outliers	187476	5217 (2.64-2.60)
Sidechain outliers	187428	5217 (2.64-2.60)
RSRZ outliers	180081	4950 (2.64-2.60)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments 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	539	6% 69% 27% ..
1	B	539	7% 70% 27% .
2	E	52	13% 52% 29% 19%
2	F	52	12% 56% 25% 19%
3	C	374	9% 65% 32% ..

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Mol	Chain	Length	Quality of chain
3	D	374	13% 63% 33% ..

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 14334 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 LRR receptor-like serine/threonine-protein kinase ERL1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	523	Total	C	N	O	S	0	0	0
			3997	2536	680	765	16			
1	B	523	Total	C	N	O	S	0	0	0
			3997	2536	680	765	16			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	546	ALA	LYS	conflict	UNP C0LGW6
B	546	ALA	LYS	conflict	UNP C0LGW6

- Molecule 2 is a protein called Protein EPIDERMAL PATTERNING FACTOR 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	F	42	Total	C	N	O	S	0	0	0
			306	188	54	54	10			
2	E	42	Total	C	N	O	S	0	0	0
			306	188	54	54	10			

- Molecule 3 is a protein called Protein TOO MANY MOUTHS.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	367	Total	C	N	O	S	0	0	0
			2864	1803	521	529	11			
3	D	367	Total	C	N	O	S	0	0	0
			2864	1803	521	529	11			

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	273	GLN	ILE	conflict	UNP Q9SSD1
C	312	ASN	THR	conflict	UNP Q9SSD1

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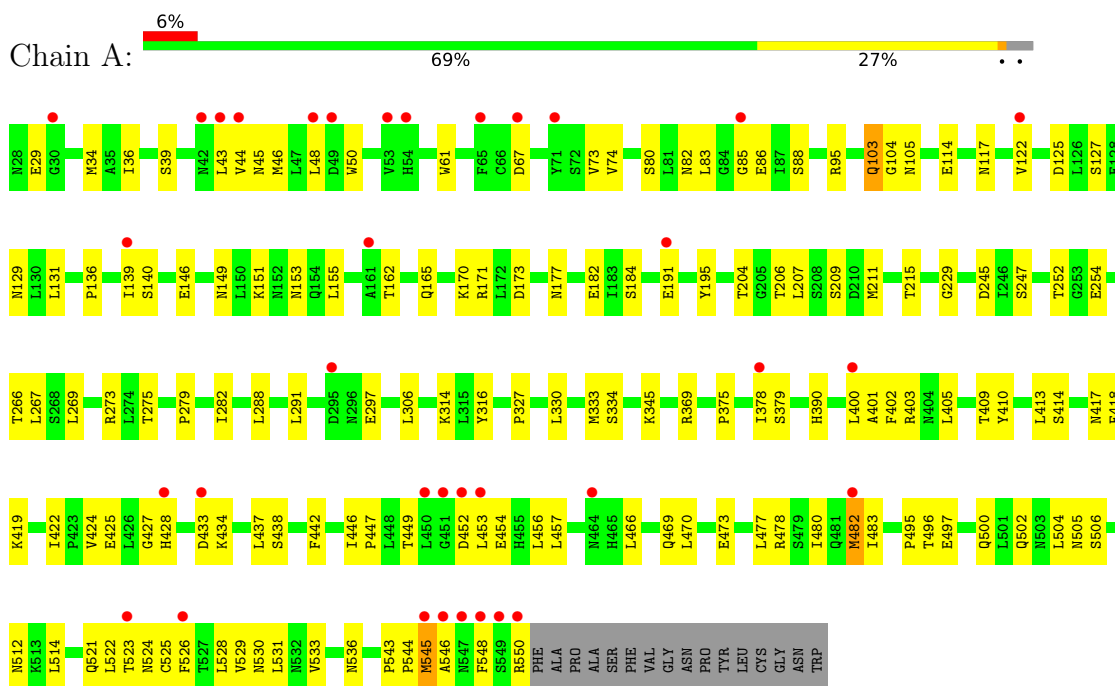
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Chain	Residue	Modelled	Actual	Comment	Reference
C	421	ALA	LEU	conflict	UNP Q9SSD1
C	422	ALA	ASP	conflict	UNP Q9SSD1
C	423	ALA	ASP	conflict	UNP Q9SSD1
D	273	GLN	ILE	conflict	UNP Q9SSD1
D	312	ASN	THR	conflict	UNP Q9SSD1
D	421	ALA	LEU	conflict	UNP Q9SSD1
D	422	ALA	ASP	conflict	UNP Q9SSD1
D	423	ALA	ASP	conflict	UNP Q9SSD1

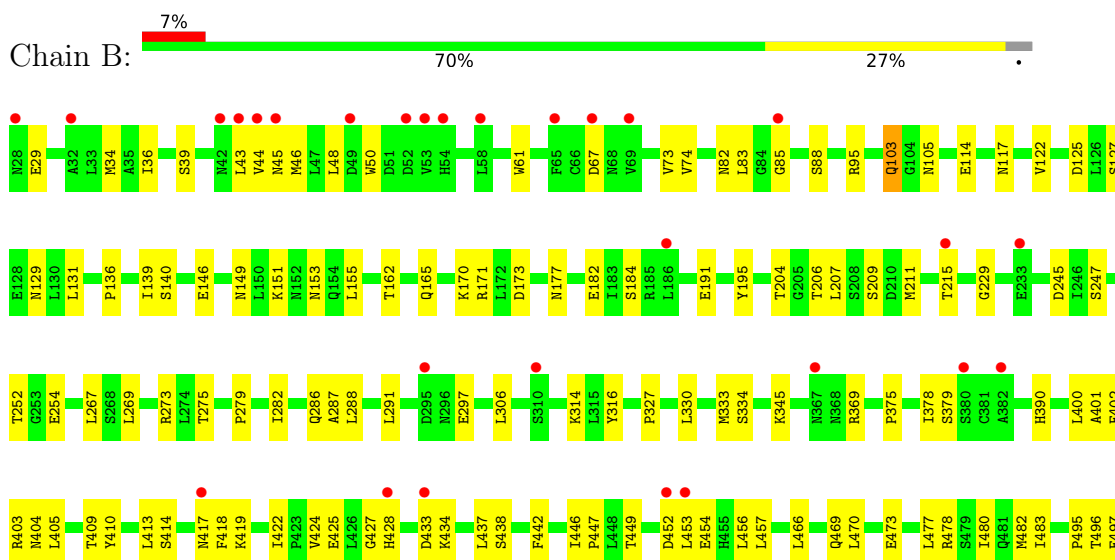
3 Residue-property plots

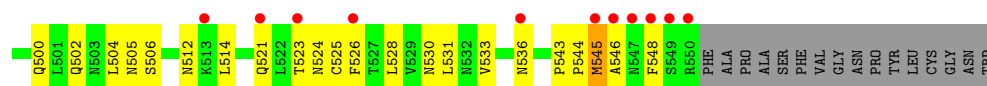
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: LRR receptor-like serine/threonine-protein kinase ERL1

