



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 12:57 AM GMT

PDB ID : 2C39
Title : RNASE PH CORE OF THE ARCHAEAL EXOSOME IN COMPLEX WITH ADP
Authors : Lorentzen, E.; Conti, E.
Deposited on : 2005-10-05
Resolution : 3.30 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

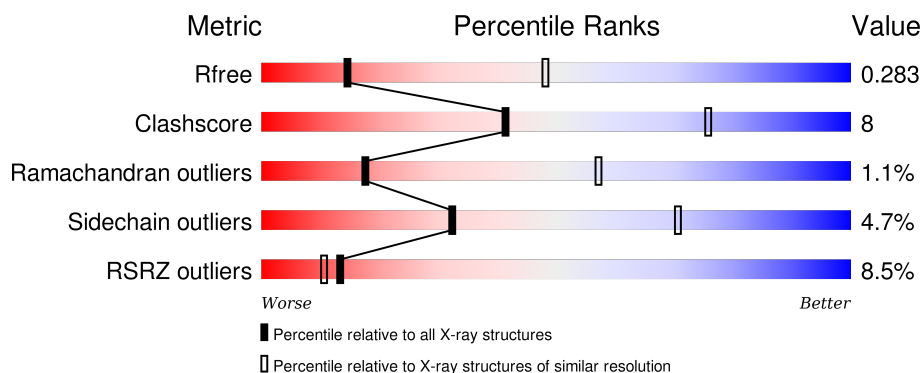
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.30 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	91344	2060 (3.40-3.20)
Clashscore	102246	1058 (3.38-3.22)
Ramachandran outliers	100387	1038 (3.38-3.22)
Sidechain outliers	100360	1037 (3.38-3.22)
RSRZ outliers	91569	2070 (3.40-3.20)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	275	<div> <div>4%</div> <div>81%</div> <div>13%</div> <div>• 5%</div> </div>
1	C	275	<div> <div>4%</div> <div>75%</div> <div>19%</div> <div>• 5%</div> </div>
1	E	275	<div> <div>6%</div> <div>77%</div> <div>17%</div> <div>• 5%</div> </div>
1	G	275	<div> <div>9%</div> <div>77%</div> <div>16%</div> <div>• 5%</div> </div>
1	I	275	<div> <div>12%</div> <div>78%</div> <div>16%</div> <div>• 5%</div> </div>

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Mol	Chain	Length	Quality of chain
1	K	275	
1	M	275	
1	O	275	
1	Q	275	
1	S	275	
1	U	275	
1	W	275	
2	B	248	
2	D	248	
2	F	248	
2	H	248	
2	J	248	
2	L	248	
2	N	248	
2	P	248	
2	R	248	
2	T	248	
2	V	248	
2	X	248	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 45814 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 PROBABLE EXOSOME COMPLEX EXONUCLEASE 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	260	Total	C	N	O	S	0	0	0
			1944	1239	320	380	5			
1	C	260	Total	C	N	O	S	0	0	0
			1947	1243	321	378	5			
1	E	260	Total	C	N	O	S	0	0	0
			1968	1253	325	385	5			
1	G	260	Total	C	N	O	S	0	0	0
			1961	1250	323	383	5			
1	I	260	Total	C	N	O	S	0	0	0
			1954	1247	323	379	5			
1	K	260	Total	C	N	O	S	0	0	0
			1958	1249	323	381	5			
1	M	260	Total	C	N	O	S	0	0	0
			1960	1249	324	382	5			
1	O	260	Total	C	N	O	S	0	0	0
			1951	1246	323	377	5			
1	Q	260	Total	C	N	O	S	0	0	0
			1953	1245	322	381	5			
1	S	259	Total	C	N	O	S	0	0	0
			1955	1245	323	382	5			
1	U	255	Total	C	N	O	S	0	0	0
			1908	1219	317	367	5			
1	W	259	Total	C	N	O	S	0	0	0
			1950	1245	322	378	5			

- Molecule 2 is a protein called PROBABLE EXOSOME COMPLEX EXONUCLEASE 1.

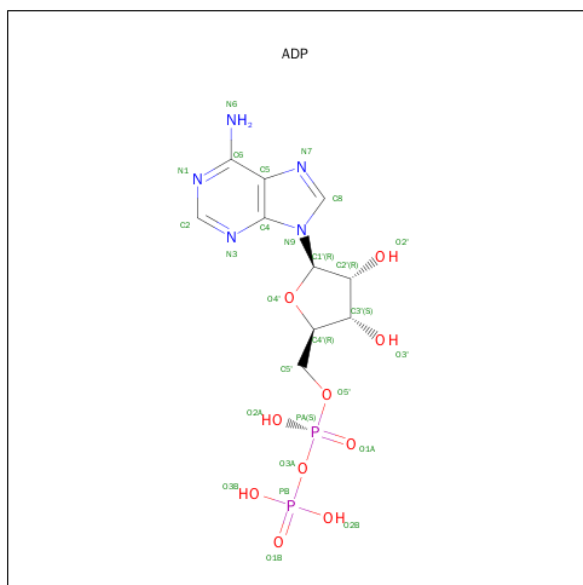
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	241	Total	C	N	O	S	0	0	0
			1812	1145	317	340	10			
2	D	248	Total	C	N	O	S	0	0	0
			1900	1198	330	360	12			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	F	241	Total	C	N	O	S	0	0	0
			1838	1161	317	350	10			
2	H	230	Total	C	N	O	S	0	0	0
			1732	1094	302	327	9			
2	J	241	Total	C	N	O	S	0	0	0
			1844	1165	321	348	10			
2	L	247	Total	C	N	O	S	0	0	0
			1890	1194	328	357	11			
2	N	239	Total	C	N	O	S	0	0	0
			1809	1144	313	342	10			
2	P	248	Total	C	N	O	S	0	0	0
			1904	1202	332	358	12			
2	R	248	Total	C	N	O	S	0	0	0
			1880	1188	332	348	12			
2	T	248	Total	C	N	O	S	0	0	0
			1884	1193	328	351	12			
2	V	239	Total	C	N	O	S	0	0	0
			1815	1148	318	339	10			
2	X	239	Total	C	N	O	S	0	0	0
			1821	1148	315	348	10			

- Molecule 3 is ADENOSINE-5'-DIPHOSPHATE (three-letter code: ADP) (formula: $C_{10}H_{15}N_5O_{10}P_2$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	B	1	Total	C	N	O	P	0	0
			27	10	5	10	2		

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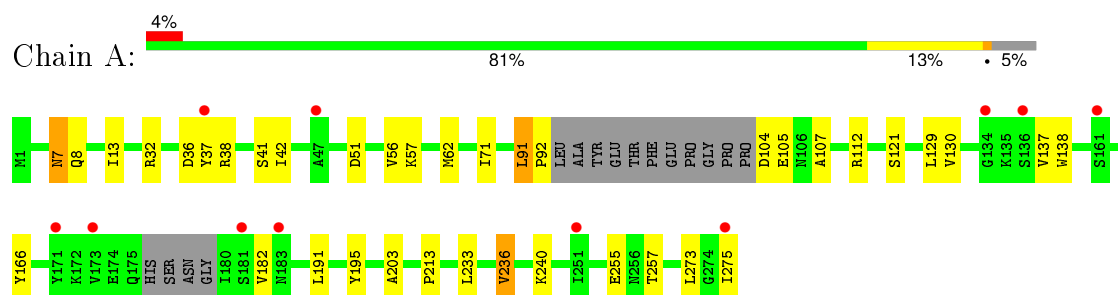
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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	D	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
3	F	1	Total	C	O	P		0	0
			17	5	10	2			
3	H	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
3	J	1	Total	O	P			0	0
			9	7	2				
3	L	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
3	N	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
3	P	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
3	R	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
3	T	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
3	V	1	Total	C	O	P		0	0
			17	5	10	2			
3	X	1	Total	C	O	P		0	0
			17	5	10	2			

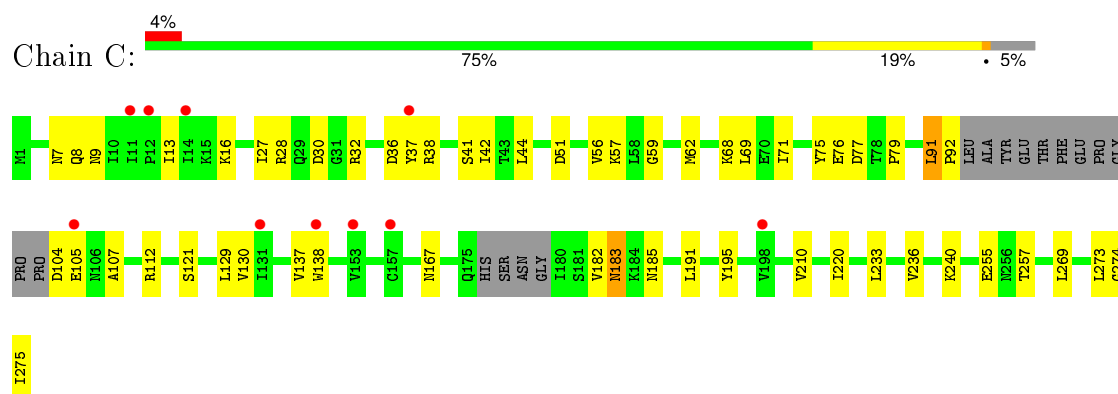
3 Residue-property plots [i](#)

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

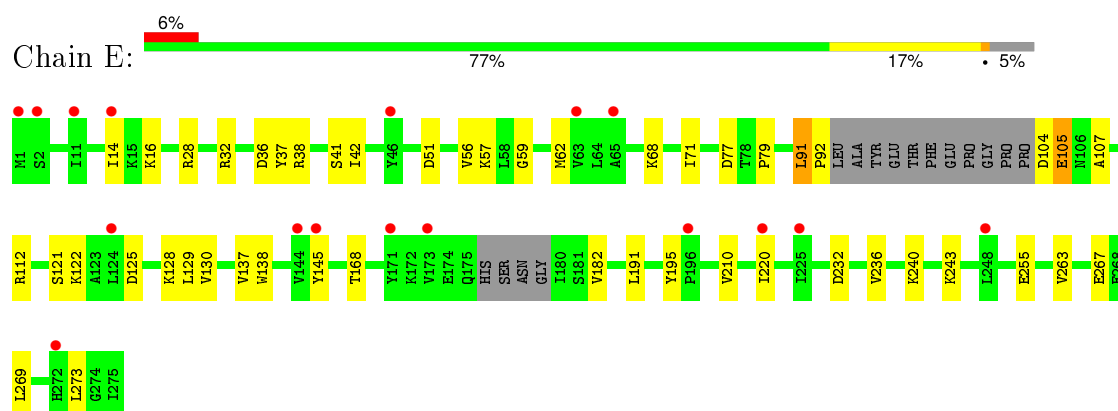
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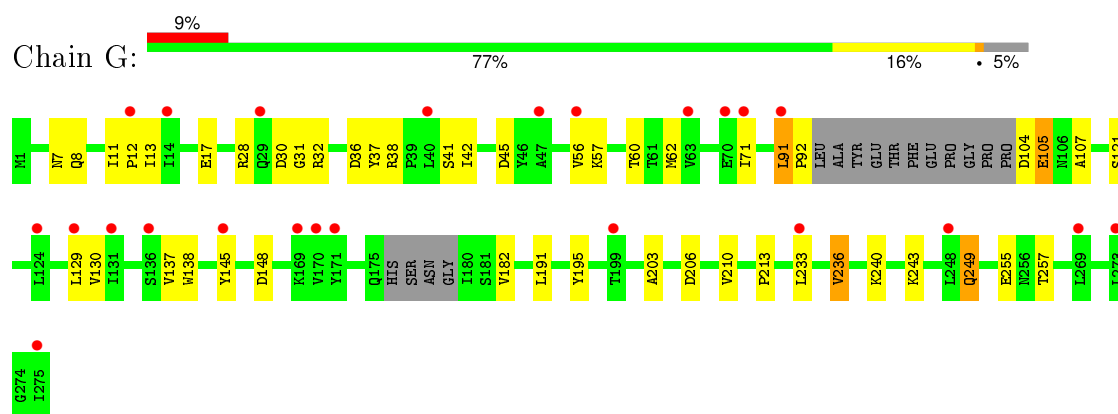
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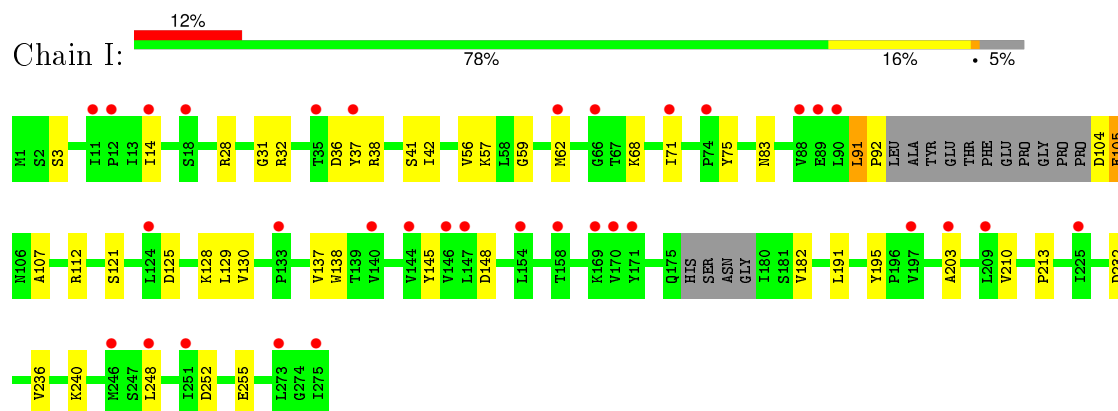
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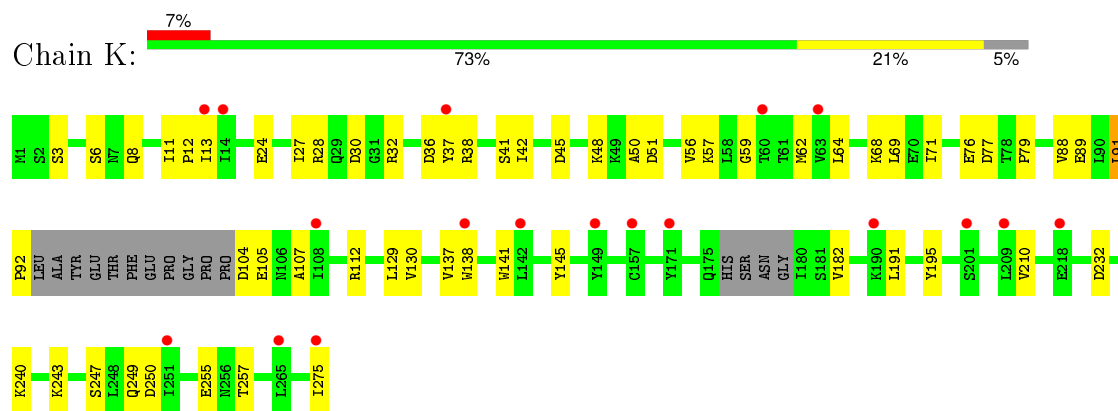
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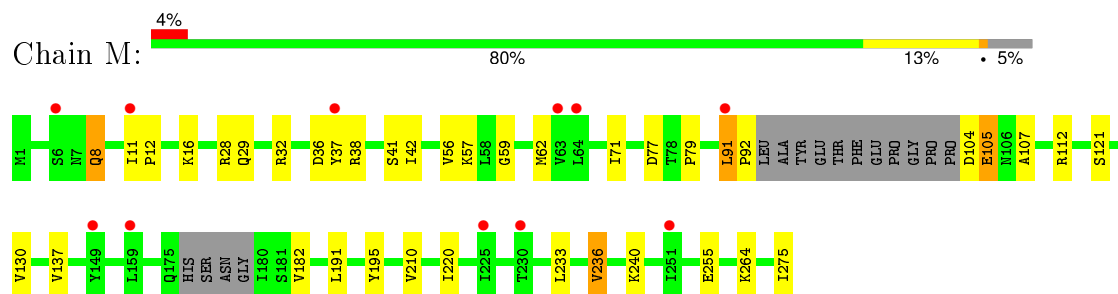
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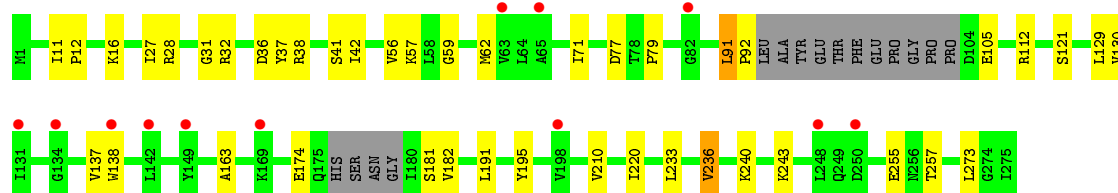
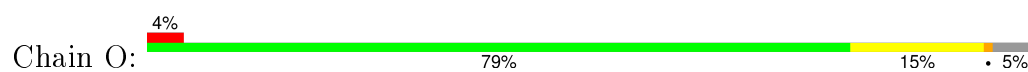
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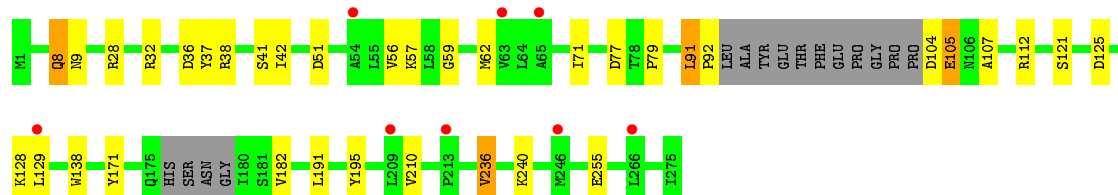
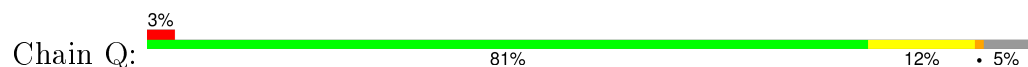
- Molecule 1: PROBABLE EXOSOME COMPLEX EXONUCLEASE 2