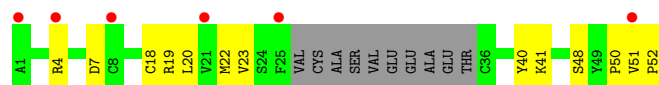


- Molecule 1: LRR receptor-like serine/threonine-protein kinase ERL1

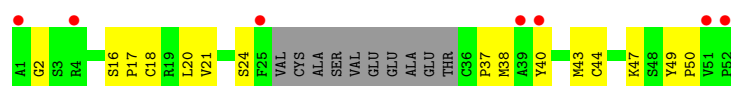




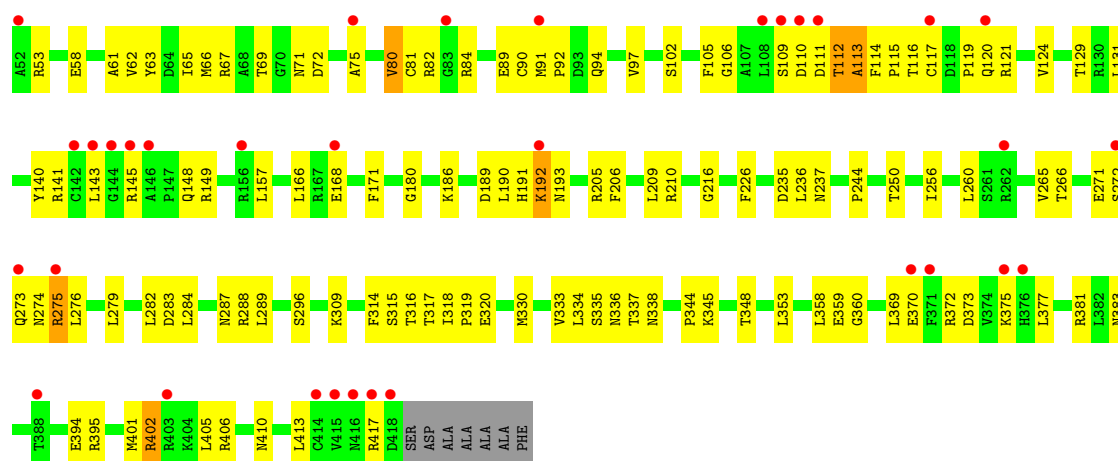
• Molecule 2: Protein EPIDERMAL PATTERNING FACTOR 1



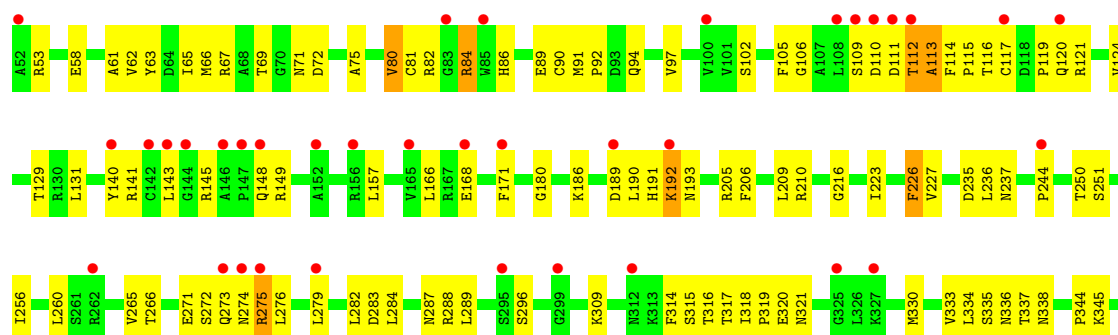
• Molecule 2: Protein EPIDERMAL PATTERNING FACTOR 1

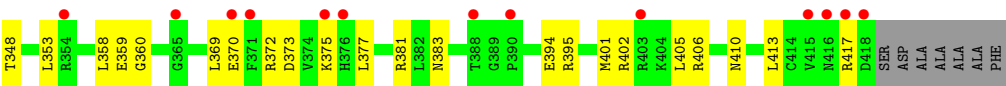


• Molecule 3: Protein TOO MANY MOUTHS



• Molecule 3: Protein TOO MANY MOUTHS





4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	66.11Å 66.15Å 143.49Å 97.61° 102.47° 93.68°	Depositor
Resolution (Å)	42.53 – 2.63 42.53 – 2.63	Depositor EDS
% Data completeness (in resolution range)	93.6 (42.53-2.63) 93.6 (42.53-2.63)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.69 (at 2.61Å)	Xtriage
Refinement program	PHENIX (1.10.1_2155: ???)	Depositor
R, R_{free}	0.252 , 0.310 0.271 , 0.281	Depositor DCC
R_{free} test set	3319 reflections (4.75%)	wwPDB-VP
Wilson B-factor (Å ²)	43.9	Xtriage
Anisotropy	0.475	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 23.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.88	EDS
Total number of atoms	14334	wwPDB-VP
Average B, all atoms (Å ²)	41.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 23.01 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 5.0799e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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	0.53	3/4066 (0.1%)	0.67	3/5532 (0.1%)
1	B	0.53	3/4066 (0.1%)	0.67	2/5532 (0.0%)
2	E	0.69	0/313	0.90	1/421 (0.2%)
2	F	0.70	0/313	0.82	0/421
3	C	0.79	2/2920 (0.1%)	0.84	6/3965 (0.2%)
3	D	0.79	2/2920 (0.1%)	0.86	8/3965 (0.2%)
All	All	0.65	10/14598 (0.1%)	0.75	20/19836 (0.1%)

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	402	ARG	C-O	-5.97	1.19	1.24
3	D	402	ARG	C-O	-5.96	1.19	1.24
1	B	103	GLN	CD-OE1	-5.82	1.12	1.23
1	A	103	GLN	CD-OE1	-5.81	1.12	1.23
1	A	103	GLN	CD-NE2	-5.78	1.21	1.33
1	B	103	GLN	CD-NE2	-5.78	1.21	1.33
3	C	105	PHE	C-O	-5.26	1.17	1.23
1	B	483	ILE	C-O	-5.25	1.18	1.24
3	D	105	PHE	C-O	-5.24	1.17	1.23
1	A	483	ILE	C-O	-5.23	1.18	1.24

All (20) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	545	MET	N-CA-C	-7.83	98.67	109.71
1	A	545	MET	N-CA-C	-7.83	98.67	109.71
3	D	192	LYS	N-CA-C	7.48	122.00	111.52
3	C	192	LYS	N-CA-C	7.47	121.98	111.52
3	D	111	ASP	N-CA-C	-7.43	103.11	111.14
3	C	111	ASP	N-CA-C	-7.41	103.14	111.14
2	E	2	GLY	N-CA-C	6.93	121.67	111.76
3	C	405	LEU	N-CA-C	-6.45	98.02	108.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	405	LEU	N-CA-C	-6.44	98.02	108.52
3	D	223	ILE	CA-C-N	-6.27	113.52	119.85
3	D	223	ILE	C-N-CA	-6.27	113.52	119.85
1	B	334	SER	N-CA-C	5.87	119.97	112.34
1	A	334	SER	N-CA-C	5.86	119.95	112.34
3	C	113	ALA	N-CA-C	5.79	119.04	110.48
3	D	113	ALA	N-CA-C	5.77	119.02	110.48
3	C	275	ARG	N-CA-C	5.60	119.38	112.54
3	D	275	ARG	N-CA-C	5.57	119.34	112.54
3	D	401	MET	N-CA-C	5.05	116.87	111.36
3	C	401	MET	N-CA-C	5.04	116.85	111.36
1	A	482	MET	N-CA-C	5.01	116.58	108.26

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3997	0	4048	120	4
1	B	3997	0	4048	118	4
2	E	306	0	294	14	0
2	F	306	0	296	13	0
3	C	2864	0	2904	99	4
3	D	2864	0	2904	106	4
All	All	14334	0	14494	457	8

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 16.

All (457) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:53:ARG:NH2	3:C:82:ARG:HH12	1.18	1.36
3:D:53:ARG:NH2	3:D:82:ARG:HH12	1.18	1.34

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:53:ARG:HH21	3:C:82:ARG:NH1	1.26	1.29
3:D:53:ARG:HH21	3:D:82:ARG:NH1	1.26	1.29
1:A:521:GLN:C	1:A:545:MET:HE1	1.56	1.28
1:B:521:GLN:C	1:B:545:MET:HE1	1.56	1.28
3:D:81:CYS:SG	3:D:90:CYS:SG	1.26	1.13
3:C:53:ARG:NH2	3:C:82:ARG:NH1	1.85	1.11
3:C:81:CYS:SG	3:C:90:CYS:SG	1.20	1.10
3:D:53:ARG:NH2	3:D:82:ARG:NH1	1.85	1.08
1:B:191:GLU:OE1	1:B:215:THR:OG1	1.73	1.05
3:D:272:SER:HB2	3:D:275:ARG:CZ	1.86	1.05
1:A:191:GLU:OE1	1:A:215:THR:OG1	1.73	1.04
3:C:272:SER:HB2	3:C:275:ARG:CZ	1.86	1.04
1:B:523:THR:HA	1:B:545:MET:HB3	1.47	0.95
1:A:523:THR:HA	1:A:545:MET:HB3	1.47	0.94
3:D:272:SER:HB2	3:D:275:ARG:NH2	1.83	0.94
3:C:272:SER:HB2	3:C:275:ARG:NH2	1.83	0.92
3:D:53:ARG:HH22	3:D:82:ARG:HH12	1.17	0.92
1:A:523:THR:CA	1:A:545:MET:HB3	1.98	0.91
3:C:53:ARG:HH22	3:C:82:ARG:HH12	1.17	0.91
3:C:81:CYS:CB	3:C:90:CYS:SG	2.60	0.90
3:C:81:CYS:SG	3:C:90:CYS:CB	2.60	0.89
1:B:523:THR:CA	1:B:545:MET:HB3	1.98	0.89
3:D:81:CYS:SG	3:D:90:CYS:CB	2.61	0.89
3:D:81:CYS:HG	3:D:90:CYS:CB	1.86	0.88
1:A:521:GLN:C	1:A:545:MET:CE	2.46	0.87
1:B:521:GLN:C	1:B:545:MET:CE	2.46	0.86
1:A:521:GLN:O	1:A:545:MET:HE1	1.75	0.86
1:B:95:ARG:NH2	1:B:117:ASN:HB3	1.91	0.85
1:A:95:ARG:NH2	1:A:117:ASN:HB3	1.91	0.85
1:B:521:GLN:O	1:B:545:MET:HE1	1.75	0.85
3:C:320:GLU:OE2	3:C:345:LYS:N	2.11	0.84
1:B:44:VAL:HG13	1:B:45:ASN:H	1.42	0.84
3:D:320:GLU:OE2	3:D:345:LYS:N	2.11	0.84
1:B:155:LEU:H	1:B:177:ASN:HD22	1.26	0.83
1:A:44:VAL:HG13	1:A:45:ASN:H	1.42	0.83
3:D:180:GLY:O	3:D:205:ARG:NH1	2.12	0.83
3:C:180:GLY:O	3:C:205:ARG:NH1	2.12	0.82
3:D:348:THR:HG21	3:D:370:GLU:HB3	1.61	0.82
3:C:140:TYR:HH	3:C:141:ARG:NH2	1.77	0.82
1:A:155:LEU:H	1:A:177:ASN:HD22	1.26	0.81
3:D:81:CYS:CB	3:D:90:CYS:SG	2.68	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:348:THR:HG21	3:C:370:GLU:HB3	1.61	0.81
1:B:433:ASP:HA	1:B:456:LEU:HA	1.64	0.80
1:A:433:ASP:HA	1:A:456:LEU:HA	1.64	0.80
3:C:272:SER:HB2	3:C:275:ARG:NH1	1.97	0.80
3:D:272:SER:HB2	3:D:275:ARG:NH1	1.97	0.78
1:B:207:LEU:HB3	1:B:211:MET:HE1	1.65	0.78
1:A:43:LEU:HG	1:A:46:MET:HB2	1.66	0.78
1:B:43:LEU:HG	1:B:46:MET:HB2	1.66	0.78
1:A:400:LEU:O	1:A:403:ARG:HG2	1.85	0.77
1:A:207:LEU:HB3	1:A:211:MET:HE1	1.65	0.77
3:C:81:CYS:HG	3:C:90:CYS:CB	1.92	0.76
1:A:170:LYS:HD3	3:C:109:SER:CB	2.14	0.76
3:C:71:ASN:HD22	3:C:115:PRO:HB3	1.50	0.76
1:B:400:LEU:O	1:B:403:ARG:HG2	1.85	0.76
3:D:109:SER:CB	1:B:170:LYS:HD3	2.16	0.76
3:D:71:ASN:HD22	3:D:115:PRO:HB3	1.50	0.75
1:A:129:ASN:HB2	1:A:153:ASN:HD21	1.51	0.75
1:B:129:ASN:HB2	1:B:153:ASN:HD21	1.51	0.75
2:E:44:CYS:O	2:E:47:LYS:HG3	1.86	0.75
3:D:272:SER:CB	3:D:275:ARG:NH2	2.51	0.74
3:C:186:LYS:HB3	3:C:210:ARG:HG2	1.70	0.74
3:C:272:SER:CB	3:C:275:ARG:NH2	2.51	0.73
3:D:186:LYS:HB3	3:D:210:ARG:HG2	1.70	0.73
1:A:524:ASN:H	1:A:545:MET:CE	2.02	0.71
3:C:140:TYR:HH	3:C:141:ARG:HH21	1.35	0.71
1:B:524:ASN:H	1:B:545:MET:CE	2.03	0.71
3:C:71:ASN:ND2	3:C:115:PRO:HB3	2.06	0.70
1:A:153:ASN:HB2	1:A:177:ASN:HD21	1.57	0.70
3:D:140:TYR:OH	3:D:141:ARG:NH2	2.24	0.70
3:D:316:THR:HG22	3:D:317:THR:H	1.56	0.70
3:D:71:ASN:ND2	3:D:115:PRO:HB3	2.06	0.70
1:A:103:GLN:HG3	1:A:127:SER:OG	1.92	0.70
1:B:521:GLN:CA	1:B:545:MET:HE1	2.22	0.70
3:C:316:THR:HG22	3:C:317:THR:H	1.56	0.70
1:B:153:ASN:HB2	1:B:177:ASN:HD21	1.57	0.70
3:C:140:TYR:OH	3:C:141:ARG:NH2	2.24	0.69
1:A:521:GLN:CA	1:A:545:MET:HE1	2.22	0.69
1:B:103:GLN:HG3	1:B:127:SER:OG	1.92	0.68
3:D:140:TYR:HH	3:D:141:ARG:NH2	1.91	0.68
1:B:524:ASN:N	1:B:545:MET:CE	2.57	0.68
1:A:131:LEU:H	1:A:153:ASN:HD22	1.41	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:131:LEU:H	1:B:153:ASN:HD22	1.41	0.68
3:C:94:GLN:CD	3:C:94:GLN:H	2.02	0.67
3:D:94:GLN:CD	3:D:94:GLN:H	2.02	0.67
1:A:500:GLN:O	1:A:502:GLN:OE1	2.14	0.65
1:A:46:MET:HE2	1:A:46:MET:HA	1.79	0.65
1:B:46:MET:HE2	1:B:46:MET:HA	1.79	0.65
1:A:375:PRO:O	1:A:378:ILE:HG22	1.97	0.65
1:A:524:ASN:N	1:A:545:MET:CE	2.56	0.65
3:D:110:ASP:HA	3:D:113:ALA:HB2	1.79	0.64
1:B:425:GLU:OE1	1:B:425:GLU:N	2.23	0.64
1:B:500:GLN:O	1:B:502:GLN:OE1	2.14	0.64
1:B:82:ASN:HA	1:B:105:ASN:HA	1.79	0.64
3:C:110:ASP:HA	3:C:113:ALA:HB2	1.79	0.64
1:A:482:MET:HG2	1:A:506:SER:HB2	1.80	0.64
1:B:375:PRO:O	1:B:378:ILE:HG22	1.97	0.64
1:A:82:ASN:HA	1:A:105:ASN:HA	1.78	0.64
1:A:497:GLU:OE2	1:A:497:GLU:N	2.31	0.64
3:C:235:ASP:OD1	3:C:237:ASN:ND2	2.31	0.64
3:D:120:GLN:O	3:D:145:ARG:HA	1.98	0.64
1:B:43:LEU:HD12	1:B:83:LEU:HD22	1.80	0.64
3:C:383:ASN:OD1	3:C:406:ARG:NH2	2.32	0.63
3:D:383:ASN:OD1	3:D:406:ARG:NH2	2.32	0.63
1:B:482:MET:HG2	1:B:506:SER:HB2	1.80	0.63
1:B:497:GLU:N	1:B:497:GLU:OE2	2.31	0.63
3:D:235:ASP:OD1	3:D:237:ASN:ND2	2.31	0.62
3:D:120:GLN:O	3:D:121:ARG:NH1	2.33	0.62
1:B:400:LEU:H	1:B:400:LEU:HD12	1.64	0.62
3:C:120:GLN:O	3:C:145:ARG:HA	1.98	0.62
3:C:120:GLN:O	3:C:121:ARG:NH1	2.33	0.62
1:A:400:LEU:HD12	1:A:400:LEU:H	1.64	0.62