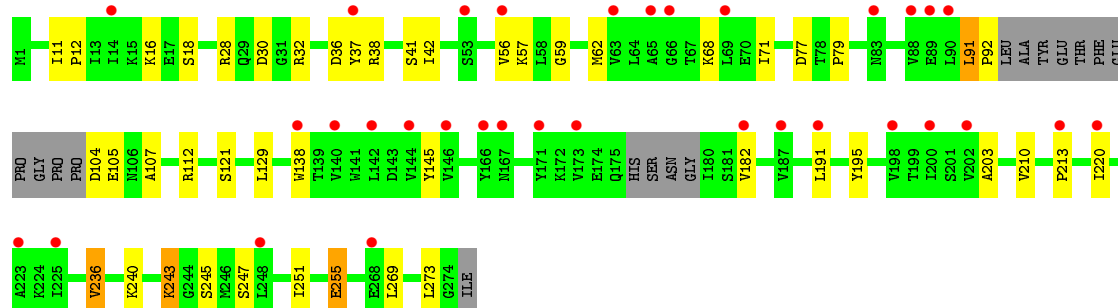
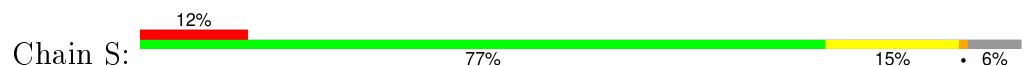
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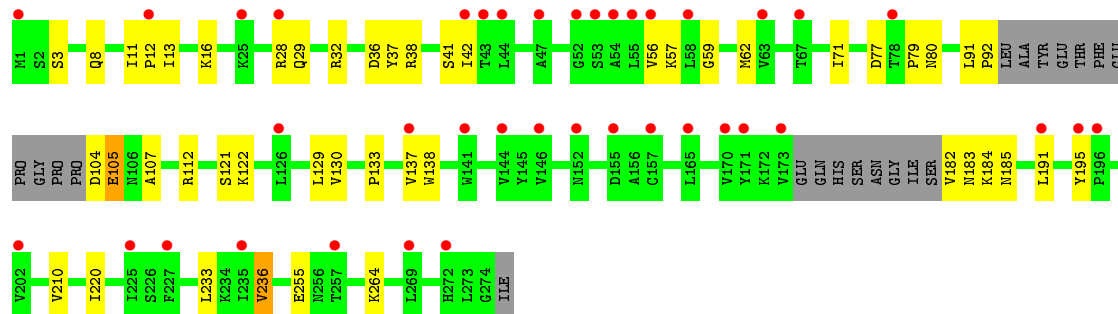
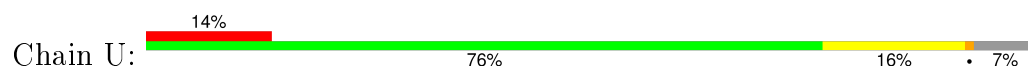
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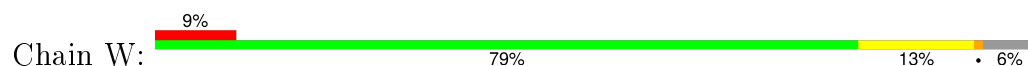
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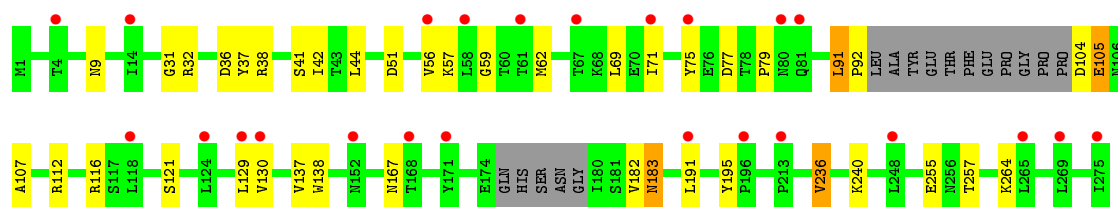


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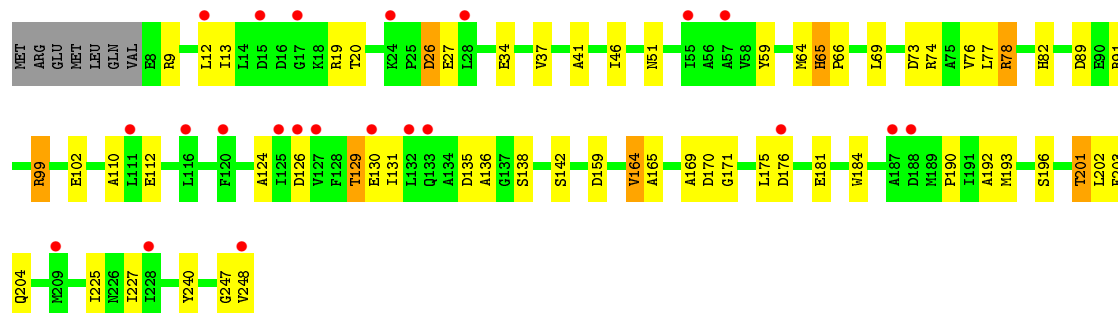


• Molecule 1: PROBABLE EXOSOME COMPLEX EXONUCLEASE 2

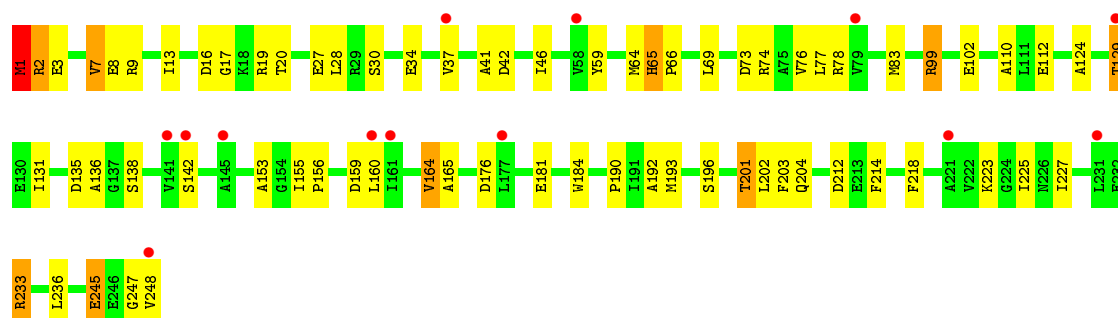




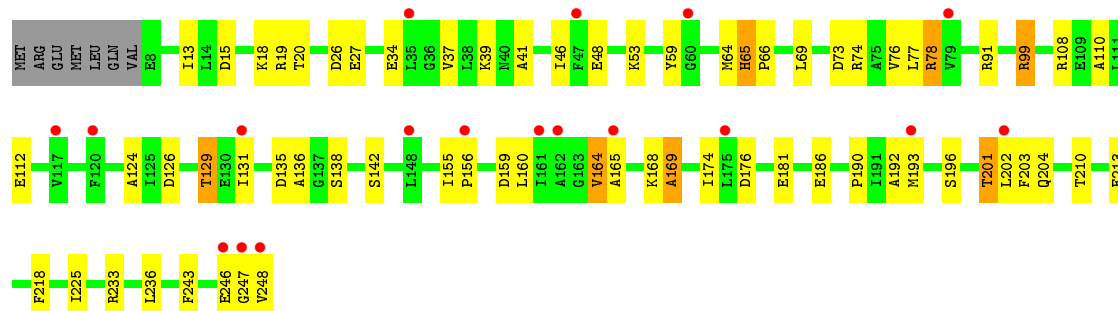
• Molecule 2: PROBABLE EXOSOME COMPLEX EXONUCLEASE 1



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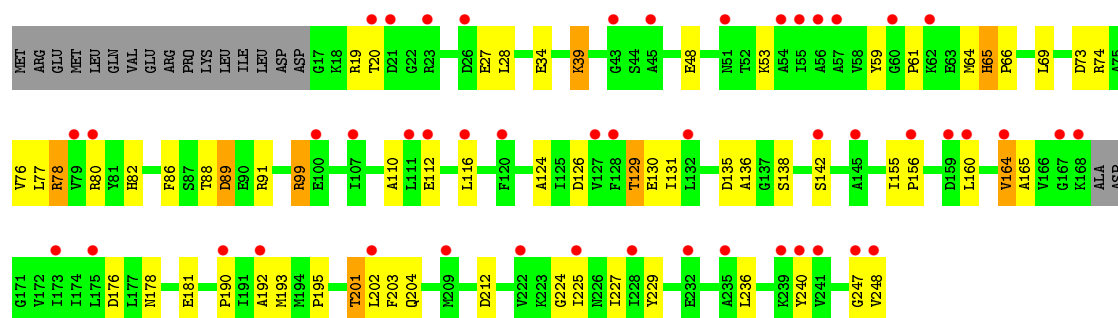


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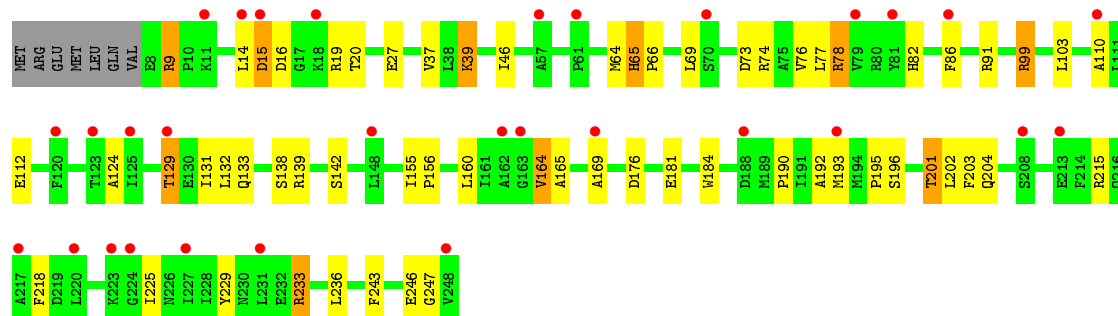


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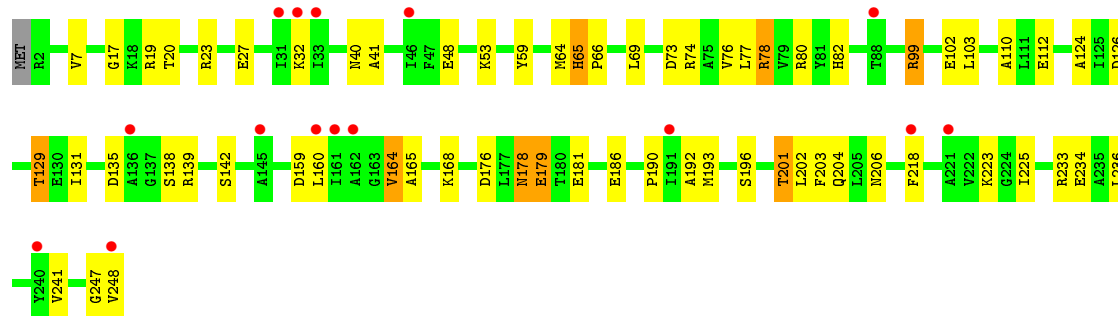
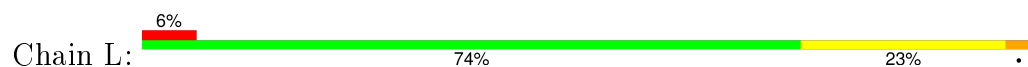




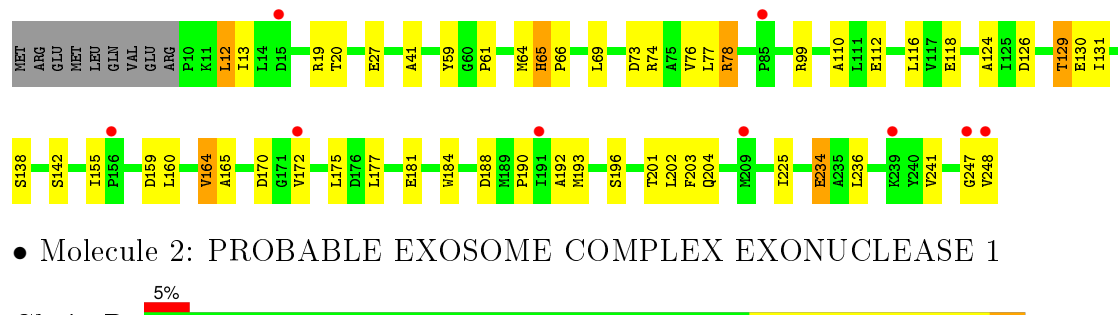
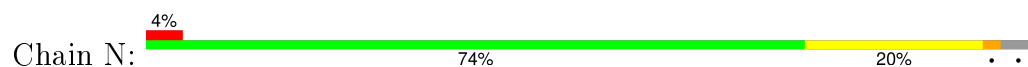
• Molecule 2: PROBABLE EXOSOME COMPLEX EXONUCLEASE 1



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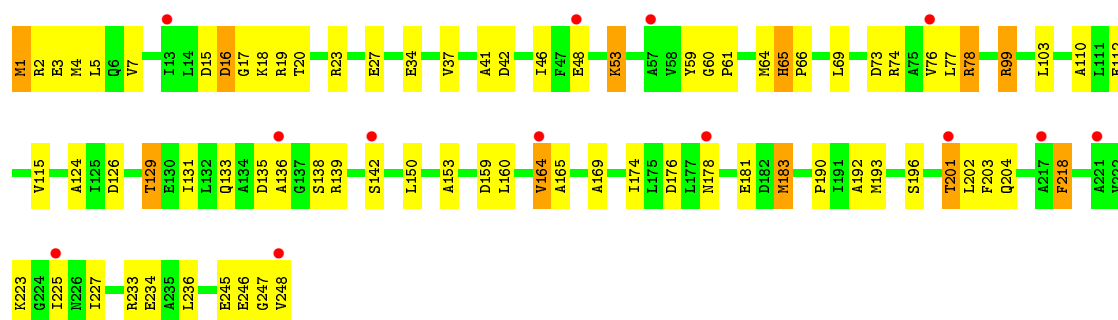