3:C:191:HIS:NE2	3:C:192:LYS:HG3	2.14	0.62
3:D:191:HIS:NE2	3:D:192:LYS:HG3	2.15	0.62
3:D:381:ARG:HD3	3:D:406:ARG:NH2	2.14	0.62
3:C:381:ARG:HD3	3:C:406:ARG:NH2	2.14	0.61
1:A:43:LEU:HD12	1:A:83:LEU:HD22	1.80	0.61
1:A:425:GLU:OE1	1:A:425:GLU:N	2.23	0.61
1:B:288:LEU:HD13	1:B:291:LEU:HB2	1.83	0.60
3:C:190:LEU:O	3:C:193:ASN:ND2	2.34	0.60
2:F:40:TYR:HB2	2:F:51:VAL:HG11	1.84	0.60
1:B:400:LEU:C	1:B:402:PHE:H	2.10	0.60
1:B:245:ASP:OD1	1:B:247:SER:OG	2.15	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:272:SER:CB	3:D:275:ARG:HH22	2.15	0.60
3:D:190:LEU:O	3:D:193:ASN:ND2	2.35	0.59
1:A:288:LEU:HD13	1:A:291:LEU:HB2	1.83	0.59
1:B:67:ASP:OD1	1:B:74:VAL:HG21	2.03	0.59
1:A:165:GLN:NE2	3:C:283:ASP:OD2	2.34	0.59
2:E:24:SER:OG	2:E:38:MET:HE3	2.02	0.59
1:B:45:ASN:HA	1:B:48:LEU:HG	1.85	0.59
1:A:427:GLY:HA2	1:A:453:LEU:HD11	1.84	0.59
1:A:67:ASP:OD1	1:A:74:VAL:HG21	2.02	0.58
3:C:410:ASN:HB2	3:C:413:LEU:HD12	1.85	0.58
1:A:400:LEU:C	1:A:402:PHE:H	2.10	0.58
2:E:20:LEU:HD11	2:E:40:TYR:HB3	1.85	0.58
3:C:309:LYS:HB2	3:C:333:VAL:HG12	1.85	0.58
3:D:410:ASN:HB2	3:D:413:LEU:HD12	1.85	0.58
3:D:309:LYS:HB2	3:D:333:VAL:HG12	1.85	0.58
1:B:427:GLY:HA2	1:B:453:LEU:HD11	1.84	0.58
3:C:272:SER:CB	3:C:275:ARG:HH22	2.15	0.58
1:A:45:ASN:HA	1:A:48:LEU:HG	1.85	0.58
1:B:306:LEU:O	1:B:333:MET:HE2	2.04	0.58
1:A:425:GLU:CD	1:A:425:GLU:H	2.07	0.58
1:A:306:LEU:O	1:A:333:MET:HE2	2.04	0.58
3:D:353:LEU:HG	3:D:377:LEU:HD21	1.85	0.57
1:B:413:LEU:HB3	1:B:418:PHE:CE2	2.39	0.57
3:C:353:LEU:HG	3:C:377:LEU:HD21	1.85	0.57
3:C:372:ARG:HD3	3:C:394:GLU:OE2	2.05	0.57
1:A:245:ASP:OD1	1:A:247:SER:OG	2.15	0.57
1:A:345:LYS:HZ1	1:A:369:ARG:HH12	1.53	0.57
1:A:413:LEU:HB3	1:A:418:PHE:CE2	2.39	0.57
3:D:372:ARG:HD3	3:D:394:GLU:OE2	2.05	0.56
3:D:265:VAL:HG12	3:D:287:ASN:OD1	2.05	0.56
3:C:265:VAL:HG12	3:C:287:ASN:OD1	2.05	0.56
3:D:129:THR:HA	3:D:157:LEU:HD21	1.87	0.56
1:B:531:LEU:HD11	1:B:533:VAL:HG13	1.87	0.56
2:E:47:LYS:HD3	2:E:49:TYR:OH	2.06	0.56
3:D:256:ILE:HA	3:D:279:LEU:HA	1.88	0.56
3:C:271:GLU:H	3:C:271:GLU:CD	2.13	0.56
3:C:129:THR:HA	3:C:157:LEU:HD21	1.87	0.55
3:C:256:ILE:HA	3:C:279:LEU:HA	1.88	0.55
1:A:153:ASN:HB2	1:A:177:ASN:ND2	2.22	0.55
1:A:531:LEU:HD11	1:A:533:VAL:HG13	1.87	0.55
3:D:148:GLN:HG2	3:D:149:ARG:N	2.22	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:153:ASN:HB2	1:B:177:ASN:ND2	2.22	0.55
1:A:207:LEU:HB3	1:A:211:MET:CE	2.35	0.55
3:D:271:GLU:H	3:D:271:GLU:CD	2.13	0.55
1:B:345:LYS:HZ1	1:B:369:ARG:HH12	1.54	0.55
3:C:250:THR:OG1	3:C:275:ARG:NH2	2.40	0.55
1:A:446:ILE:HD11	1:A:466:LEU:HD13	1.89	0.54
1:A:505:ASN:HA	1:A:528:LEU:HA	1.89	0.54
3:D:283:ASP:OD2	1:B:165:GLN:NE2	2.38	0.54
1:B:114:GLU:OE1	1:B:114:GLU:N	2.33	0.54
3:C:148:GLN:HG2	3:C:149:ARG:N	2.22	0.54
3:C:276:LEU:HD12	3:C:279:LEU:HD22	1.89	0.54
1:B:345:LYS:NZ	1:B:369:ARG:HH12	2.04	0.54
1:B:151:LYS:HE2	1:B:173:ASP:OD2	2.07	0.54
1:A:345:LYS:NZ	1:A:369:ARG:HH12	2.04	0.54
1:B:446:ILE:HD11	1:B:466:LEU:HD13	1.89	0.54
1:B:505:ASN:HA	1:B:528:LEU:HA	1.89	0.54
3:C:273:GLN:NE2	3:C:282:LEU:HD11	2.23	0.54
3:D:315:SER:OG	3:D:338:ASN:OD1	2.15	0.54
3:D:395:ARG:NH2	3:D:417:ARG:HB3	2.23	0.54
3:D:250:THR:OG1	3:D:275:ARG:NH2	2.40	0.54
1:A:400:LEU:C	1:A:402:PHE:N	2.64	0.54
1:A:151:LYS:HE2	1:A:173:ASP:OD2	2.07	0.54
2:F:23:VAL:HG22	2:F:41:LYS:HE2	1.90	0.54
3:C:315:SER:OG	3:C:338:ASN:OD1	2.15	0.53
3:D:272:SER:CB	3:D:275:ARG:NH1	2.71	0.53
3:D:273:GLN:NE2	3:D:282:LEU:HD11	2.23	0.53
3:D:317:THR:O	3:D:319:PRO:HD3	2.08	0.53
2:F:50:PRO:HB3	3:D:112:THR:HA	1.90	0.53
2:E:50:PRO:HB3	3:C:112:THR:HG23	1.89	0.53
3:D:276:LEU:HD12	3:D:279:LEU:HD22	1.89	0.53
1:B:207:LEU:HB3	1:B:211:MET:CE	2.35	0.53
3:C:317:THR:O	3:C:319:PRO:HD3	2.08	0.53
1:B:473:GLU:OE2	1:B:473:GLU:N	2.36	0.53
3:C:121:ARG:HA	3:C:145:ARG:HB3	1.91	0.53
1:B:452:ASP:OD1	1:B:452:ASP:O	2.26	0.53
3:C:191:HIS:NE2	3:C:192:LYS:CD	2.71	0.53
3:C:334:LEU:HB2	3:C:358:LEU:HD23	1.91	0.53
3:C:395:ARG:NH2	3:C:417:ARG:HB3	2.23	0.53
3:D:121:ARG:HA	3:D:145:ARG:HB3	1.91	0.53
3:D:191:HIS:NE2	3:D:192:LYS:CD	2.71	0.53
3:C:120:GLN:HG2	3:C:121:ARG:HD2	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:206:PHE:HB3	3:C:209:LEU:HB2	1.90	0.53
3:D:191:HIS:CE1	3:D:192:LYS:HG3	2.44	0.53
3:D:206:PHE:HB3	3:D:209:LEU:HB2	1.90	0.53
3:D:334:LEU:HB2	3:D:358:LEU:HD23	1.91	0.53
1:A:114:GLU:OE1	1:A:114:GLU:N	2.33	0.53
1:A:514:LEU:H	1:A:536:ASN:HD22	1.57	0.52
3:C:67:ARG:HD3	3:C:72:ASP:OD2	2.10	0.52
3:D:67:ARG:HD3	3:D:72:ASP:OD2	2.10	0.52
1:A:524:ASN:N	1:A:545:MET:HE3	2.25	0.52
3:D:353:LEU:HG	3:D:377:LEU:CD2	2.40	0.52
1:B:400:LEU:C	1:B:402:PHE:N	2.64	0.52
1:A:452:ASP:O	1:A:452:ASP:OD1	2.26	0.52
3:C:191:HIS:CE1	3:C:192:LYS:HG3	2.44	0.52
3:D:120:GLN:HG2	3:D:121:ARG:HD2	1.90	0.52
3:C:272:SER:CB	3:C:275:ARG:NH1	2.71	0.52
1:A:469:GLN:HG2	1:A:470:LEU:N	2.25	0.51
1:B:469:GLN:HG2	1:B:470:LEU:N	2.25	0.51
3:C:353:LEU:HG	3:C:377:LEU:CD2	2.40	0.51
1:B:514:LEU:H	1:B:536:ASN:HD22	1.57	0.51
1:B:524:ASN:N	1:B:545:MET:HE3	2.25	0.51