• Molecule 2: PROBABLE EXOSOME COMPLEX EXONUCLEASE 1

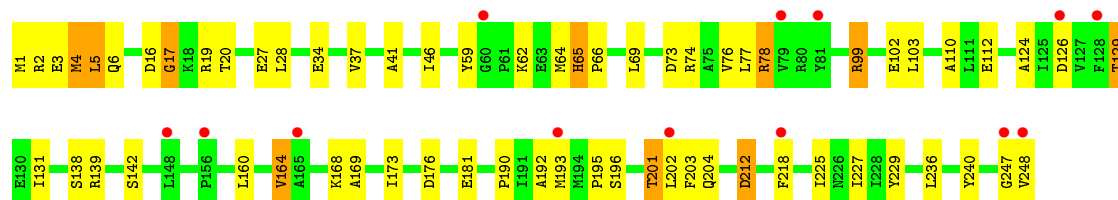
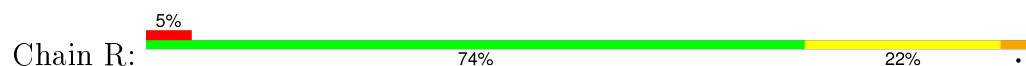


• Molecule 2: PROBABLE EXOSOME COMPLEX EXONUCLEASE 1

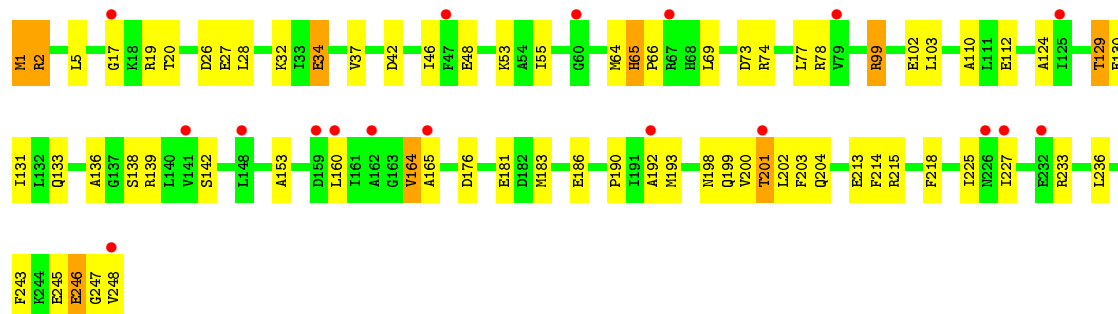




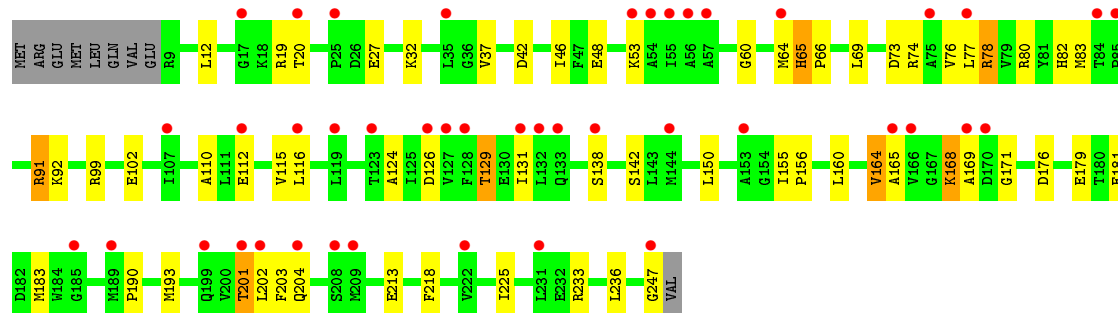
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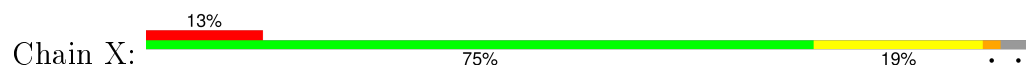
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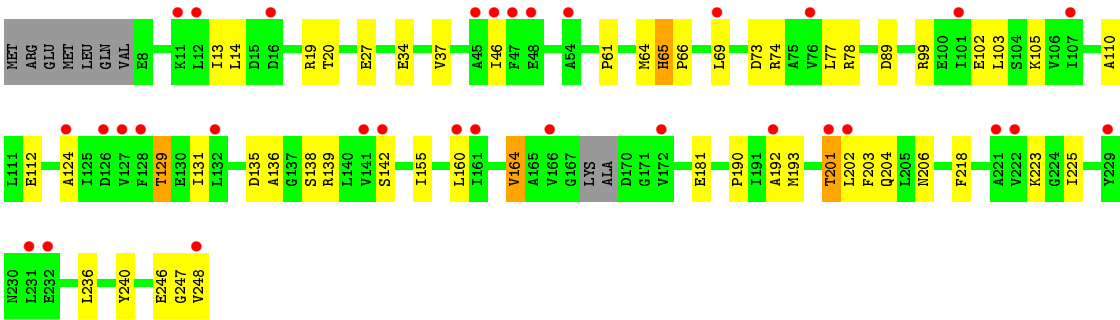


• Molecule 2: PROBABLE EXOSOME COMPLEX EXONUCLEASE 1



• Molecule 2: PROBABLE EXOSOME COMPLEX EXONUCLEASE 1





4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	206.20 Å 214.00 Å 432.50 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	93.25 – 3.30 93.06 – 3.30	Depositor EDS
% Data completeness (in resolution range)	100.0 (93.25-3.30) 84.6 (93.06-3.30)	Depositor EDS
R_{merge}	0.18	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.99 (at 3.33 Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.274 , 0.295 0.265 , 0.283	Depositor DCC
R_{free} test set	4015 reflections (3.09%)	DCC
Wilson B-factor (Å ²)	86.3	Xtriage
Anisotropy	0.060	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	(Not available) , (Not available)	EDS
Estimated twinning fraction	0.048 for -k,-h,-l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.42$, $\langle L^2 \rangle = 0.24$	Xtriage
Outliers	0 of 133792 reflections	Xtriage
F_o, F_c correlation	0.89	EDS
Total number of atoms	45814	wwPDB-VP
Average B, all atoms (Å ²)	54.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 18.35% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: ADP

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	0.47	0/1969	0.58	0/2678
1	C	0.54	0/1972	0.59	0/2680
1	E	0.47	0/1993	0.58	0/2706
1	G	0.49	0/1986	0.57	0/2697
1	I	0.44	0/1979	0.56	0/2688
1	K	0.54	0/1983	0.60	0/2693
1	M	0.49	0/1985	0.58	0/2696
1	O	0.52	0/1976	0.60	0/2684
1	Q	0.49	0/1978	0.58	0/2688
1	S	0.47	0/1980	0.58	0/2690
1	U	0.43	0/1933	0.58	0/2628
1	W	0.47	0/1975	0.57	0/2682
2	B	0.45	0/1840	0.60	0/2494
2	D	0.51	0/1928	0.64	0/2606
2	F	0.47	0/1866	0.60	0/2524
2	H	0.45	0/1757	0.59	0/2377
2	J	0.46	0/1872	0.58	0/2530
2	L	0.51	0/1918	0.65	0/2592
2	N	0.48	0/1837	0.60	0/2487
2	P	0.51	0/1932	0.65	0/2609
2	R	0.50	0/1908	0.65	1/2578 (0.0%)
2	T	0.49	0/1912	0.63	0/2584
2	V	0.47	0/1843	0.60	0/2494
2	X	0.46	0/1848	0.60	0/2501
All	All	0.48	0/46170	0.60	1/62586 (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
2	D	0	2
2	L	0	1
2	P	0	1
2	R	0	2
2	T	0	1
All	All	0	7

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
2	R	4	MET	N-CA-C	-5.96	94.91	111.00

There are no chirality outliers.

All (7) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	D	1	MET	Peptide
2	D	17	GLY	Peptide
2	L	17	GLY	Peptide
2	P	17	GLY	Peptide
2	R	17	GLY	Peptide
2	R	5	LEU	Peptide
2	T	17	GLY	Peptide

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	1944	0	1969	20	0
1	C	1947	0	1982	30	0
1	E	1968	0	2013	35	0
1	G	1961	0	2003	33	0
1	I	1954	0	1997	33	0
1	K	1958	0	2001	35	0
1	M	1960	0	2003	20	0
1	O	1951	0	1995	23	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	Q	1953	0	1988	23	0
1	S	1955	0	1996	29	0
1	U	1908	0	1950	26	0
1	W	1950	0	1997	25	0
2	B	1812	0	1810	41	0
2	D	1900	0	1920	45	0
2	F	1838	0	1852	47	0
2	H	1732	0	1740	49	0
2	J	1844	0	1870	47	0
2	L	1890	0	1915	50	0
2	N	1809	0	1817	41	0
2	P	1904	0	1938	47	0
2	R	1880	0	1904	39	0
2	T	1884	0	1913	49	0
2	V	1815	0	1836	41	0
2	X	1821	0	1820	31	0
3	B	27	0	12	5	0
3	D	27	0	12	3	0
3	F	17	0	7	1	0
3	H	27	0	12	2	0
3	J	9	0	0	1	0
3	L	27	0	12	3	0
3	N	27	0	12	3	0
3	P	27	0	12	3	0
3	R	27	0	12	0	0
3	T	27	0	12	3	0
3	V	17	0	7	2	0
3	X	17	0	7	0	0
All	All	45814	0	46346	777	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 8.

All (777) 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)
2:T:1:MET:H2	2:T:2:ARG:HA	1.24	1.00
2:T:1:MET:N	2:T:2:ARG:HA	1.75	1.00
1:E:243:LYS:HG2	2:F:112:GLU:OE1	1.61	0.98
1:G:249:GLN:H	1:G:249:GLN:HE21	1.18	0.90
2:P:99:ARG:NH1	3:P:404:ADP:O2A	2.07	0.87

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L:78:ARG:HD3	2:L:126:ASP:OD1	1.75	0.86
2:H:227:ILE:HD12	2:H:248:VAL:HG13	1.59	0.83
2:V:99:ARG:NH1	3:V:404:ADP:O2A	2.12	0.81
2:T:99:ARG:NH1	3:T:404:ADP:O2A	2.13	0.81
1:G:249:GLN:N	1:G:249:GLN:HE21	1.77	0.81
2:J:64:MET:HE2	2:J:124:ALA:HB2	1.66	0.77
2:F:99:ARG:NH1	3:F:404:ADP:O2A	2.16	0.77
2:L:64:MET:HE2	2:L:124:ALA:HB2	1.67	0.76
2:T:53:LYS:HG3	2:T:133:GLN:HB2	1.67	0.76
2:H:48:GLU:HG2	2:H:53:LYS:HG2	1.67	0.75
2:L:99:ARG:NH1	3:L:404:ADP:O2A	2.19	0.75
2:N:77:LEU:HD12	2:N:112:GLU:HG3	1.69	0.74
2:N:99:ARG:HH12	3:N:404:ADP:PA	2.09	0.74
2:R:78:ARG:HD3	2:R:126:ASP:OD1	1.88	0.74
2:X:64:MET:HE2	2:X:124:ALA:HB2	1.70	0.73
2:P:53:LYS:HG3	2:P:133:GLN:HB2	1.69	0.72
2:H:64:MET:HE2	2:H:124:ALA:HB2	1.69	0.72
2:T:243:PHE:HZ	2:T:246:GLU:HG2	1.54	0.72
2:T:64:MET:HE2	2:T:124:ALA:HB2	1.72	0.72
2:B:64:MET:HE2	2:B:124:ALA:HB2	1.70	0.72
2:L:77:LEU:HD12	2:L:112:GLU:HG3	1.72	0.72
2:H:99:ARG:NH1	3:H:404:ADP:O2A	2.22	0.72
2:J:99:ARG:HH12	3:J:404:ADP:PB	2.11	0.72
2:P:64:MET:HE2	2:P:124:ALA:HB2	1.71	0.72
2:B:175:LEU:HD22	2:B:248:VAL:HG21	1.72	0.71
1:W:51:ASP:OD2	1:W:69:LEU:HB2	1.92	0.70
2:F:77:LEU:HD12	2:F:112:GLU:HG3	1.73	0.70
2:D:64:MET:HE2	2:D:124:ALA:HB2	1.72	0.70
2:X:223:LYS:HB3	2:X:248:VAL:HG11	1.72	0.70
2:F:129:THR:HG21	2:F:142:SER:OG	1.90	0.70
2:R:77:LEU:HD12	2:R:112:GLU:HG3	1.73	0.70
2:H:78:ARG:HD3	2:H:126:ASP:OD1	1.92	0.70
2:L:48:GLU:HG2	2:L:53:LYS:HG2	1.72	0.70
2:T:66:PRO:HG2	2:T:69:LEU:HD12	1.74	0.69
2:N:99:ARG:NH1	3:N:404:ADP:O2A	2.25	0.69
2:R:64:MET:HE2	2:R:124:ALA:HB2	1.73	0.69
2:F:48:GLU:OE1	2:F:53:LYS:HE2	1.92	0.69
2:D:77:LEU:HD12	2:D:112:GLU:HG3	1.73	0.69
2:T:77:LEU:HD12	2:T:112:GLU:HG3	1.74	0.69
1:G:243:LYS:HG2	2:H:112:GLU:OE1	1.92	0.69
2:B:66:PRO:HG2	2:B:69:LEU:HD12	1.75	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:64:MET:HE2	2:F:124:ALA:HB2	1.75	0.69
2:D:65:HIS:CB	2:D:66:PRO:HD3	2.22	0.68
2:N:64:MET:HE2	2:N:124:ALA:HB2	1.74	0.68
2:X:129:THR:HG21	2:X:142:SER:OG	1.93	0.68
2:J:77:LEU:HD12	2:J:112:GLU:HG3	1.75	0.68
2:T:1:MET:N	2:T:2:ARG:CA	2.56	0.68
2:B:34:GLU:HB3	2:B:240:TYR:HD1	1.59	0.68
1:K:42:ILE:HG12	1:K:56:VAL:HG22	1.76	0.68
2:N:12:LEU:HD21	2:N:184:TRP:HB2	1.75	0.67
2:B:77:LEU:HD12	2:B:112:GLU:HG3	1.77	0.67
2:J:243:PHE:HZ	2:J:246:GLU:HG2	1.60	0.67
2:V:77:LEU:HD12	2:V:112:GLU:HG3	1.75	0.67
2:X:66:PRO:HG2	2:X:69:LEU:HD12	1.77	0.67
2:L:65:HIS:CB	2:L:66:PRO:HD3	2.23	0.67
1:I:112:ARG:NH2	2:J:99:ARG:HB2	2.10	0.67
2:V:65:HIS:CB	2:V:66:PRO:HD3	2.24	0.67
2:N:66:PRO:HG2	2:N:69:LEU:HD12	1.77	0.67
2:H:34:GLU:HB3	2:H:240:TYR:HD1	1.58	0.66
1:M:42:ILE:HG12	1:M:56:VAL:HG22	1.76	0.66
2:N:129:THR:HG21	2:N:142:SER:OG	1.95	0.66
2:P:65:HIS:CB	2:P:66:PRO:HD3	2.25	0.66
1:G:42:ILE:HG12	1:G:56:VAL:HG22	1.78	0.66
1:U:41:SER:HB2	1:U:57:LYS:HB2	1.78	0.66
2:B:136:ALA:HA	3:B:404:ADP:O3'	1.95	0.66
1:E:243:LYS:CE	2:F:108:ARG:HH21	2.08	0.66
2:L:66:PRO:HG2	2:L:69:LEU:HD12	1.76	0.66
2:H:227:ILE:HD13	2:H:248:VAL:HG22	1.78	0.66
2:F:65:HIS:CB	2:F:66:PRO:HD3	2.25	0.66
2:V:168:LYS:HD2	2:V:213:GLU:OE1	1.96	0.66
1:K:112:ARG:NH2	2:L:99:ARG:HB2	2.10	0.65
2:P:77:LEU:HD12	2:P:112:GLU:HG3	1.78	0.65
2:B:99:ARG:HH12	3:B:404:ADP:PA	2.20	0.65
2:R:66:PRO:HG2	2:R:69:LEU:HD12	1.79	0.65
2:X:77:LEU:HD12	2:X:112:GLU:HG3	1.79	0.65
2:B:78:ARG:HD3	2:B:126:ASP:OD1	1.96	0.65
2:V:64:MET:HE2	2:V:124:ALA:HB2	1.77	0.65
2:N:65:HIS:CB	2:N:66:PRO:HD3	2.27	0.65
2:H:66:PRO:HG2	2:H:69:LEU:HD12	1.79	0.65
1:Q:42:ILE:HG12	1:Q:56:VAL:HG22	1.79	0.65
2:J:65:HIS:CB	2:J:66:PRO:HD3	2.26	0.65
1:Q:51:ASP:OD1	1:Q:171:TYR:HE1	1.79	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:65:HIS:CB	2:H:66:PRO:HD3	2.26	0.65
2:H:129:THR:HG21	2:H:142:SER:OG	1.97	0.64
2:B:65:HIS:CB	2:B:66:PRO:HD3	2.26	0.64
2:X:65:HIS:CB	2:X:66:PRO:HD3	2.27	0.64
2:J:66:PRO:HG2	2:J:69:LEU:HD12	1.79	0.64
2:H:77:LEU:HD12	2:H:112:GLU:HG3	1.78	0.64
2:B:164:VAL:HG22	2:B:225:ILE:HG13	1.80	0.64
2:T:65:HIS:CB	2:T:66:PRO:HD3	2.28	0.64
2:L:19:ARG:HD2	2:L:181:GLU:OE2	1.98	0.64
2:R:164:VAL:HG22	2:R:225:ILE:HG13	1.80	0.64
2:P:66:PRO:HG2	2:P:69:LEU:HD12	1.79	0.63
2:V:78:ARG:HD3	2:V:126:ASP:OD1	1.99	0.63
2:V:129:THR:HG21	2:V:142:SER:OG	1.97	0.63
2:V:66:PRO:HG2	2:V:69:LEU:HD12	1.79	0.63
2:F:164:VAL:HG22	2:F:225:ILE:HG13	1.80	0.63
3:P:404:ADP:O2B	3:P:404:ADP:O2A	2.16	0.63
2:T:1:MET:O	2:T:1:MET:HG3	1.98	0.63
2:F:66:PRO:HG2	2:F:69:LEU:HD12	1.81	0.63
1:S:240:LYS:HB2	2:T:203:PHE:HB3	1.81	0.63
2:D:66:PRO:HG2	2:D:69:LEU:HD12	1.81	0.63
2:V:64:MET:HE1	2:V:76:VAL:HB	1.81	0.62
2:H:164:VAL:HG22	2:H:225:ILE:HG13	1.80	0.62
1:G:91:LEU:HD22	2:L:80:ARG:HH12	1.65	0.62
2:R:65:HIS:CB	2:R:66:PRO:HD3	2.29	0.62
2:B:129:THR:HG21	2:B:142:SER:OG	2.00	0.62
1:W:42:ILE:HG12	1:W:56:VAL:HG22	1.82	0.62
2:R:227:ILE:HD12	2:R:248:VAL:HG13	1.82	0.62
2:F:48:GLU:HG2	2:F:53:LYS:HG2	1.81	0.61
2:N:175:LEU:CD2	2:N:248:VAL:HG21	2.30	0.61
1:S:41:SER:HB2	1:S:57:LYS:HB2	1.81	0.61
2:J:164:VAL:HG22	2:J:225:ILE:HG13	1.82	0.61
2:T:129:THR:HG21	2:T:142:SER:OG	2.01	0.61
2:T:164:VAL:HG22	2:T:225:ILE:HG13	1.82	0.61
2:X:34:GLU:HB3	2:X:240:TYR:HD1	1.65	0.61
2:L:129:THR:HG21	2:L:142:SER:OG	2.00	0.61
2:X:73:ASP:OD2	2:X:74:ARG:HG3	2.00	0.61
1:O:41:SER:HB2	1:O:57:LYS:HB2	1.83	0.61
1:K:41:SER:HB2	1:K:57:LYS:HB2	1.83	0.61
1:M:41:SER:HB2	1:M:57:LYS:HB2	1.82	0.61
2:J:129:THR:HG21	2:J:142:SER:OG	2.01	0.61
2:B:138:SER:OG	3:B:404:ADP:O2B	2.18	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:V:179:GLU:O	2:V:183:MET:HB2	2.01	0.60
1:S:42:ILE:HG12	1:S:56:VAL:HG22	1.82	0.60
2:B:9:ARG:NH2	2:B:184:TRP:O	2.34	0.60
1:A:42:ILE:HG12	1:A:56:VAL:HG22	1.83	0.60
2:P:1:MET:HG3	2:P:3:GLU:H	1.67	0.60
1:C:41:SER:HB2	1:C:57:LYS:HB2	1.83	0.60
1:W:116:ARG:HD3	2:X:206:ASN:HB3	1.83	0.60
1:Q:71:ILE:HD12	1:Q:182:VAL:HG22	1.83	0.60
1:E:71:ILE:HD12	1:E:182:VAL:HG22	1.83	0.60
2:P:164:VAL:HG22	2:P:225:ILE:HG13	1.84	0.60
1:K:51:ASP:OD2	1:K:69:LEU:HB2	2.02	0.60
1:U:42:ILE:HG12	1:U:56:VAL:HG22	1.84	0.60
2:N:177:LEU:HD12	2:N:188:ASP:OD1	2.01	0.60
2:T:55:ILE:HG22	2:T:130:GLU:HB2	1.82	0.60
1:Q:41:SER:HB2	1:Q:57:LYS:HB2	1.82	0.59
1:G:148:ASP:OD1	2:L:40:ASN:HB2	2.02	0.59
1:U:112:ARG:NH2	2:V:99:ARG:HB2	2.17	0.59
1:I:42:ILE:HG12	1:I:56:VAL:HG22	1.84	0.59
2:V:164:VAL:HG22	2:V:225:ILE:HG13	1.84	0.59
1:W:41:SER:HB2	1:W:57:LYS:HB2	1.84	0.59
1:M:71:ILE:HD12	1:M:182:VAL:HG22	1.85	0.59
2:X:164:VAL:HG22	2:X:225:ILE:HG13	1.83	0.59
2:J:82:HIS:HE1	1:K:145:TYR:OH	1.86	0.59
1:O:42:ILE:HG12	1:O:56:VAL:HG22	1.85	0.59
1:I:14:ILE:HG22	2:V:116:LEU:HD22	1.85	0.59
1:C:42:ILE:HG12	1:C:56:VAL:HG22	1.85	0.59
2:L:164:VAL:HG22	2:L:225:ILE:HG13	1.85	0.59
2:N:130:GLU:HG3	1:Q:91:LEU:HD13	1.84	0.59
1:S:71:ILE:HD12	1:S:182:VAL:HG22	1.84	0.59
1:I:248:LEU:HD23	2:J:218:PHE:CZ	2.38	0.58
1:E:41:SER:HB2	1:E:57:LYS:HB2	1.86	0.58
2:F:64:MET:HE1	2:F:76:VAL:HB	1.84	0.58
2:N:164:VAL:HG22	2:N:225:ILE:HG13	1.83	0.58
1:G:41:SER:HB2	1:G:57:LYS:HB2	1.84	0.58
2:N:110:ALA:HB1	2:N:201:THR:CG2	2.34	0.58
2:L:73:ASP:OD2	2:L:74:ARG:HG3	2.04	0.58
2:L:234:GLU:HG3	2:L:241:VAL:CG2	2.33	0.58
2:H:48:GLU:HG2	2:H:53:LYS:CG	2.35	0.57
1:C:71:ILE:HD12	1:C:182:VAL:HG22	1.86	0.57
2:D:129:THR:HG21	2:D:142:SER:OG	2.03	0.57
2:P:110:ALA:HB1	2:P:201:THR:CG2	2.34	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:T:26:ASP:O	2:T:248:VAL:HB	2.03	0.57
2:R:129:THR:HG21	2:R:142:SER:OG	2.04	0.57
2:F:73:ASP:OD2	2:F:74:ARG:HG3	2.05	0.57
1:G:71:ILE:HD12	1:G:182:VAL:HG22	1.87	0.57
2:D:110:ALA:HB1	2:D:201:THR:CG2	2.35	0.57
1:E:14:ILE:HG21	2:N:118:GLU:OE1	2.04	0.57
2:N:129:THR:HG21	2:N:142:SER:HG	1.67	0.57
2:V:19:ARG:HD2	2:V:181:GLU:OE2	2.04	0.57
2:N:78:ARG:HD3	2:N:126:ASP:OD1	2.04	0.57
2:B:136:ALA:HA	3:B:404:ADP:HO3'	1.69	0.57
2:L:110:ALA:HB1	2:L:201:THR:CG2	2.34	0.57
2:T:19:ARG:HD2	2:T:181:GLU:OE2	2.04	0.56
2:H:89:ASP:N	2:H:89:ASP:OD2	2.27	0.56
1:E:42:ILE:HG12	1:E:56:VAL:HG22	1.86	0.56
2:R:73:ASP:OD2	2:R:74:ARG:HG3	2.06	0.56
1:A:71:ILE:HD12	1:A:182:VAL:HG22	1.87	0.56
2:T:110:ALA:HB1	2:T:201:THR:CG2	2.35	0.56
2:R:110:ALA:HB1	2:R:201:THR:CG2	2.35	0.56
1:W:71:ILE:HD12	1:W:182:VAL:HG22	1.88	0.56
2:X:110:ALA:HB1	2:X:201:THR:CG2	2.36	0.56
2:P:19:ARG:HD2	2:P:181:GLU:OE2	2.05	0.56
2:R:64:MET:HE1	2:R:76:VAL:HB	1.87	0.56
1:A:32:ARG:HB2	1:A:36:ASP:HB2	1.87	0.56
1:I:31:GLY:HA2	2:V:233:ARG:NH1	2.20	0.56
2:L:32:LYS:HB3	2:L:48:GLU:HB2	1.88	0.56
1:K:57:LYS:HG2	1:K:62:MET:HG2	1.88	0.56
1:S:255:GLU:OE2	2:T:215:ARG:NH2	2.39	0.56
2:P:129:THR:HG21	2:P:142:SER:OG	2.06	0.56
2:D:164:VAL:HG22	2:D:225:ILE:HG13	1.87	0.56
1:G:249:GLN:H	1:G:249:GLN:NE2	1.96	0.56
1:K:32:ARG:HB2	1:K:36:ASP:HB2	1.88	0.56
2:P:203:PHE:HE1	2:P:218:PHE:CE1	2.24	0.56
2:L:168:LYS:HE2	2:L:186:GLU:HB2	1.88	0.56
2:F:110:ALA:HB1	2:F:201:THR:CG2	2.36	0.56
1:O:57:LYS:HG2	1:O:62:MET:HG2	1.87	0.55
2:F:233:ARG:CZ	1:W:31:GLY:HA2	2.35	0.55
2:D:19:ARG:HD2	2:D:181:GLU:OE2	2.06	0.55
2:T:55:ILE:CG2	2:T:130:GLU:HB2	2.35	0.55
2:J:133:GLN:NE2	1:K:48:LYS:HB2	2.22	0.55
1:C:32:ARG:HB2	1:C:36:ASP:HB2	1.87	0.55
2:F:243:PHE:CZ	2:F:246:GLU:HG2	2.42	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:41:SER:HB2	1:I:57:LYS:HB2	1.88	0.55
2:H:227:ILE:CD1	2:H:248:VAL:HG13	2.35	0.55
1:K:6:SER:C	1:K:8:GLN:H	2.10	0.55
2:H:73:ASP:OD2	2:H:74:ARG:HG3	2.07	0.55
2:T:28:LEU:HG	2:T:248:VAL:HG21	1.89	0.55
1:I:71:ILE:HD12	1:I:182:VAL:HG22	1.89	0.55
2:H:135:ASP:O	2:H:136:ALA:HB3	2.07	0.55
2:P:73:ASP:OD2	2:P:74:ARG:HG3	2.07	0.55
2:H:88:THR:HG21	3:H:404:ADP:C2	2.43	0.54
2:J:86:PHE:HA	1:K:68:LYS:HD3	1.87	0.54
1:I:32:ARG:HB2	1:I:36:ASP:HB2	1.89	0.54
2:D:64:MET:HE1	2:D:76:VAL:HB	1.89	0.54
1:O:71:ILE:HD12	1:O:182:VAL:HG22	1.90	0.54
2:T:73:ASP:OD2	2:T:74:ARG:HG3	2.08	0.54
1:E:243:LYS:CE	2:F:108:ARG:NH2	2.70	0.54
1:K:71:ILE:HD12	1:K:182:VAL:HG22	1.89	0.54
1:U:32:ARG:HB2	1:U:36:ASP:HB2	1.89	0.54
2:H:110:ALA:HB1	2:H:201:THR:CG2	2.37	0.54
1:E:51:ASP:O	1:E:168:THR:HA	2.07	0.54
2:N:19:ARG:HD2	2:N:181:GLU:OE2	2.07	0.54
1:O:240:LYS:HB2	2:P:203:PHE:HB3	1.90	0.54
1:E:121:SER:O	1:E:122:LYS:HB3	2.07	0.54
1:C:240:LYS:HB2	2:D:203:PHE:HB3	1.89	0.53
2:H:80:ARG:NH1	2:H:130:GLU:OE2	2.42	0.53
2:V:73:ASP:OD2	2:V:74:ARG:HG3	2.08	0.53
1:U:71:ILE:HD12	1:U:182:VAL:HG22	1.90	0.53
2:T:243:PHE:CZ	2:T:246:GLU:HG2	2.41	0.53
2:H:227:ILE:CD1	2:H:248:VAL:HG22	2.38	0.53
1:U:57:LYS:HG2	1:U:62:MET:HG2	1.91	0.53
2:T:34:GLU:HG3	2:T:46:ILE:HB	1.90	0.53
1:O:32:ARG:HB2	1:O:36:ASP:HB2	1.91	0.53
2:P:48:GLU:HG2	2:P:53:LYS:HB3	1.91	0.53
2:J:64:MET:HE1	2:J:76:VAL:HB	1.91	0.53
1:G:32:ARG:HB2	1:G:36:ASP:HB2	1.91	0.53
2:D:223:LYS:HB3	2:D:248:VAL:CG1	2.39	0.53
2:B:110:ALA:HB1	2:B:201:THR:CG2	2.39	0.53
1:I:57:LYS:HG2	1:I:62:MET:HG2	1.91	0.53
1:E:32:ARG:HB2	1:E:36:ASP:HB2	1.90	0.53
2:P:159:ASP:OD2	2:P:196:SER:HB2	2.08	0.53
2:D:99:ARG:HH12	3:D:404:ADP:PA	2.29	0.53
2:X:223:LYS:HB3	2:X:248:VAL:CG1	2.38	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:233:ARG:HG3	2:D:233:ARG:NH1	2.24	0.53
2:B:51:ASN:HB2	2:B:135:ASP:OD2	2.09	0.53
2:R:212:ASP:N	2:R:212:ASP:OD1	2.39	0.53
1:E:243:LYS:HE3	2:F:108:ARG:HH21	1.73	0.52
1:M:32:ARG:HB2	1:M:36:ASP:HB2	1.90	0.52
1:G:91:LEU:H	1:G:92:PRO:CD	2.23	0.52
1:Q:57:LYS:HG2	1:Q:62:MET:HG2	1.90	0.52
2:T:42:ASP:O	2:T:153:ALA:HA	2.09	0.52
2:X:223:LYS:CB	2:X:248:VAL:HG11	2.38	0.52
2:J:91:ARG:HB2	1:K:68:LYS:HG2	1.91	0.52
2:H:131:ILE:HG12	2:H:138:SER:HB2	1.91	0.52
2:P:193:MET:HG3	2:P:225:ILE:HD13	1.92	0.52
1:E:125:ASP:HB3	1:E:128:LYS:HD2	1.91	0.52
1:W:32:ARG:HB2	1:W:36:ASP:HB2	1.91	0.52
2:H:192:ALA:HB3	2:H:202:LEU:HB3	1.92	0.52
2:F:78:ARG:HD3	2:F:126:ASP:OD1	2.10	0.52
2:H:129:THR:HG21	2:H:142:SER:HG	1.73	0.52
2:L:23:ARG:HH21	2:L:178:ASN:HD21	1.56	0.52
1:S:269:LEU:O	1:S:273:LEU:HG	2.10	0.52
1:C:112:ARG:NH1	2:D:102:GLU:OE1	2.42	0.52
2:L:193:MET:HG3	2:L:225:ILE:HD13	1.92	0.52
2:D:73:ASP:OD2	2:D:74:ARG:HG3	2.10	0.52
2:H:82:HIS:HE1	1:I:145:TYR:OH	1.92	0.52
1:E:112:ARG:NH2	2:F:99:ARG:HB2	2.25	0.52
2:L:131:ILE:HD11	2:L:142:SER:HB2	1.92	0.52
1:S:57:LYS:HG2	1:S:62:MET:HG2	1.92	0.51
2:B:193:MET:HG3	2:B:225:ILE:HD13	1.92	0.51
1:Q:32:ARG:HB2	1:Q:36:ASP:HB2	1.91	0.51
1:G:91:LEU:H	1:G:92:PRO:HD3	1.75	0.51
1:C:51:ASP:OD2	1:C:69:LEU:HB2	2.10	0.51
2:R:19:ARG:HD2	2:R:181:GLU:OE2	2.09	0.51
2:R:34:GLU:HB3	2:R:240:TYR:HD1	1.75	0.51
1:W:91:LEU:H	1:W:92:PRO:CD	2.23	0.51
1:A:57:LYS:HG2	1:A:62:MET:HG2	1.93	0.51
2:X:131:ILE:HG12	2:X:138:SER:HB2	1.93	0.51
1:S:32:ARG:HB2	1:S:36:ASP:HB2	1.91	0.51
2:J:133:GLN:OE1	1:K:48:LYS:HG2	2.10	0.51
1:S:91:LEU:H	1:S:92:PRO:CD	2.24	0.51
2:D:28:LEU:O	2:D:245:GLU:HB2	2.11	0.51
1:S:145:TYR:OH	2:V:82:HIS:HE1	1.92	0.51
2:X:135:ASP:O	2:X:136:ALA:HB3	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:P:190:PRO:HG2	2:P:204:GLN:HB2	1.92	0.51
2:P:42:ASP:O	2:P:153:ALA:HA	2.11	0.51
1:E:263:VAL:O	1:E:267:GLU:HG3	2.11	0.51
2:B:19:ARG:HD2	2:B:181:GLU:OE2	2.11	0.51
1:E:91:LEU:H	1:E:92:PRO:CD	2.23	0.51
2:T:136:ALA:N	3:T:404:ADP:O3'	2.36	0.50
2:F:131:ILE:HG12	2:F:138:SER:HB2	1.94	0.50
1:Q:240:LYS:HB2	2:R:203:PHE:HB3	1.93	0.50
2:L:135:ASP:OD1	2:L:179:GLU:HB2	2.11	0.50
1:G:30:ASP:OD1	1:G:31:GLY:N	2.44	0.50
2:B:73:ASP:OD2	2:B:74:ARG:HG3	2.10	0.50
1:A:91:LEU:H	1:A:92:PRO:HD3	1.76	0.50
2:R:168:LYS:HG3	2:R:173:ILE:HG13	1.92	0.50
2:F:19:ARG:HD2	2:F:181:GLU:OE2	2.11	0.50
1:K:91:LEU:H	1:K:92:PRO:CD	2.25	0.50
2:T:227:ILE:HD12	2:T:248:VAL:HG13	1.94	0.50
1:C:91:LEU:H	1:C:92:PRO:HD3	1.76	0.50
2:T:27:GLU:HG2	2:T:247:GLY:HA2	1.94	0.50
1:C:91:LEU:H	1:C:92:PRO:CD	2.24	0.50
2:J:110:ALA:HB1	2:J:201:THR:CG2	2.42	0.50
2:L:131:ILE:HG12	2:L:138:SER:HB2	1.92	0.50
2:P:131:ILE:HG12	2:P:138:SER:HB2	1.92	0.50
2:V:131:ILE:HD11	2:V:142:SER:HB2	1.93	0.50
1:E:91:LEU:H	1:E:92:PRO:HD3	1.76	0.50
2:V:110:ALA:HB1	2:V:201:THR:CG2	2.41	0.50
1:A:41:SER:HB2	1:A:57:LYS:HB2	1.92	0.49
2:R:2:ARG:HG2	2:R:3:GLU:H	1.77	0.49
1:E:243:LYS:HE2	2:F:108:ARG:HH21	1.74	0.49
1:C:57:LYS:HG2	1:C:62:MET:HG2	1.93	0.49
1:E:57:LYS:HG2	1:E:62:MET:HG2	1.94	0.49
1:O:91:LEU:H	1:O:92:PRO:CD	2.25	0.49
2:J:73:ASP:OD2	2:J:74:ARG:HG3	2.12	0.49
2:H:19:ARG:HD2	2:H:181:GLU:OE2	2.12	0.49
1:E:243:LYS:HE3	2:F:108:ARG:NH2	2.27	0.49
1:C:112:ARG:NH2	2:D:99:ARG:HB2	2.27	0.49
1:G:91:LEU:HD22	2:L:80:ARG:NH1	2.27	0.49
1:Q:91:LEU:H	1:Q:92:PRO:HD3	1.76	0.49
1:E:28:ARG:CZ	1:E:210:VAL:HG13	2.43	0.49
2:L:223:LYS:HB3	2:L:248:VAL:CG1	2.43	0.49
1:C:183:ASN:C	1:C:183:ASN:ND2	2.65	0.49
1:E:91:LEU:N	1:E:92:PRO:CD	2.76	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:P:192:ALA:HB3	2:P:202:LEU:HB3	1.95	0.49
2:P:1:MET:HG2	2:P:4:MET:HG3	1.95	0.49
2:J:27:GLU:HG2	2:J:247:GLY:HA2	1.95	0.49
2:T:131:ILE:HG12	2:T:138:SER:HB2	1.94	0.49
2:D:131:ILE:HD11	2:D:142:SER:HB2	1.94	0.49
1:C:68:LYS:HG2	2:F:91:ARG:HB2	1.94	0.49
2:V:27:GLU:HG2	2:V:247:GLY:HA2	1.95	0.49
1:A:91:LEU:H	1:A:92:PRO:CD	2.26	0.49
1:Q:129:LEU:HB3	1:Q:138:TRP:HB2	1.95	0.49
1:M:91:LEU:H	1:M:92:PRO:CD	2.25	0.49
2:D:131:ILE:HG12	2:D:138:SER:HB2	1.95	0.49
1:W:91:LEU:H	1:W:92:PRO:HD3	1.77	0.49
1:A:104:ASP:HB3	1:A:107:ALA:HB3	1.95	0.49
2:B:131:ILE:HG12	2:B:138:SER:HB2	1.95	0.49
1:E:38:ARG:HD2	1:E:59:GLY:HA3	1.95	0.49
1:I:240:LYS:HB2	2:J:203:PHE:HB3	1.95	0.49
1:O:121:SER:HB3	1:O:236:VAL:HG11	1.94	0.49
1:W:57:LYS:HG2	1:W:62:MET:HG2	1.94	0.48
1:M:91:LEU:H	1:M:92:PRO:HD3	1.78	0.48
2:F:168:LYS:HE2	2:F:186:GLU:HB2	1.93	0.48
2:B:169:ALA:O	2:B:171:GLY:N	2.42	0.48
2:D:233:ARG:NH2	1:G:31:GLY:HA2	2.28	0.48
1:C:27:ILE:HD11	2:T:233:ARG:HH12	1.78	0.48
1:K:112:ARG:NH1	2:L:102:GLU:OE1	2.46	0.48
2:X:129:THR:HG21	2:X:142:SER:HG	1.77	0.48
1:G:91:LEU:N	1:G:92:PRO:CD	2.76	0.48
2:H:27:GLU:HG2	2:H:247:GLY:HA2	1.96	0.48
2:N:190:PRO:HG2	2:N:204:GLN:HB2	1.94	0.48
1:S:121:SER:HB3	1:S:236:VAL:HG11	1.95	0.48
2:V:131:ILE:HG12	2:V:138:SER:HB2	1.96	0.48
1:W:91:LEU:N	1:W:92:PRO:CD	2.76	0.48
1:O:91:LEU:H	1:O:92:PRO:HD3	1.78	0.48
2:D:159:ASP:OD2	2:D:196:SER:HB2	2.13	0.48
2:N:234:GLU:HG3	2:N:241:VAL:HG21	1.94	0.48
2:X:192:ALA:HB3	2:X:202:LEU:HB3	1.96	0.48
2:N:131:ILE:HG12	2:N:138:SER:HB2	1.94	0.48
2:D:193:MET:HG3	2:D:225:ILE:HD13	1.94	0.48
2:B:175:LEU:HD22	2:B:248:VAL:CG2	2.43	0.48
2:T:190:PRO:HG2	2:T:204:GLN:HB2	1.96	0.48
2:X:103:LEU:HD21	2:X:139:ARG:CZ	2.43	0.48
1:O:163:ALA:HA	1:O:273:LEU:HD21	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:7:ASN:H	1:A:7:ASN:ND2	2.11	0.48
2:H:64:MET:HE1	2:H:76:VAL:HB	1.95	0.48
2:J:193:MET:HG3	2:J:225:ILE:HD13	1.95	0.48
2:R:27:GLU:HG2	2:R:247:GLY:HA2	1.95	0.48
2:T:192:ALA:HB3	2:T:202:LEU:HB3	1.96	0.48
2:F:131:ILE:HD11	2:F:142:SER:HB2	1.96	0.48
1:M:91:LEU:N	1:M:92:PRO:CD	2.77	0.48
1:U:91:LEU:H	1:U:92:PRO:HD3	1.78	0.48
1:S:68:LYS:HG2	2:V:91:ARG:HB2	1.94	0.48
2:N:73:ASP:OD2	2:N:74:ARG:HG3	2.14	0.48
2:N:12:LEU:HD22	2:N:181:GLU:HA	1.95	0.48
1:Q:91:LEU:H	1:Q:92:PRO:CD	2.26	0.48
2:D:233:ARG:HG3	2:D:233:ARG:HH11	1.79	0.48
1:A:166:TYR:HB3	1:A:273:LEU:HD22	1.96	0.48
2:P:183:MET:HE3	2:P:183:MET:HA	1.96	0.48