1:A:252:THR:HG21	1:A:273:ARG:NH1	2.25	0.51
3:D:106:GLY:O	3:D:114:PHE:HB2	2.11	0.51
1:B:252:THR:HG21	1:B:273:ARG:NH1	2.25	0.51
1:B:425:GLU:H	1:B:425:GLU:CD	2.07	0.51
1:B:506:SER:HA	1:B:530:ASN:O	2.11	0.51
3:C:191:HIS:CE1	3:C:192:LYS:HE3	2.45	0.51
1:A:506:SER:HA	1:A:530:ASN:O	2.11	0.50
2:F:40:TYR:OH	1:B:287:ALA:O	2.17	0.50
1:A:122:VAL:HG13	1:A:146:GLU:HG3	1.92	0.50
3:D:63:TYR:CD1	3:D:75:ALA:HA	2.46	0.50
3:C:63:TYR:CD1	3:C:75:ALA:HA	2.46	0.50
3:D:191:HIS:CE1	3:D:192:LYS:HE3	2.45	0.50
1:A:400:LEU:O	1:A:402:PHE:N	2.45	0.50
1:B:400:LEU:O	1:B:402:PHE:N	2.45	0.50
2:F:7:ASP:O	2:F:52:PRO:HG2	2.11	0.50
3:C:106:GLY:O	3:C:114:PHE:HB2	2.11	0.50
3:D:318:ILE:O	3:D:344:PRO:HG3	2.11	0.50
1:B:122:VAL:HG13	1:B:146:GLU:HG3	1.92	0.50
3:C:318:ILE:O	3:C:344:PRO:HG3	2.11	0.50
1:B:36:ILE:HA	1:B:88:SER:HB3	1.93	0.50
1:B:433:ASP:HB2	1:B:457:LEU:HG	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:91:MET:HE2	3:C:91:MET:HA	1.94	0.49
1:A:473:GLU:OE2	1:A:473:GLU:N	2.36	0.49
3:C:276:LEU:CD1	3:C:279:LEU:HD22	2.43	0.49
3:C:186:LYS:HA	3:C:209:LEU:HA	1.94	0.49
3:C:189:ASP:OD2	3:C:191:HIS:HB3	2.12	0.49
3:D:91:MET:HE2	3:D:91:MET:HA	1.94	0.49
3:D:189:ASP:OD2	3:D:191:HIS:HB3	2.12	0.49
1:B:34:MET:HE1	1:B:50:TRP:HB3	1.94	0.49
1:B:67:ASP:OD2	1:B:74:VAL:HG11	2.13	0.49
1:B:500:GLN:O	1:B:502:GLN:CD	2.56	0.49
1:A:67:ASP:OD2	1:A:74:VAL:HG11	2.13	0.49
3:C:148:GLN:HG2	3:C:149:ARG:O	2.13	0.49
1:A:182:GLU:HA	1:A:204:THR:O	2.13	0.48
3:C:119:PRO:HA	3:C:143:LEU:O	2.13	0.48
3:D:276:LEU:CD1	3:D:279:LEU:HD22	2.43	0.48
1:A:34:MET:HE1	1:A:50:TRP:HB3	1.95	0.48
1:A:36:ILE:HA	1:A:88:SER:HB3	1.93	0.48
1:A:433:ASP:HB2	1:A:457:LEU:HG	1.94	0.48
2:E:20:LEU:HD11	2:E:40:TYR:HD1	1.77	0.48
3:D:148:GLN:HG2	3:D:149:ARG:O	2.13	0.48
1:B:424:VAL:N	1:B:425:GLU:OE1	2.47	0.48
1:A:500:GLN:O	1:A:502:GLN:CD	2.56	0.48
1:A:413:LEU:HB3	1:A:418:PHE:HE2	1.78	0.48
3:D:315:SER:HA	3:D:338:ASN:O	2.13	0.48
1:B:182:GLU:HA	1:B:204:THR:O	2.13	0.48
3:D:186:LYS:HA	3:D:209:LEU:HA	1.94	0.48
3:D:119:PRO:HA	3:D:143:LEU:O	2.13	0.48
3:D:166:LEU:HB3	3:D:171:PHE:HE2	1.79	0.48
1:A:543:PRO:HA	1:A:544:PRO:HD3	1.72	0.48
3:C:315:SER:HA	3:C:338:ASN:O	2.13	0.48
1:A:39:SER:O	1:A:85:GLY:HA3	2.14	0.48
1:A:424:VAL:N	1:A:425:GLU:OE1	2.47	0.48
1:B:502:GLN:HG3	1:B:526:PHE:HE1	1.79	0.48
3:C:191:HIS:NE2	3:C:192:LYS:CG	2.77	0.48
3:D:314:PHE:HB3	3:D:337:THR:O	2.14	0.48
1:A:502:GLN:HG3	1:A:526:PHE:HE1	1.79	0.47
3:C:166:LEU:HB3	3:C:171:PHE:HE2	1.79	0.47
3:D:191:HIS:NE2	3:D:192:LYS:HD2	2.29	0.47
1:A:275:THR:HG22	1:A:297:GLU:HB2	1.96	0.47
2:E:16:SER:O	2:E:18:CYS:N	2.45	0.47
1:B:413:LEU:HB3	1:B:418:PHE:HE2	1.78	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:275:THR:HG22	1:B:297:GLU:HB2	1.96	0.47
2:E:17:PRO:HD2	2:E:44:CYS:SG	2.55	0.47
3:C:191:HIS:NE2	3:C:192:LYS:HD2	2.29	0.47
3:D:191:HIS:NE2	3:D:192:LYS:CG	2.77	0.47
1:B:279:PRO:HD2	1:B:282:ILE:HD12	1.96	0.47
3:C:314:PHE:HB3	3:C:337:THR:O	2.14	0.47
1:B:171:ARG:HG3	1:B:195:TYR:HB3	1.97	0.47
3:D:67:ARG:CD	3:D:72:ASP:OD2	2.63	0.47
1:B:44:VAL:HG13	1:B:45:ASN:N	2.21	0.47
1:A:279:PRO:HD2	1:A:282:ILE:HD12	1.96	0.47
3:C:244:PRO:HA	3:C:266:THR:O	2.14	0.47
1:A:44:VAL:CG1	1:A:45:ASN:H	2.22	0.47
3:C:67:ARG:CD	3:C:72:ASP:OD2	2.63	0.47
1:B:39:SER:O	1:B:85:GLY:HA3	2.14	0.47
1:A:171:ARG:HG3	1:A:195:TYR:HB3	1.97	0.46
3:D:244:PRO:HA	3:D:266:THR:O	2.14	0.46
1:A:379:SER:HA	1:A:405:LEU:HD21	1.97	0.46
2:E:20:LEU:HD12	2:E:21:VAL:N	2.31	0.46
2:E:43:MET:HE3	2:E:43:MET:HB2	1.83	0.46
1:B:330:LEU:HD23	1:B:333:MET:CE	2.45	0.46
1:A:446:ILE:CD1	1:A:466:LEU:HD13	2.46	0.46
1:B:314:LYS:HE2	1:B:316:TYR:OH	2.16	0.46
2:F:50:PRO:HB3	3:D:112:THR:HG23	1.98	0.46
3:C:63:TYR:CE1	3:C:75:ALA:HA	2.51	0.46
3:D:120:GLN:O	3:D:121:ARG:HD2	2.15	0.46
1:A:330:LEU:HD23	1:A:333:MET:CE	2.45	0.46
3:C:120:GLN:O	3:C:121:ARG:HD2	2.15	0.46
3:C:236:LEU:HD12	3:C:260:LEU:CD2	2.46	0.46
3:D:236:LEU:HD12	3:D:260:LEU:CD2	2.45	0.46
1:A:314:LYS:HE2	1:A:316:TYR:OH	2.16	0.46
3:D:63:TYR:CE1	3:D:75:ALA:HA	2.51	0.46
1:B:446:ILE:CD1	1:B:466:LEU:HD13	2.46	0.46
3:C:92:PRO:HA	3:C:97:VAL:O	2.16	0.45
3:D:92:PRO:HA	3:D:97:VAL:O	2.16	0.45
1:B:546:ALA:HB1	1:B:548:PHE:CE2	2.51	0.45
1:B:379:SER:HA	1:B:405:LEU:HD21	1.97	0.45
1:A:345:LYS:NZ	1:A:369:ARG:NH1	2.65	0.45
2:E:44:CYS:O	2:E:47:LYS:CG	2.62	0.45
3:D:226:PHE:CD1	3:D:226:PHE:C	2.93	0.45
1:A:546:ALA:HB1	1:A:548:PHE:CE2	2.51	0.45
3:C:359:GLU:HB2	3:C:383:ASN:O	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:18:CYS:C	2:F:19:ARG:HG2	2.42	0.45
3:D:226:PHE:C	3:D:226:PHE:HD1	2.24	0.45
1:B:306:LEU:C	1:B:333:MET:HE2	2.42	0.45
1:A:470:LEU:HD23	1:A:495:PRO:HD3	1.98	0.45
2:F:22:MET:HE2	2:F:22:MET:HB3	1.75	0.45
3:D:66:MET:O	3:D:69:THR:HG22	2.17	0.45
1:B:345:LYS:NZ	1:B:369:ARG:NH1	2.65	0.45
1:B:267:LEU:HD11	1:B:269:LEU:HD21	1.99	0.44
1:A:378:ILE:O	1:A:378:ILE:HG13	2.17	0.44
1:B:44:VAL:CG1	1:B:45:ASN:H	2.22	0.44
1:B:496:THR:HG23	1:B:521:GLN:CD	2.43	0.44
1:A:50:TRP:CD1	1:A:61:TRP:HB3	2.53	0.44
3:C:66:MET:O	3:C:69:THR:HG22	2.17	0.44
1:A:306:LEU:C	1:A:333:MET:HE2	2.42	0.44
3:D:359:GLU:HB2	3:D:383:ASN:O	2.17	0.44
1:B:140:SER:HB3	1:B:162:THR:HB	2.00	0.44
1:A:400:LEU:HD23	1:A:425:GLU:OE2	2.17	0.44
1:B:470:LEU:HD23	1:B:495:PRO:HD3	1.98	0.44
2:F:20:LEU:HD11	2:F:40:TYR:HB3	1.99	0.43
1:B:400:LEU:HD23	1:B:425:GLU:OE2	2.17	0.43
1:A:390:HIS:HA	1:A:414:SER:O	2.18	0.43
1:A:437:LEU:HB3	1:A:442:PHE:CE2	2.52	0.43
1:B:50:TRP:CD1	1:B:61:TRP:HB3	2.53	0.43
1:B:437:LEU:HB3	1:B:442:PHE:CE2	2.52	0.43
1:A:129:ASN:HB2	1:A:153:ASN:ND2	2.27	0.43
2:E:20:LEU:HD11	2:E:40:TYR:CD1	2.53	0.43
3:C:89:GLU:HB2	3:C:102:SER:HB3	2.01	0.43
3:D:124:VAL:H	3:D:148:GLN:HE22	1.67	0.43
3:D:274:ASN:HD21	3:D:296:SER:HB3	1.83	0.43
3:C:274:ASN:HD21	3:C:296:SER:HB3	1.83	0.43
1:A:267:LEU:HD11	1:A:269:LEU:HD21	1.99	0.43
3:D:266:THR:HG22	3:D:288:ARG:HB2	2.00	0.43
1:A:86:GLU:OE2	3:C:402:ARG:NH1	2.49	0.43
1:A:254:GLU:HG2	1:A:275:THR:O	2.19	0.43
1:A:496:THR:HG23	1:A:521:GLN:CD	2.43	0.43
3:C:336:ASN:HA	3:C:360:GLY:O	2.19	0.43
3:D:89:GLU:HB2	3:D:102:SER:HB3	2.00	0.43
1:B:254:GLU:HG2	1:B:275:THR:O	2.19	0.43
1:A:417:ASN:OD1	1:A:419:LYS:NZ	2.52	0.43
3:D:66:MET:HA	3:D:69:THR:HG22	2.01	0.43
1:B:417:ASN:O	1:B:419:LYS:NZ	2.51	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:425:GLU:HA	1:B:428:HIS:ND1	2.34	0.43
1:B:543:PRO:C	1:B:545:MET:H	2.27	0.43
3:C:266:THR:HG22	3:C:288:ARG:HB2	2.00	0.43
1:A:125:ASP:OD1	1:A:149:ASN:ND2	2.52	0.43
1:A:543:PRO:C	1:A:545:MET:H	2.27	0.43
1:A:417:ASN:O	1:A:419:LYS:NZ	2.51	0.42
1:A:504:LEU:HD11	1:A:506:SER:O	2.20	0.42
3:C:66:MET:HA	3:C:69:THR:HG22	2.01	0.42
1:B:125:ASP:OD1	1:B:149:ASN:ND2	2.52	0.42
1:B:378:ILE:HG13	1:B:378:ILE:O	2.17	0.42
1:B:546:ALA:HB1	1:B:548:PHE:CD2	2.54	0.42
3:C:124:VAL:H	3:C:148:GLN:HE22	1.66	0.42
1:B:390:HIS:HA	1:B:414:SER:O	2.19	0.42
3:D:227:VAL:HG13	3:D:251:SER:HB2	2.02	0.42
1:B:129:ASN:HB2	1:B:153:ASN:ND2	2.27	0.42
1:A:410:TYR:HD1	1:A:434:LYS:HB2	1.85	0.42
1:A:477:LEU:O	1:A:480:ILE:HG22	2.20	0.42
3:D:191:HIS:CD2	3:D:192:LYS:HG3	2.54	0.42
3:D:192:LYS:HA	3:D:216:GLY:O	2.19	0.42
1:B:410:TYR:HD1	1:B:434:LYS:HB2	1.85	0.42
1:B:504:LEU:HD11	1:B:506:SER:O	2.20	0.42
1:A:140:SER:HB3	1:A:162:THR:HB	2.00	0.42
1:A:378:ILE:CG2	1:A:402:PHE:HE1	2.33	0.42
3:D:336:ASN:HA	3:D:360:GLY:O	2.19	0.42
1:B:477:LEU:O	1:B:480:ILE:HG22	2.20	0.42
1:A:425:GLU:HA	1:A:428:HIS:ND1	2.34	0.42
3:C:191:HIS:CD2	3:C:192:LYS:HG3	2.54	0.42
1:A:266:THR:HG21	2:E:37:PRO:HB3	2.00	0.42
1:B:427:GLY:HA3	1:B:449:THR:HB	2.02	0.42
1:B:523:THR:HB	1:B:545:MET:HE3	1.12	0.42
1:A:427:GLY:HA3	1:A:449:THR:HB	2.02	0.42
1:A:522:LEU:N	1:A:545:MET:CE	2.83	0.42
1:B:417:ASN:OD1	1:B:419:LYS:NZ	2.52	0.42
1:A:546:ALA:HB1	1:A:548:PHE:CD2	2.54	0.42
2:F:51:VAL:O	3:D:86:HIS:HB2	2.20	0.42
1:B:378:ILE:CG2	1:B:402:PHE:HE1	2.33	0.42
1:B:525:CYS:HB3	1:B:528:LEU:HB2	2.02	0.42
1:A:523:THR:HB	1:A:545:MET:HE3	1.12	0.41
3:C:61:ALA:O	3:C:65:ILE:HD12	2.20	0.41
3:C:141:ARG:NH1	3:C:168:GLU:OE2	2.53	0.41
3:C:192:LYS:HA	3:C:216:GLY:O	2.19	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:58:GLU:HG2	3:D:131:LEU:HD23	2.02	0.41
1:A:136:PRO:HD2	1:A:139:ILE:HG13	2.02	0.41
3:C:335:SER:O	3:C:337:THR:HG23	2.20	0.41
3:D:61:ALA:O	3:D:65:ILE:HD12	2.20	0.41
1:A:252:THR:HG22	1:A:273:ARG:HB2	2.02	0.41
1:A:327:PRO:O	1:A:330:LEU:HD12	2.20	0.41
2:F:4:ARG:HA	1:B:286:GLN:HB2	2.03	0.41
2:F:41:LYS:HD2	2:F:48:SER:HB2	2.01	0.41
3:D:141:ARG:NH1	3:D:168:GLU:OE2	2.53	0.41
1:B:422:ILE:HG22	1:B:447:PRO:HG2	2.03	0.41
1:A:414:SER:HA	1:A:438:SER:O	2.20	0.41
1:A:525:CYS:HB3	1:A:528:LEU:HB2	2.02	0.41
2:F:52:PRO:HA	3:D:86:HIS:N	2.36	0.41
2:E:20:LEU:HD12	2:E:21:VAL:H	1.85	0.41
1:A:422:ILE:HG22	1:A:447:PRO:HG2	2.03	0.41
1:A:424:VAL:O	1:A:449:THR:OG1	2.37	0.41
1:B:29:GLU:OE1	1:B:73:VAL:HG23	2.21	0.41
1:B:136:PRO:HD2	1:B:139:ILE:HG13	2.02	0.41
1:A:512:ASN:HB2	1:A:536:ASN:HD21	1.86	0.41
3:C:116:THR:HG22	3:C:117:CYS:N	2.36	0.41
1:B:95:ARG:HH22	1:B:117:ASN:HB3	1.80	0.41
1:A:29:GLU:OE1	1:A:73:VAL:HG23	2.21	0.41
3:D:62:VAL:HG11	3:D:80:VAL:HG11	2.02	0.41
3:D:321:ASN:N	3:D:321:ASN:HD22	2.19	0.41
1:B:206:THR:HG22	1:B:229:GLY:HA3	2.03	0.41
1:B:252:THR:HG22	1:B:273:ARG:HB2	2.02	0.41
1:B:512:ASN:HB2	1:B:536:ASN:HD21	1.86	0.41
1:B:543:PRO:HA	1:B:544:PRO:HD3	1.72	0.41
3:D:284:LEU:HB3	3:D:289:LEU:HD11	2.03	0.41
1:B:327:PRO:O	1:B:330:LEU:HD12	2.20	0.41
1:A:44:VAL:HG13	1:A:45:ASN:N	2.21	0.40
3:C:62:VAL:HG11	3:C:80:VAL:HG11	2.02	0.40
3:D:116:THR:HG22	3:D:117:CYS:N	2.36	0.40
3:D:335:SER:O	3:D:337:THR:HG23	2.20	0.40
3:C:330:MET:HA	3:C:353:LEU:HA	2.03	0.40
1:B:402:PHE:C	1:B:404:ASN:N	2.78	0.40
3:C:58:GLU:HG2	3:C:131:LEU:HD23	2.02	0.40
3:C:284:LEU:HB3	3:C:289:LEU:HD11	2.03	0.40
3:D:273:GLN:HE21	3:D:282:LEU:HD11	1.84	0.40
3:D:330:MET:HA	3:D:353:LEU:HA	2.04	0.40
1:B:414:SER:HA	1:B:438:SER:O	2.20	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:206:THR:HG22	1:A:229:GLY:HA3	2.03	0.40
1:A:529:VAL:HG22	1:A:550:ARG:HB2	2.04	0.40
1:A:80:SER:HA	1:A:104:GLY:O	2.22	0.40
3:D:84:ARG:HH21	3:D:89:GLU:HA	1.87	0.40