1:Q:112:ARG:NH2	2:R:99:ARG:HB2	2.29	0.47
1:S:251:ILE:HD12	2:T:200:VAL:HG21	1.96	0.47
2:V:37:VAL:HG11	2:V:46:ILE:HG13	1.96	0.47
2:N:202:LEU:HD23	2:N:203:PHE:N	2.29	0.47
2:N:234:GLU:HG3	2:N:241:VAL:CG2	2.44	0.47
1:W:121:SER:HB3	1:W:236:VAL:HG11	1.96	0.47
2:J:14:LEU:O	2:J:16:ASP:N	2.44	0.47
2:R:2:ARG:HG2	2:R:3:GLU:N	2.29	0.47
1:U:121:SER:O	1:U:122:LYS:HB2	2.14	0.47
1:U:104:ASP:HB3	1:U:107:ALA:HB3	1.97	0.47
1:I:104:ASP:HB3	1:I:107:ALA:HB3	1.96	0.47
2:V:99:ARG:HH12	3:V:404:ADP:PA	2.37	0.47
2:N:131:ILE:HD11	2:N:142:SER:HB2	1.95	0.47
2:T:28:LEU:O	2:T:245:GLU:HB3	2.15	0.47
2:P:135:ASP:O	2:P:136:ALA:HB3	2.14	0.47
2:V:83:MET:HB2	2:V:92:LYS:HD3	1.97	0.47
2:B:27:GLU:HG2	2:B:247:GLY:HA2	1.97	0.47
1:E:129:LEU:HB3	1:E:138:TRP:HB2	1.96	0.47
1:S:129:LEU:HB3	1:S:138:TRP:HB2	1.96	0.47
2:D:13:ILE:HD13	2:D:19:ARG:HG2	1.95	0.47
2:H:86:PHE:HA	1:I:68:LYS:HD3	1.97	0.47
1:A:121:SER:HB3	1:A:236:VAL:HG11	1.95	0.47
1:I:38:ARG:HD2	1:I:59:GLY:HA3	1.97	0.47
1:S:91:LEU:H	1:S:92:PRO:HD3	1.79	0.47
1:A:91:LEU:N	1:A:92:PRO:CD	2.77	0.47
2:F:27:GLU:HG2	2:F:247:GLY:HA2	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:J:190:PRO:HG2	2:J:204:GLN:HB2	1.96	0.47
1:C:38:ARG:HD2	1:C:59:GLY:HA3	1.97	0.47
2:V:32:LYS:HB3	2:V:48:GLU:HB2	1.97	0.47
1:W:183:ASN:C	1:W:183:ASN:ND2	2.66	0.47
2:F:26:ASP:HB2	2:F:248:VAL:HG12	1.95	0.47
2:H:131:ILE:HD11	2:H:142:SER:HB2	1.97	0.47
2:H:193:MET:HG3	2:H:225:ILE:HD13	1.97	0.47
1:I:121:SER:HB3	1:I:236:VAL:HG11	1.96	0.47
1:M:104:ASP:HB3	1:M:107:ALA:HB3	1.97	0.47
1:I:28:ARG:CZ	1:I:210:VAL:HG13	2.45	0.47
2:L:179:GLU:HG3	3:L:404:ADP:O2'	2.15	0.46
2:P:41:ALA:HA	2:P:59:TYR:CE2	2.50	0.46
1:Q:91:LEU:N	1:Q:92:PRO:CD	2.78	0.46
1:U:91:LEU:H	1:U:92:PRO:CD	2.28	0.46
1:O:77:ASP:O	1:O:79:PRO:HD3	2.15	0.46
2:N:27:GLU:HG2	2:N:247:GLY:HA2	1.98	0.46
2:B:34:GLU:HB3	2:B:240:TYR:CD1	2.46	0.46
1:S:91:LEU:N	1:S:92:PRO:CD	2.78	0.46
2:J:19:ARG:HD2	2:J:181:GLU:OE2	2.15	0.46
2:L:234:GLU:HG3	2:L:241:VAL:HG21	1.98	0.46
1:Q:38:ARG:HD2	1:Q:59:GLY:HA3	1.97	0.46
1:K:91:LEU:N	1:K:92:PRO:CD	2.79	0.46
2:P:227:ILE:HD12	2:P:248:VAL:HG22	1.97	0.46
1:G:91:LEU:CD2	2:L:80:ARG:HH12	2.28	0.46
2:V:193:MET:HG3	2:V:225:ILE:HD13	1.97	0.46
1:C:91:LEU:N	1:C:92:PRO:CD	2.78	0.46
2:J:192:ALA:HB3	2:J:202:LEU:HB3	1.96	0.46
1:W:129:LEU:HB3	1:W:138:TRP:HB2	1.97	0.46
2:J:196:SER:HB3	1:O:27:ILE:HG21	1.96	0.46
2:P:23:ARG:HH21	2:P:178:ASN:ND2	2.14	0.46
2:X:193:MET:HG3	2:X:225:ILE:HD13	1.98	0.46
2:R:131:ILE:HD11	2:R:142:SER:HB2	1.98	0.46
1:U:38:ARG:HD2	1:U:59:GLY:HA3	1.98	0.46
2:P:27:GLU:HG2	2:P:247:GLY:HA2	1.98	0.46
2:H:28:LEU:HG	2:H:248:VAL:HG21	1.98	0.46
2:D:202:LEU:HD23	2:D:203:PHE:N	2.31	0.46
1:K:91:LEU:H	1:K:92:PRO:HD3	1.80	0.46
2:R:192:ALA:HB3	2:R:202:LEU:HB3	1.97	0.46
1:E:104:ASP:HB3	1:E:107:ALA:HB3	1.98	0.46
2:L:64:MET:HE1	2:L:76:VAL:HB	1.98	0.46
1:E:32:ARG:CZ	1:E:38:ARG:HG3	2.46	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:202:LEU:HD23	2:H:203:PHE:N	2.31	0.46
2:R:190:PRO:HG2	2:R:204:GLN:HB2	1.97	0.46
2:J:160:LEU:HD11	2:J:236:LEU:HD22	1.98	0.46
1:C:28:ARG:CZ	1:C:210:VAL:HG13	2.46	0.46
2:P:16:ASP:C	2:P:18:LYS:H	2.19	0.46
1:M:57:LYS:HG2	1:M:62:MET:HG2	1.97	0.45
1:G:57:LYS:HG2	1:G:62:MET:HG2	1.98	0.45
2:F:192:ALA:HB3	2:F:202:LEU:HB3	1.98	0.45
2:P:64:MET:HE1	2:P:76:VAL:HB	1.98	0.45
2:D:65:HIS:CB	2:D:66:PRO:CD	2.94	0.45
1:O:91:LEU:N	1:O:92:PRO:CD	2.79	0.45
2:X:27:GLU:HG2	2:X:247:GLY:HA2	1.97	0.45
1:W:240:LYS:HB2	2:X:203:PHE:HB3	1.98	0.45
1:W:77:ASP:O	1:W:79:PRO:HD3	2.16	0.45
2:P:37:VAL:HG11	2:P:46:ILE:HG13	1.98	0.45
2:V:168:LYS:HE3	2:V:171:GLY:HA2	1.97	0.45
1:K:243:LYS:HD3	2:L:74:ARG:HH12	1.81	0.45
1:I:125:ASP:OD2	1:I:128:LYS:HE3	2.16	0.45
1:C:269:LEU:O	1:C:273:LEU:HG	2.17	0.45
1:K:3:SER:HB3	2:L:78:ARG:HG3	1.97	0.45
2:N:64:MET:HE1	2:N:76:VAL:HB	1.97	0.45
1:W:38:ARG:HD2	1:W:59:GLY:HA3	1.99	0.45
2:V:48:GLU:OE1	2:V:53:LYS:HE2	2.17	0.45
2:V:160:LEU:HD11	2:V:236:LEU:HD22	1.99	0.45
2:J:233:ARG:NH1	1:O:31:GLY:HA2	2.31	0.45
1:Q:8:GLN:HG2	1:Q:8:GLN:O	2.16	0.45
2:L:23:ARG:HH12	2:L:176:ASP:HB3	1.82	0.45
1:I:91:LEU:H	1:I:92:PRO:HD3	1.82	0.45
1:Q:121:SER:HB3	1:Q:236:VAL:HG11	1.97	0.45
1:C:75:TYR:CD1	1:C:75:TYR:N	2.85	0.45
1:A:129:LEU:HB3	1:A:138:TRP:HB2	1.99	0.45
2:J:131:ILE:HG12	2:J:138:SER:HB2	1.97	0.45
1:I:75:TYR:CE2	1:I:83:ASN:OD1	2.70	0.45
1:K:77:ASP:O	1:K:79:PRO:HD3	2.16	0.45
2:B:192:ALA:HB3	2:B:202:LEU:HB3	1.99	0.45
2:T:213:GLU:O	2:T:214:PHE:C	2.54	0.45
3:D:404:ADP:H5'2	3:D:404:ADP:O3B	2.16	0.45
2:R:131:ILE:HG12	2:R:138:SER:HB2	1.99	0.45
1:A:32:ARG:CZ	1:A:38:ARG:HG3	2.47	0.45
2:D:192:ALA:HB3	2:D:202:LEU:HB3	1.99	0.45
1:I:91:LEU:H	1:I:92:PRO:CD	2.30	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:R:195:PRO:HG2	2:R:229:TYR:CD1	2.52	0.45
2:X:61:PRO:HD3	2:X:155:ILE:HD11	1.99	0.45
2:F:210:THR:HG23	2:F:213:GLU:OE1	2.16	0.45
2:B:131:ILE:HD11	2:B:142:SER:HB2	1.99	0.45
2:J:131:ILE:HD11	2:J:142:SER:HB2	1.99	0.45
1:E:14:ILE:HG22	2:N:116:LEU:HD22	1.99	0.45
2:X:19:ARG:HD2	2:X:181:GLU:OE2	2.16	0.45
2:T:32:LYS:HB3	2:T:48:GLU:HB2	1.98	0.44
2:P:15:ASP:C	2:P:16:ASP:O	2.55	0.44
1:C:129:LEU:HB3	1:C:138:TRP:HB2	1.99	0.44
1:Q:104:ASP:CG	1:Q:105:GLU:N	2.71	0.44
2:J:37:VAL:HG11	2:J:46:ILE:HG13	1.99	0.44
2:H:91:ARG:HB2	1:I:68:LYS:HG2	1.99	0.44
1:I:130:VAL:HA	1:I:137:VAL:HG12	1.98	0.44
1:G:104:ASP:HB3	1:G:107:ALA:HB3	1.99	0.44
2:V:190:PRO:HG2	2:V:204:GLN:HB2	1.99	0.44
2:J:86:PHE:HB2	1:K:50:ALA:HB2	1.98	0.44
1:E:121:SER:HB3	1:E:236:VAL:HG11	1.98	0.44
2:T:37:VAL:HG11	2:T:46:ILE:HG13	1.99	0.44
1:U:91:LEU:N	1:U:92:PRO:CD	2.79	0.44
2:B:91:ARG:HB2	1:E:68:LYS:HG2	2.00	0.44
1:O:130:VAL:HA	1:O:137:VAL:HG12	1.99	0.44
1:W:104:ASP:HB3	1:W:107:ALA:HB3	1.99	0.44
1:K:130:VAL:HA	1:K:137:VAL:HG12	1.99	0.44
2:L:27:GLU:HG2	2:L:247:GLY:HA2	2.00	0.44
2:R:62:LYS:NZ	2:R:126:ASP:OD2	2.48	0.44
2:B:99:ARG:NH1	3:B:404:ADP:O2A	2.50	0.44
2:L:41:ALA:HA	2:L:59:TYR:CE2	2.53	0.44
1:S:16:LYS:HG3	1:S:220:ILE:HB	2.00	0.44
1:M:130:VAL:HA	1:M:137:VAL:HG12	1.99	0.44
2:H:48:GLU:CG	2:H:53:LYS:HG2	2.41	0.44
1:O:32:ARG:CZ	1:O:38:ARG:HG3	2.47	0.44
1:W:32:ARG:CZ	1:W:38:ARG:HG3	2.48	0.44
2:B:190:PRO:HG2	2:B:204:GLN:HB2	1.99	0.44
1:S:28:ARG:CZ	1:S:210:VAL:HG13	2.48	0.44
1:W:264:LYS:HG3	1:W:264:LYS:H	1.66	0.44
2:J:39:LYS:HA	2:J:39:LYS:HD2	1.85	0.44
2:X:131:ILE:HD11	2:X:142:SER:HB2	2.00	0.44
1:E:104:ASP:CG	1:E:105:GLU:N	2.71	0.44
2:L:192:ALA:HB3	2:L:202:LEU:HB3	1.99	0.44
2:F:159:ASP:OD2	2:F:196:SER:HB2	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:112:ARG:NH2	2:P:99:ARG:HB2	2.33	0.44
2:P:1:MET:HG3	2:P:3:GLU:N	2.30	0.44
1:U:104:ASP:CG	1:U:105:GLU:N	2.71	0.44
2:D:160:LEU:HD11	2:D:236:LEU:HD22	2.00	0.44
1:K:28:ARG:CZ	1:K:210:VAL:HG13	2.48	0.44
1:G:240:LYS:HB2	2:H:203:PHE:HB3	2.00	0.44
1:S:38:ARG:HD2	1:S:59:GLY:HA3	1.99	0.44
1:U:129:LEU:HB3	1:U:138:TRP:HB2	2.00	0.44
2:H:227:ILE:HD12	2:H:248:VAL:CG1	2.41	0.44
2:T:64:MET:HB2	2:T:64:MET:HE3	1.82	0.44
2:N:118:GLU:CD	2:N:118:GLU:H	2.20	0.44
1:A:240:LYS:HB2	2:B:203:PHE:HB3	2.00	0.44
2:P:169:ALA:HB2	2:P:174:ILE:HD13	2.00	0.44
1:I:104:ASP:CG	1:I:105:GLU:N	2.71	0.43
1:E:130:VAL:HA	1:E:137:VAL:HG12	2.00	0.43
2:F:135:ASP:O	2:F:136:ALA:HB3	2.18	0.43
2:T:165:ALA:HA	2:T:190:PRO:HA	2.00	0.43
2:L:165:ALA:HA	2:L:190:PRO:HA	1.99	0.43
2:N:13:ILE:CD1	2:N:172:VAL:HB	2.48	0.43
1:I:3:SER:HB3	2:J:78:ARG:CG	2.47	0.43
1:K:27:ILE:HG21	2:R:196:SER:HB3	2.00	0.43
2:V:12:LEU:HD22	2:V:181:GLU:HG3	2.00	0.43
1:C:121:SER:HB3	1:C:236:VAL:HG11	2.00	0.43
2:D:214:PHE:O	2:D:218:PHE:HB2	2.18	0.43
2:P:160:LEU:HD11	2:P:236:LEU:HD22	2.00	0.43
1:M:121:SER:HB3	1:M:236:VAL:HG11	2.01	0.43
2:B:41:ALA:HA	2:B:59:TYR:CE2	2.54	0.43
1:G:203:ALA:HB2	1:G:213:PRO:HG3	1.99	0.43
1:U:13:ILE:H	1:U:13:ILE:HG13	1.61	0.43
1:O:38:ARG:HD2	1:O:59:GLY:HA3	2.00	0.43
1:I:91:LEU:N	1:I:92:PRO:CD	2.81	0.43
1:U:80:ASN:OD1	1:U:133:PRO:HB3	2.18	0.43
2:J:103:LEU:HD21	2:J:139:ARG:CZ	2.48	0.43
2:F:41:ALA:HA	2:F:59:TYR:CE2	2.54	0.43
1:S:112:ARG:NH1	2:T:102:GLU:OE1	2.52	0.43
1:A:112:ARG:NH1	2:B:102:GLU:OE1	2.51	0.43
1:K:38:ARG:HD2	1:K:59:GLY:HA3	2.00	0.43
1:Q:104:ASP:HB3	1:Q:107:ALA:HB3	2.00	0.43
2:L:190:PRO:HG2	2:L:204:GLN:HB2	2.00	0.43
1:S:11:ILE:HA	1:S:12:PRO:HD3	1.93	0.43
1:Q:77:ASP:O	1:Q:79:PRO:HD3	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:X:190:PRO:HG2	2:X:204:GLN:HB2	1.99	0.43
2:B:202:LEU:HD23	2:B:203:PHE:N	2.33	0.43
1:G:121:SER:HB3	1:G:236:VAL:HG11	1.99	0.43
1:U:77:ASP:O	1:U:79:PRO:HD3	2.18	0.43
2:D:190:PRO:HG2	2:D:204:GLN:HB2	1.99	0.43
2:N:61:PRO:HD3	2:N:155:ILE:HD11	2.01	0.43
1:Q:125:ASP:CG	1:Q:128:LYS:HG3	2.39	0.43
1:A:130:VAL:HA	1:A:137:VAL:HG12	2.00	0.43
2:T:131:ILE:HD11	2:T:142:SER:HB2	2.01	0.43
2:T:160:LEU:HD11	2:T:236:LEU:HD22	2.00	0.43
1:G:145:TYR:OH	2:L:82:HIS:HE1	2.01	0.43
2:D:27:GLU:HG2	2:D:247:GLY:HA2	2.01	0.43
2:N:12:LEU:HD12	2:N:170:ASP:OD1	2.17	0.43
1:S:32:ARG:CZ	1:S:38:ARG:HG3	2.49	0.43
1:S:91:LEU:HD22	2:V:80:ARG:HH12	1.83	0.43
2:P:165:ALA:HA	2:P:190:PRO:HA	2.00	0.43
1:W:105:GLU:OE1	2:X:105:LYS:HG3	2.19	0.43
2:F:65:HIS:CB	2:F:66:PRO:CD	2.97	0.43
1:M:32:ARG:CZ	1:M:38:ARG:HG3	2.48	0.43
2:L:23:ARG:HH21	2:L:178:ASN:ND2	2.15	0.43
1:E:240:LYS:HB2	2:F:203:PHE:HB3	2.00	0.43
2:H:61:PRO:HD3	2:H:155:ILE:HD11	2.01	0.43
2:J:155:ILE:HA	2:J:156:PRO:HD3	1.88	0.43
1:G:130:VAL:HA	1:G:137:VAL:HG12	2.00	0.43
2:N:193:MET:HG3	2:N:225:ILE:HD13	2.00	0.43
2:P:223:LYS:HB3	2:P:248:VAL:CG1	2.48	0.43
2:V:155:ILE:HA	2:V:156:PRO:HD3	1.88	0.43
1:C:104:ASP:HB3	1:C:107:ALA:HB3	2.01	0.43
1:U:112:ARG:NH1	2:V:102:GLU:OE1	2.49	0.42
2:V:165:ALA:HA	2:V:190:PRO:HA	2.01	0.42
1:C:130:VAL:HA	1:C:137:VAL:HG12	2.01	0.42
1:S:104:ASP:HB3	1:S:107:ALA:HB3	2.01	0.42
2:L:65:HIS:CB	2:L:66:PRO:CD	2.95	0.42
1:I:32:ARG:CZ	1:I:38:ARG:HG3	2.48	0.42
2:H:160:LEU:HD11	2:H:236:LEU:HD22	2.00	0.42
1:U:11:ILE:HA	1:U:12:PRO:HD3	1.94	0.42
1:S:77:ASP:O	1:S:79:PRO:HD3	2.19	0.42
2:D:135:ASP:O	2:D:136:ALA:HB3	2.20	0.42
2:X:34:GLU:HB3	2:X:240:TYR:CD1	2.50	0.42
1:U:32:ARG:CZ	1:U:38:ARG:HG3	2.49	0.42
1:U:121:SER:HB3	1:U:236:VAL:HG11	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:82:HIS:HB3	2:B:130:GLU:OE2	2.19	0.42
2:V:115:VAL:CG2	2:V:150:LEU:HD13	2.49	0.42
2:R:41:ALA:HA	2:R:59:TYR:CE2	2.54	0.42
2:H:165:ALA:HA	2:H:190:PRO:HA	2.02	0.42
2:B:159:ASP:OD2	2:B:196:SER:HB2	2.19	0.42
2:X:160:LEU:HD11	2:X:236:LEU:HD22	2.02	0.42
1:M:28:ARG:CZ	1:M:210:VAL:HG13	2.49	0.42
1:A:13:ILE:HG13	1:A:13:ILE:H	1.69	0.42
1:G:60:THR:HB	2:L:40:ASN:ND2	2.35	0.42
2:P:131:ILE:HD11	2:P:142:SER:HB2	2.01	0.42
2:V:202:LEU:HD23	2:V:203:PHE:N	2.34	0.42
1:M:11:ILE:HA	1:M:12:PRO:HD3	1.92	0.42
1:E:16:LYS:HG3	1:E:220:ILE:HB	2.01	0.42
2:N:159:ASP:OD2	2:N:196:SER:HB2	2.19	0.42
2:D:136:ALA:HA	3:D:404:ADP:H5'2	2.02	0.42
2:H:224:GLY:HA2	2:H:248:VAL:HG11	2.01	0.42
2:F:129:THR:HG21	2:F:142:SER:HG	1.80	0.42
2:F:19:ARG:HD3	2:F:174:ILE:HG21	2.01	0.42
2:N:192:ALA:HB3	2:N:202:LEU:HB3	2.01	0.42
1:C:77:ASP:O	1:C:79:PRO:HD3	2.19	0.42
1:O:174:GLU:O	1:O:181:SER:N	2.47	0.42
1:K:13:ILE:H	1:K:13:ILE:HG13	1.67	0.42
3:N:404:ADP:O3B	3:N:404:ADP:O3'	2.30	0.42
1:M:112:ARG:NH2	2:N:99:ARG:HB2	2.34	0.42
1:G:60:THR:HB	2:L:40:ASN:HD21	1.83	0.42
2:P:23:ARG:HH12	2:P:176:ASP:HB3	1.85	0.42
2:B:82:HIS:HE1	1:E:145:TYR:OH	2.02	0.42
2:F:190:PRO:HG2	2:F:204:GLN:HB2	2.02	0.42
1:U:130:VAL:HA	1:U:137:VAL:HG12	2.00	0.42
1:G:13:ILE:O	1:G:17:GLU:HG3	2.20	0.42
2:N:41:ALA:HA	2:N:59:TYR:CE2	2.55	0.42
2:L:159:ASP:OD1	2:L:160:LEU:N	2.53	0.42
1:Q:112:ARG:NH1	2:R:102:GLU:OE1	2.53	0.42
2:L:99:ARG:HH12	3:L:404:ADP:PA	2.40	0.42
2:R:193:MET:HG3	2:R:225:ILE:HD13	2.00	0.42
2:D:233:ARG:CG	2:D:233:ARG:HH11	2.33	0.42
1:G:32:ARG:CZ	1:G:38:ARG:HG3	2.50	0.42
2:F:160:LEU:HD11	2:F:236:LEU:HD22	2.01	0.42
1:U:28:ARG:CZ	1:U:210:VAL:HG13	2.50	0.42
2:B:227:ILE:HD12	2:B:248:VAL:HG13	2.01	0.42
1:G:30:ASP:OD1	1:G:32:ARG:HG2	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:227:ILE:HD12	2:D:248:VAL:HG22	2.01	0.42
2:R:2:ARG:CD	2:R:4:MET:HG2	2.50	0.42
2:N:165:ALA:HA	2:N:190:PRO:HA	2.01	0.42
1:Q:28:ARG:CZ	1:Q:210:VAL:HG13	2.50	0.42
1:E:77:ASP:O	1:E:79:PRO:HD3	2.20	0.42
1:K:88:VAL:HG12	1:K:89:GLU:N	2.35	0.42
1:S:247:SER:HA	2:T:198:ASN:O	2.20	0.42
2:D:9:ARG:HG3	2:D:184:TRP:HB3	2.01	0.42
1:U:3:SER:HB3	2:V:78:ARG:CG	2.50	0.42
2:F:165:ALA:HA	2:F:190:PRO:HA	2.02	0.42
2:P:78:ARG:HD3	2:P:126:ASP:OD1	2.20	0.42
2:D:83:MET:HE2	2:D:99:ARG:HH21	1.84	0.41
2:R:129:THR:O	2:R:129:THR:HG22	2.20	0.41
1:M:38:ARG:HD2	1:M:59:GLY:HA3	2.02	0.41
2:R:3:GLU:CB	2:R:5:LEU:N	2.83	0.41
1:A:166:TYR:HB2	1:A:273:LEU:HD21	2.01	0.41
1:C:75:TYR:HD1	1:C:75:TYR:N	2.17	0.41
2:L:159:ASP:OD2	2:L:196:SER:HB2	2.19	0.41
1:I:129:LEU:HB3	1:I:138:TRP:HB2	2.02	0.41
2:J:132:LEU:HD22	1:K:64:LEU:CD2	2.50	0.41
2:R:103:LEU:HD21	2:R:139:ARG:CZ	2.50	0.41
1:W:130:VAL:HA	1:W:137:VAL:HG12	2.02	0.41
2:J:243:PHE:CZ	2:J:246:GLU:HG2	2.47	0.41
2:T:193:MET:HG3	2:T:225:ILE:HD13	2.01	0.41
2:D:129:THR:O	2:D:129:THR:HG22	2.20	0.41
2:R:16:ASP:HB3	2:R:17:GLY:H	1.76	0.41
2:D:42:ASP:O	2:D:153:ALA:HA	2.19	0.41
1:O:16:LYS:HG3	1:O:220:ILE:HB	2.02	0.41
1:O:11:ILE:HA	1:O:12:PRO:HD3	1.92	0.41
1:C:13:ILE:H	1:C:13:ILE:HG13	1.69	0.41
2:D:37:VAL:HG11	2:D:46:ILE:HG13	2.02	0.41
2:P:99:ARG:NH2	3:P:404:ADP:O2B	2.53	0.41
2:F:48:GLU:CG	2:F:53:LYS:HG2	2.48	0.41
1:O:28:ARG:CZ	1:O:210:VAL:HG13	2.50	0.41
2:R:37:VAL:HG11	2:R:46:ILE:HG13	2.02	0.41
2:B:37:VAL:HG11	2:B:46:ILE:HG13	2.02	0.41
2:R:160:LEU:HD11	2:R:236:LEU:HD22	2.03	0.41
1:M:104:ASP:CG	1:M:105:GLU:N	2.73	0.41
2:H:59:TYR:CE1	1:I:92:PRO:HA	2.55	0.41
2:L:202:LEU:HD23	2:L:203:PHE:N	2.35	0.41
1:I:203:ALA:HB2	1:I:213:PRO:HG3	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:X:37:VAL:HG11	2:X:46:ILE:HG13	2.02	0.41
1:U:16:LYS:HG3	1:U:220:ILE:HB	2.03	0.41
2:J:65:HIS:CB	2:J:66:PRO:CD	2.97	0.41
2:H:59:TYR:CZ	1:I:92:PRO:HA	2.55	0.41
1:G:104:ASP:CG	1:G:105:GLU:N	2.73	0.41
2:P:103:LEU:HD21	2:P:139:ARG:CZ	2.51	0.41
1:O:129:LEU:HB3	1:O:138:TRP:HB2	2.02	0.41
2:F:37:VAL:HG11	2:F:46:ILE:HG13	2.01	0.41
1:K:11:ILE:HA	1:K:12:PRO:HD3	1.94	0.41
2:B:165:ALA:HA	2:B:190:PRO:HA	2.03	0.41
1:C:16:LYS:HG3	1:C:220:ILE:HB	2.03	0.41
2:D:155:ILE:HA	2:D:156:PRO:HD3	1.88	0.41
2:F:155:ILE:HA	2:F:156:PRO:HD3	1.89	0.41
2:R:28:LEU:HG	2:R:248:VAL:HG21	2.03	0.41
2:T:32:LYS:HE2	2:T:34:GLU:OE2	2.20	0.41
2:H:195:PRO:HG2	2:H:229:TYR:CD1	2.55	0.41
1:G:11:ILE:HA	1:G:12:PRO:HD3	1.93	0.41
1:K:104:ASP:HB3	1:K:107:ALA:HB3	2.03	0.41
2:J:195:PRO:HG2	2:J:229:TYR:CD1	2.56	0.41
1:I:252:ASP:OD1	2:J:215:ARG:NH1	2.54	0.41
1:S:245:SER:HB2	2:T:199:GLN:HB3	2.02	0.41
1:M:77:ASP:O	1:M:79:PRO:HD3	2.21	0.41
1:C:183:ASN:ND2	1:C:185:ASN:OD1	2.38	0.41
1:M:240:LYS:HB2	2:N:203:PHE:HB3	2.03	0.41
2:P:169:ALA:HB2	2:P:174:ILE:CD1	2.51	0.41
2:N:159:ASP:OD1	2:N:160:LEU:N	2.54	0.41
2:D:1:MET:C	2:D:3:GLU:N	2.73	0.41
2:B:26:ASP:O	2:B:248:VAL:HG23	2.21	0.41
2:X:65:HIS:CB	2:X:66:PRO:CD	2.98	0.41
1:I:248:LEU:CD2	2:J:218:PHE:CZ	3.04	0.41
1:Q:32:ARG:CZ	1:Q:38:ARG:HG3	2.50	0.41
2:H:190:PRO:HG2	2:H:204:GLN:HB2	2.02	0.41
2:J:9:ARG:HG2	2:J:184:TRP:CE3	2.56	0.41
1:M:16:LYS:HG3	1:M:220:ILE:HB	2.03	0.41
1:S:203:ALA:HB2	1:S:213:PRO:HG3	2.02	0.41
2:D:30:SER:N	2:D:245:GLU:HB3	2.36	0.41
2:J:202:LEU:HD23	2:J:203:PHE:N	2.36	0.41
1:K:240:LYS:HB2	2:L:203:PHE:HB3	2.02	0.41
2:D:165:ALA:HA	2:D:190:PRO:HA	2.03	0.41
2:F:13:ILE:HD11	2:F:169:ALA:HB3	2.03	0.41
2:P:60:GLY:O	2:P:61:PRO:C	2.60	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:129:LEU:HB3	1:K:138:TRP:HB2	2.03	0.41
1:C:274:GLY:O	1:C:275:ILE:HB	2.21	0.41
2:H:116:LEU:HD12	2:H:156:PRO:HB2	2.03	0.41
1:E:269:LEU:O	1:E:273:LEU:HG	2.20	0.41
2:T:138:SER:OG	3:T:404:ADP:O3B	2.29	0.40
2:B:64:MET:HE1	2:B:76:VAL:HB	2.03	0.40
2:J:129:THR:HG21	2:J:142:SER:HG	1.87	0.40
2:L:160:LEU:HD11	2:L:236:LEU:HD22	2.03	0.40
2:T:103:LEU:HD21	2:T:139:ARG:CZ	2.51	0.40
1:W:75:TYR:HD2	1:W:75:TYR:N	2.20	0.40
2:V:42:ASP:CG	2:V:60:GLY:H	2.24	0.40
1:S:243:LYS:HG2	2:T:112:GLU:OE1	2.21	0.40
2:R:2:ARG:HD2	2:R:4:MET:HG2	2.02	0.40
2:J:165:ALA:HA	2:J:190:PRO:HA	2.03	0.40
2:D:41:ALA:HA	2:D:59:TYR:CE2	2.56	0.40
1:A:203:ALA:HB2	1:A:213:PRO:HG3	2.04	0.40
2:L:103:LEU:HD21	2:L:139:ARG:CZ	2.51	0.40
2:P:245:GLU:O	2:P:246:GLU:HB3	2.22	0.40
2:V:129:THR:HG21	2:V:142:SER:HG	1.83	0.40
1:K:32:ARG:CZ	1:K:38:ARG:HG3	2.51	0.40
2:N:160:LEU:HD11	2:N:236:LEU:HD22	2.04	0.40
2:P:115:VAL:CG2	2:P:150:LEU:HD13	2.51	0.40
1:U:183:ASN:O	1:U:185:ASN:N	2.52	0.40
2:F:193:MET:HG3	2:F:225:ILE:HD13	2.03	0.40
2:J:91:ARG:HD2	1:K:141:TRP:CG	2.57	0.40
1:K:247:SER:O	1:K:250:ASP:HB2	2.21	0.40
1:C:44:LEU:HD22	1:C:167:ASN:HB2	2.03	0.40
1:W:112:ARG:NH1	2:X:102:GLU:OE1	2.53	0.40
2:H:39:LYS:HG2	1:I:148:ASP:OD2	2.22	0.40
1:G:129:LEU:HB3	1:G:138:TRP:HB2	2.02	0.40
1:G:28:ARG:CZ	1:G:210:VAL:HG13	2.51	0.40
2:H:135:ASP:O	2:H:136:ALA:CB	2.70	0.40
2:F:202:LEU:HD23	2:F:203:PHE:N	2.37	0.40
1:W:44:LEU:HD22	1:W:167:ASN:HB2	2.03	0.40