All (8) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:375:LYS:NZ	1:B:454:GLU:OE1[1_655]	1.90	0.30
1:A:478:ARG:NH2	3:C:373:ASP:OD2[1_565]	1.94	0.26
3:D:373:ASP:OD2	1:B:478:ARG:NH2[1_655]	1.94	0.26
1:A:454:GLU:OE1	3:C:375:LYS:NZ[1_565]	1.98	0.22
3:D:375:LYS:NZ	1:B:454:GLU:CD[1_655]	2.11	0.09
3:D:375:LYS:NZ	1:B:454:GLU:OE2[1_655]	2.11	0.09
1:A:454:GLU:OE2	3:C:375:LYS:NZ[1_565]	2.15	0.05
1:A:454:GLU:CD	3:C:375:LYS:NZ[1_565]	2.17	0.03

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	521/539 (97%)	464 (89%)	56 (11%)	1 (0%)	43	64
1	B	521/539 (97%)	464 (89%)	56 (11%)	1 (0%)	43	64
2	E	38/52 (73%)	35 (92%)	3 (8%)	0	100	100
2	F	38/52 (73%)	36 (95%)	2 (5%)	0	100	100
3	C	365/374 (98%)	331 (91%)	34 (9%)	0	100	100
3	D	365/374 (98%)	331 (91%)	34 (9%)	0	100	100
All	All	1848/1930 (96%)	1661 (90%)	185 (10%)	2 (0%)	48	69