There are no symmetry-related clashes.

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	254/275 (92%)	241 (95%)	10 (4%)	3 (1%)	16	54
1	C	254/275 (92%)	240 (94%)	8 (3%)	6 (2%)	7	38
1	E	254/275 (92%)	241 (95%)	11 (4%)	2 (1%)	24	62
1	G	254/275 (92%)	239 (94%)	11 (4%)	4 (2%)	12	48
1	I	254/275 (92%)	242 (95%)	10 (4%)	2 (1%)	24	62
1	K	254/275 (92%)	240 (94%)	11 (4%)	3 (1%)	16	54
1	M	254/275 (92%)	240 (94%)	11 (4%)	3 (1%)	16	54
1	O	254/275 (92%)	245 (96%)	7 (3%)	2 (1%)	24	62
1	Q	254/275 (92%)	238 (94%)	13 (5%)	3 (1%)	16	54
1	S	253/275 (92%)	242 (96%)	9 (4%)	2 (1%)	24	62
1	U	249/275 (90%)	236 (95%)	11 (4%)	2 (1%)	24	62
1	W	253/275 (92%)	241 (95%)	9 (4%)	3 (1%)	16	54
2	B	239/248 (96%)	221 (92%)	15 (6%)	3 (1%)	15	52
2	D	246/248 (99%)	231 (94%)	10 (4%)	5 (2%)	9	43
2	F	239/248 (96%)	226 (95%)	10 (4%)	3 (1%)	15	52
2	H	226/248 (91%)	216 (96%)	8 (4%)	2 (1%)	21	60
2	J	239/248 (96%)	225 (94%)	10 (4%)	4 (2%)	11	47
2	L	245/248 (99%)	231 (94%)	13 (5%)	1 (0%)	39	76
2	N	237/248 (96%)	224 (94%)	12 (5%)	1 (0%)	39	76
2	P	246/248 (99%)	230 (94%)	13 (5%)	3 (1%)	16	54
2	R	246/248 (99%)	230 (94%)	13 (5%)	3 (1%)	16	54
2	T	246/248 (99%)	233 (95%)	11 (4%)	2 (1%)	24	62
2	V	237/248 (96%)	218 (92%)	15 (6%)	4 (2%)	11	47
2	X	235/248 (95%)	223 (95%)	11 (5%)	1 (0%)	39	76
All	All	5922/6276 (94%)	5593 (94%)	262 (4%)	67 (1%)	17	57

All (67) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	G	8	GLN
2	J	15	ASP
2	P	16	ASP
1	Q	8	GLN
2	V	91	ARG
2	V	169	ALA
1	A	8	GLN
1	A	105	GLU
1	C	8	GLN
1	C	9	ASN
1	C	105	GLU
2	D	7	VAL
1	E	105	GLU
1	G	7	ASN
1	G	105	GLU
1	I	105	GLU
1	K	105	GLU
1	M	105	GLU
1	O	105	GLU
1	Q	105	GLU
2	R	169	ALA
1	S	105	GLU
1	U	105	GLU
1	U	184	LYS
1	W	105	GLU
1	C	7	ASN
1	C	76	GLU
2	F	169	ALA
1	W	9	ASN
2	B	170	ASP
2	D	176	ASP
2	H	176	ASP
2	V	176	ASP
2	B	176	ASP
2	D	2	ARG
2	D	16	ASP
2	F	176	ASP
2	J	65	HIS
2	J	169	ALA
1	K	76	GLU
2	P	7	VAL
2	R	176	ASP

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Mol	Chain	Res	Type
2	T	176	ASP
2	V	65	HIS
2	B	65	HIS
2	D	65	HIS
2	F	65	HIS
2	H	65	HIS
2	J	176	ASP
2	L	65	HIS
1	M	8	GLN
2	N	65	HIS
2	P	65	HIS
2	R	65	HIS
2	X	65	HIS
2	T	65	HIS
1	C	91	LEU
1	K	91	LEU
1	O	91	LEU
1	S	91	LEU
1	W	91	LEU
1	E	91	LEU
1	G	91	LEU
1	Q	91	LEU
1	A	91	LEU
1	I	91	LEU
1	M	91	LEU

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	212/242 (88%)	202 (95%)	10 (5%)	32	70
1	C	212/242 (88%)	204 (96%)	8 (4%)	40	75
1	E	218/242 (90%)	213 (98%)	5 (2%)	58	83
1	G	216/242 (89%)	206 (95%)	10 (5%)	33	71
1	I	214/242 (88%)	209 (98%)	5 (2%)	58	83