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	401	ALA
1	B	401	ALA

5.3.2 Protein sidechains ⓘ

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	459/471 (98%)	456 (99%)	3 (1%)	76	89
1	B	459/471 (98%)	456 (99%)	3 (1%)	76	89
2	E	37/45 (82%)	37 (100%)	0	100	100
2	F	37/45 (82%)	37 (100%)	0	100	100
3	C	324/328 (99%)	319 (98%)	5 (2%)	57	79
3	D	324/328 (99%)	319 (98%)	5 (2%)	57	79
All	All	1640/1688 (97%)	1624 (99%)	16 (1%)	68	85

All (16) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	184	SER
1	A	209	SER
1	A	409	THR
3	C	80	VAL
3	C	84	ARG
3	C	112	THR
3	C	226	PHE
3	C	369	LEU
3	D	80	VAL
3	D	84	ARG
3	D	112	THR
3	D	226	PHE
3	D	369	LEU
1	B	184	SER
1	B	209	SER

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Mol	Chain	Res	Type
1	B	409	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (31) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	103	GLN
1	A	153	ASN
1	A	177	ASN
1	A	194	GLN
1	A	286	GLN
1	A	441	ASN
1	A	465	HIS
1	A	481	GLN
1	A	536	ASN
3	C	71	ASN
3	C	133	HIS
3	C	148	GLN
3	C	169	ASN
3	C	304	GLN
3	C	321	ASN
3	D	59	GLN
3	D	71	ASN
3	D	133	HIS
3	D	148	GLN
3	D	169	ASN
3	D	304	GLN
3	D	321	ASN
1	B	103	GLN
1	B	153	ASN
1	B	177	ASN
1	B	194	GLN
1	B	286	GLN
1	B	441	ASN
1	B	465	HIS
1	B	481	GLN
1	B	536	ASN

5.3.3 RNA ⓘ

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 oligosaccharides 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	523/539 (97%)	0.57	35 (6%)	24 19	27, 38, 62, 84	0
1	B	523/539 (97%)	0.77	39 (7%)	20 16	27, 38, 62, 84	0
2	E	42/52 (80%)	1.17	7 (16%)	4 3	35, 50, 57, 59	0
2	F	42/52 (80%)	1.25	6 (14%)	6 5	38, 51, 58, 64	0
3	C	367/374 (98%)	0.88	33 (8%)	15 12	25, 40, 60, 77	0
3	D	367/374 (98%)	1.03	49 (13%)	7 5	25, 40, 60, 77	0
All	All	1864/1930 (96%)	0.81	169 (9%)	15 11	25, 39, 61, 84	0

All (169) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	C	144	GLY	9.1
1	A	67	ASP	7.4
1	B	549	SER	6.8
3	C	143	LEU	6.7
1	B	67	ASP	6.6
3	C	83	GLY	6.6
1	B	545	MET	5.3
3	C	108	LEU	5.3
3	C	417	ARG	5.3
3	C	415	VAL	5.1
3	D	418	ASP	4.9
3	D	83	GLY	4.8
3	D	108	LEU	4.7
3	D	417	ARG	4.7
3	C	109	SER	4.5
3	C	145	ARG	4.5
1	A	548	PHE	4.4
1	B	548	PHE	4.3
3	D	144	GLY	4.2

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Mol	Chain	Res	Type	RSRZ
3	D	415	VAL	4.0
3	D	192	LYS	3.9
1	A	549	SER	3.9
3	D	110	ASP	3.9
1	B	523	THR	3.9
2	F	4	ARG	3.9
1	A	42	ASN	3.8
3	C	192	LYS	3.8
3	D	273	GLN	3.7
2	F	1	ALA	3.7
1	B	53	VAL	3.7
2	E	25	PHE	3.7
1	A	545	MET	3.7
3	C	418	ASP	3.7
1	B	550	ARG	3.6
1	B	44	VAL	3.5
1	A	71	TYR	3.4
3	C	416	ASN	3.4
3	D	390	PRO	3.4
3	C	388	THR	3.3
1	B	42	ASN	3.3
1	A	48	LEU	3.3
3	D	168	GLU	3.3
3	D	262	ARG	3.3
1	B	453	LEU	3.3
1	A	550	ARG	3.2
3	C	111	ASP	3.2
3	C	52	ALA	3.2
3	D	143	LEU	3.1
3	D	370	GLU	3.1
3	D	275	ARG	3.1
1	A	43	LEU	3.1
1	B	295	ASP	3.1
3	C	146	ALA	3.1
1	B	310	SER	3.1
3	D	156	ARG	3.1
3	C	168	GLU	3.0
1	B	54	HIS	3.0
3	C	91	MET	3.0
1	B	547	ASN	3.0
3	C	375	LYS	2.9
3	C	273	GLN	2.9

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Mol	Chain	Res	Type	RSRZ
3	C	142	CYS	2.9
1	A	295	ASP	2.9
1	A	30	GLY	2.9
3	C	403	ARG	2.9
3	D	325	GLY	2.9
1	B	546	ALA	2.9
1	B	428	HIS	2.9
2	E	52	PRO	2.8
2	E	1	ALA	2.8
3	C	120	GLN	2.8
3	D	274	ASN	2.8
2	E	4	ARG	2.8
3	D	109	SER	2.8
1	A	65	PHE	2.8
1	A	547	ASN	2.8
1	A	450	LEU	2.8
1	B	452	ASP	2.8
1	A	44	VAL	2.8
3	D	165	VAL	2.7
3	C	370	GLU	2.7
3	D	146	ALA	2.7
1	A	54	HIS	2.7
3	C	371	PHE	2.7
3	C	376	HIS	2.7
1	A	191	GLU	2.7
1	A	139	ILE	2.6
1	A	433	ASP	2.6
1	B	433	ASP	2.6
2	E	40	TYR	2.6
3	D	403	ARG	2.6
3	D	142	CYS	2.6
3	D	295	SER	2.6
1	B	43	LEU	2.6
3	D	388	THR	2.5
2	E	39	ALA	2.5
2	E	51	VAL	2.5
1	A	526	PHE	2.5
2	F	25	PHE	2.5
3	D	279	LEU	2.5
1	B	28	ASN	2.5
3	C	117	CYS	2.5
3	D	375	LYS	2.5

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Mol	Chain	Res	Type	RSRZ
3	C	272	SER	2.5
2	F	21	VAL	2.5
3	D	112	THR	2.4
3	D	117	CYS	2.4
3	D	148	GLN	2.4
1	B	45	ASN	2.4
3	D	416	ASN	2.4
3	C	156	ARG	2.4
1	A	523	THR	2.4
1	B	32	ALA	2.4
3	D	147	PRO	2.3
3	D	244	PRO	2.3
1	B	382	ALA	2.3
3	D	376	HIS	2.3
1	B	380	SER	2.3
3	D	312	ASN	2.3
1	B	52	ASP	2.3
1	B	65	PHE	2.3
1	A	428	HIS	2.3
3	D	140	TYR	2.3
1	B	233	GLU	2.3
1	B	417	ASN	2.3
1	A	452	ASP	2.3
1	A	161	ALA	2.2
1	B	215	THR	2.2
3	C	262	ARG	2.2
1	B	521	GLN	2.2
1	A	451	GLY	2.2
1	A	53	VAL	2.2
1	B	69	VAL	2.2
1	A	546	ALA	2.2
3	D	152	ALA	2.2
3	D	189	ASP	2.2
3	D	299	GLY	2.2
1	B	513	LYS	2.2
1	B	526	PHE	2.2
1	A	453	LEU	2.2
3	D	365	GLY	2.2
3	C	275	ARG	2.2
1	A	464	ASN	2.2
1	B	536	ASN	2.2
3	D	52	ALA	2.1

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Mol	Chain	Res	Type	RSRZ
1	B	367	ASN	2.1
3	D	327	LYS	2.1
1	A	85	GLY	2.1
1	B	85	GLY	2.1
3	D	371	PHE	2.1
3	C	414	CYS	2.1
1	A	122	VAL	2.1
1	B	49	ASP	2.1
3	D	100	VAL	2.1
3	D	171	PHE	2.1
3	D	85	TRP	2.1
1	A	482	MET	2.1
1	A	400	LEU	2.1
1	A	49	ASP	2.1
3	D	354	ARG	2.1
3	D	120	GLN	2.1
1	B	58	LEU	2.1
1	A	378	ILE	2.1
2	F	51	VAL	2.1
3	C	110	ASP	2.0
3	D	111	ASP	2.0
2	F	8	CYS	2.0
3	C	75	ALA	2.0
1	B	186	LEU	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 oligosaccharides 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.