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	K	215/242 (89%)	204 (95%)	11 (5%)	29	68
1	M	216/242 (89%)	206 (95%)	10 (5%)	33	71
1	O	213/242 (88%)	205 (96%)	8 (4%)	40	75
1	Q	214/242 (88%)	208 (97%)	6 (3%)	51	80
1	S	216/242 (89%)	208 (96%)	8 (4%)	41	76
1	U	208/242 (86%)	199 (96%)	9 (4%)	35	72
1	W	214/242 (88%)	207 (97%)	7 (3%)	45	78
2	B	186/208 (89%)	176 (95%)	10 (5%)	27	66
2	D	200/208 (96%)	186 (93%)	14 (7%)	19	56
2	F	193/208 (93%)	182 (94%)	11 (6%)	25	65
2	H	179/208 (86%)	169 (94%)	10 (6%)	26	65
2	J	194/208 (93%)	184 (95%)	10 (5%)	29	67
2	L	199/208 (96%)	187 (94%)	12 (6%)	24	62
2	N	188/208 (90%)	182 (97%)	6 (3%)	46	79
2	P	201/208 (97%)	186 (92%)	15 (8%)	17	52
2	R	194/208 (93%)	184 (95%)	10 (5%)	29	67
2	T	196/208 (94%)	182 (93%)	14 (7%)	18	55
2	V	189/208 (91%)	182 (96%)	7 (4%)	41	76
2	X	191/208 (92%)	180 (94%)	11 (6%)	25	64
All	All	4878/5400 (90%)	4651 (95%)	227 (5%)	32	70

All (227) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	7	ASN
1	A	37	TYR
1	A	51	ASP
1	A	191	LEU
1	A	195	TYR
1	A	233	LEU
1	A	236	VAL
1	A	255	GLU
1	A	257	THR
1	A	275	ILE
2	B	12	LEU

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Mol	Chain	Res	Type
2	B	13	ILE
2	B	20	THR
2	B	26	ASP
2	B	78	ARG
2	B	89	ASP
2	B	99	ARG
2	B	129	THR
2	B	164	VAL
2	B	201	THR
1	C	30	ASP
1	C	37	TYR
1	C	183	ASN
1	C	191	LEU
1	C	195	TYR
1	C	233	LEU
1	C	255	GLU
1	C	257	THR
2	D	1	MET
2	D	2	ARG
2	D	7	VAL
2	D	8	GLU
2	D	20	THR
2	D	34	GLU
2	D	78	ARG
2	D	99	ARG
2	D	129	THR
2	D	164	VAL
2	D	201	THR
2	D	212	ASP
2	D	233	ARG
2	D	245	GLU
1	E	37	TYR
1	E	191	LEU
1	E	195	TYR
1	E	232	ASP
1	E	255	GLU
2	F	15	ASP
2	F	18	LYS
2	F	20	THR
2	F	34	GLU
2	F	39	LYS
2	F	78	ARG

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Mol	Chain	Res	Type
2	F	99	ARG
2	F	129	THR
2	F	164	VAL
2	F	201	THR
2	F	218	PHE
1	G	37	TYR
1	G	45	ASP
1	G	191	LEU
1	G	195	TYR
1	G	206	ASP
1	G	233	LEU
1	G	236	VAL
1	G	249	GLN
1	G	255	GLU
1	G	257	THR
2	H	20	THR
2	H	39	LYS
2	H	78	ARG
2	H	89	ASP
2	H	99	ARG
2	H	129	THR
2	H	164	VAL
2	H	178	ASN
2	H	201	THR
2	H	212	ASP
1	I	37	TYR
1	I	191	LEU
1	I	195	TYR
1	I	232	ASP
1	I	255	GLU
2	J	9	ARG
2	J	15	ASP
2	J	20	THR
2	J	39	LYS
2	J	78	ARG
2	J	99	ARG
2	J	129	THR
2	J	164	VAL
2	J	201	THR
2	J	233	ARG
1	K	24	GLU
1	K	30	ASP

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Mol	Chain	Res	Type
1	K	37	TYR
1	K	45	ASP
1	K	191	LEU
1	K	195	TYR
1	K	232	ASP
1	K	249	GLN
1	K	255	GLU
1	K	257	THR
1	K	275	ILE
2	L	7	VAL
2	L	20	THR
2	L	78	ARG
2	L	99	ARG
2	L	129	THR
2	L	164	VAL
2	L	178	ASN
2	L	179	GLU
2	L	201	THR
2	L	206	ASN
2	L	218	PHE
2	L	233	ARG
1	M	8	GLN
1	M	29	GLN
1	M	37	TYR
1	M	191	LEU
1	M	195	TYR
1	M	233	LEU
1	M	236	VAL
1	M	255	GLU
1	M	264	LYS
1	M	275	ILE
2	N	12	LEU
2	N	20	THR
2	N	78	ARG
2	N	129	THR
2	N	164	VAL
2	N	234	GLU
1	O	37	TYR
1	O	191	LEU
1	O	195	TYR
1	O	233	LEU
1	O	236	VAL

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Mol	Chain	Res	Type
1	O	243	LYS
1	O	255	GLU
1	O	257	THR
2	P	1	MET
2	P	2	ARG
2	P	5	LEU
2	P	20	THR
2	P	34	GLU
2	P	53	LYS
2	P	78	ARG
2	P	99	ARG
2	P	129	THR
2	P	164	VAL
2	P	183	MET
2	P	201	THR
2	P	218	PHE
2	P	233	ARG
2	P	234	GLU
1	Q	9	ASN
1	Q	37	TYR
1	Q	191	LEU
1	Q	195	TYR
1	Q	236	VAL
1	Q	255	GLU
2	R	1	MET
2	R	6	GLN
2	R	20	THR
2	R	78	ARG
2	R	99	ARG
2	R	129	THR
2	R	164	VAL
2	R	201	THR
2	R	212	ASP
2	R	218	PHE
1	S	18	SER
1	S	30	ASP
1	S	37	TYR
1	S	191	LEU
1	S	195	TYR
1	S	236	VAL
1	S	243	LYS
1	S	255	GLU

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Mol	Chain	Res	Type
2	T	1	MET
2	T	2	ARG
2	T	5	LEU
2	T	20	THR
2	T	34	GLU
2	T	78	ARG
2	T	99	ARG
2	T	129	THR
2	T	164	VAL
2	T	183	MET
2	T	186	GLU
2	T	201	THR
2	T	218	PHE
2	T	246	GLU
1	U	8	GLN
1	U	29	GLN
1	U	37	TYR
1	U	191	LEU
1	U	195	TYR
1	U	233	LEU
1	U	236	VAL
1	U	255	GLU
1	U	264	LYS
2	V	20	THR
2	V	78	ARG
2	V	129	THR
2	V	164	VAL
2	V	168	LYS
2	V	201	THR
2	V	218	PHE
1	W	37	TYR
1	W	183	ASN
1	W	191	LEU
1	W	195	TYR
1	W	236	VAL
1	W	255	GLU
1	W	257	THR
2	X	13	ILE
2	X	14	LEU
2	X	20	THR
2	X	78	ARG
2	X	89	ASP

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Mol	Chain	Res	Type
2	X	99	ARG
2	X	129	THR
2	X	164	VAL
2	X	201	THR
2	X	218	PHE
2	X	246	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (19) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	7	ASN
2	B	178	ASN
2	D	178	ASN
2	F	82	HIS
1	G	249	GLN
2	H	178	ASN
1	I	29	GLN
2	J	82	HIS
2	L	40	ASN
2	L	82	HIS
2	L	178	ASN
1	O	8	GLN
2	P	178	ASN
2	R	6	GLN
2	R	82	HIS
1	S	29	GLN
2	T	82	HIS
2	V	82	HIS
2	X	82	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

12 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
3	ADP	B	404	-	22,29,29	1.18	2 (9%)	27,45,45	1.87	3 (11%)
3	ADP	D	404	2	22,29,29	1.18	3 (13%)	27,45,45	2.33	6 (22%)
3	ADP	F	404	-	15,17,29	1.57	2 (13%)	23,26,45	1.07	1 (4%)
3	ADP	H	404	-	22,29,29	1.11	2 (9%)	27,45,45	2.25	5 (18%)
3	ADP	J	404	-	6,8,29	0.95	0	11,13,45	1.23	1 (9%)
3	ADP	L	404	-	22,29,29	1.09	1 (4%)	27,45,45	2.18	7 (25%)
3	ADP	N	404	-	22,29,29	1.19	2 (9%)	27,45,45	1.85	3 (11%)
3	ADP	P	404	-	22,29,29	1.06	2 (9%)	27,45,45	2.49	5 (18%)
3	ADP	R	404	2	22,29,29	1.22	3 (13%)	27,45,45	1.78	7 (25%)
3	ADP	T	404	-	22,29,29	1.01	1 (4%)	27,45,45	2.19	4 (14%)
3	ADP	V	404	-	15,17,29	0.85	1 (6%)	23,26,45	1.13	2 (8%)
3	ADP	X	404	-	15,17,29	1.84	2 (13%)	23,26,45	1.36	3 (13%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	ADP	B	404	-	-	0/12/32/32	0/3/3/3
3	ADP	D	404	2	-	0/12/32/32	0/3/3/3
3	ADP	F	404	-	-	0/12/25/32	0/1/1/3
3	ADP	H	404	-	-	0/12/32/32	0/3/3/3
3	ADP	J	404	-	-	0/6/6/32	0/0/0/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	ADP	L	404	-	-	0/12/32/32	0/3/3/3
3	ADP	N	404	-	-	0/12/32/32	0/3/3/3
3	ADP	P	404	-	-	0/12/32/32	0/3/3/3
3	ADP	R	404	2	-	0/12/32/32	0/3/3/3
3	ADP	T	404	-	-	0/12/32/32	0/3/3/3
3	ADP	V	404	-	-	0/12/25/32	0/1/1/3
3	ADP	X	404	-	-	0/12/25/32	0/1/1/3

All (21) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	V	404	ADP	O4'-C1'	2.03	1.48	1.43
3	P	404	ADP	C2-N3	2.11	1.35	1.32
3	R	404	ADP	C2-N3	2.12	1.35	1.32
3	D	404	ADP	C2-N3	2.14	1.36	1.32
3	F	404	ADP	C1'-C2'	2.31	1.56	1.51
3	H	404	ADP	O4'-C1'	2.35	1.44	1.41
3	B	404	ADP	O4'-C1'	2.42	1.44	1.41
3	D	404	ADP	O4'-C1'	2.43	1.44	1.41
3	R	404	ADP	O4'-C1'	2.58	1.44	1.41
3	N	404	ADP	O4'-C1'	2.63	1.44	1.41
3	T	404	ADP	C5-C4	2.75	1.46	1.40
3	P	404	ADP	C5-C4	2.99	1.47	1.40
3	X	404	ADP	C1'-C2'	3.06	1.57	1.51
3	D	404	ADP	C5-C4	3.13	1.47	1.40
3	H	404	ADP	C5-C4	3.29	1.47	1.40
3	L	404	ADP	C5-C4	3.41	1.48	1.40
3	N	404	ADP	C5-C4	3.43	1.48	1.40
3	R	404	ADP	C5-C4	3.51	1.48	1.40
3	B	404	ADP	C5-C4	3.56	1.48	1.40
3	F	404	ADP	O4'-C1'	5.07	1.55	1.43
3	X	404	ADP	O4'-C1'	5.86	1.57	1.43

All (47) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	P	404	ADP	N3-C2-N1	-8.58	122.33	128.89
3	D	404	ADP	N3-C2-N1	-7.96	122.80	128.89
3	N	404	ADP	N3-C2-N1	-7.64	123.05	128.89
3	H	404	ADP	N3-C2-N1	-7.47	123.17	128.89
3	B	404	ADP	N3-C2-N1	-7.29	123.31	128.89
3	T	404	ADP	N3-C2-N1	-6.89	123.62	128.89

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	T	404	ADP	C2'-C1'-N9	-6.55	104.29	114.29
3	L	404	ADP	N3-C2-N1	-6.53	123.90	128.89
3	R	404	ADP	N3-C2-N1	-6.33	124.04	128.89
3	P	404	ADP	C2'-C1'-N9	-6.30	104.66	114.29
3	H	404	ADP	C2'-C1'-N9	-6.15	104.89	114.29
3	D	404	ADP	C2'-C1'-N9	-4.63	107.21	114.29
3	L	404	ADP	C4-C5-N7	-4.24	105.58	109.48
3	L	404	ADP	C2'-C1'-N9	-4.19	107.89	114.29
3	P	404	ADP	PA-O3A-PB	-3.92	119.53	132.67
3	L	404	ADP	PA-O3A-PB	-3.69	120.29	132.67
3	B	404	ADP	C2'-C1'-N9	-3.59	108.81	114.29
3	D	404	ADP	C4-C5-N7	-3.29	106.45	109.48
3	P	404	ADP	C4-C5-N7	-3.21	106.53	109.48
3	T	404	ADP	PA-O3A-PB	-3.02	122.54	132.67
3	D	404	ADP	PA-O3A-PB	-3.02	122.54	132.67
3	B	404	ADP	C4-C5-N7	-2.96	106.75	109.48
3	R	404	ADP	C4-C5-N7	-2.94	106.78	109.48
3	X	404	ADP	PA-O3A-PB	-2.85	123.10	132.67
3	H	404	ADP	PA-O3A-PB	-2.81	123.24	132.67
3	X	404	ADP	O4'-C1'-C2'	-2.64	100.75	106.16
3	H	404	ADP	C4-C5-N7	-2.52	107.16	109.48
3	D	404	ADP	C1'-N9-C4	-2.39	123.33	126.94
3	V	404	ADP	PA-O3A-PB	-2.27	125.04	132.67
3	N	404	ADP	C4-C5-N7	-2.27	107.39	109.48
3	L	404	ADP	C1'-N9-C4	-2.24	123.56	126.94
3	T	404	ADP	C4'-O4'-C1'	-2.24	107.26	109.72
3	N	404	ADP	PA-O3A-PB	-2.16	125.41	132.67
3	R	404	ADP	C1'-N9-C4	-2.14	123.72	126.94
3	R	404	ADP	PA-O3A-PB	-2.01	125.92	132.67
3	R	404	ADP	C4'-O4'-C1'	2.06	111.99	109.72
3	P	404	ADP	O3B-PB-O2B	2.17	115.65	107.38
3	R	404	ADP	O3B-PB-O2B	2.22	115.84	107.38
3	R	404	ADP	O4'-C1'-N9	2.36	113.04	108.10
3	J	404	ADP	O3B-PB-O1B	2.51	118.67	110.58
3	L	404	ADP	O3B-PB-O2B	2.58	117.19	107.38
3	H	404	ADP	O4'-C1'-N9	2.71	113.77	108.10
3	L	404	ADP	O4'-C1'-N9	2.77	113.91	108.10
3	F	404	ADP	C1'-C2'-C3'	3.00	106.47	101.64
3	D	404	ADP	O4'-C1'-N9	3.29	114.98	108.10
3	V	404	ADP	C1'-C2'-C3'	3.41	107.13	101.64
3	X	404	ADP	C1'-C2'-C3'	3.67	107.55	101.64

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

10 monomers are involved in 26 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	404	ADP	5	0
3	D	404	ADP	3	0
3	F	404	ADP	1	0
3	H	404	ADP	2	0
3	J	404	ADP	1	0
3	L	404	ADP	3	0
3	N	404	ADP	3	0
3	P	404	ADP	3	0
3	T	404	ADP	3	0
3	V	404	ADP	2	0

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	260/275 (94%)	0.71	11 (4%) 40 33	46, 53, 67, 74	0
1	C	260/275 (94%)	0.79	10 (3%) 44 37	46, 53, 67, 75	0
1	E	260/275 (94%)	0.72	17 (6%) 22 18	46, 53, 67, 74	0
1	G	260/275 (94%)	0.85	24 (9%) 11 9	46, 53, 67, 74	0
1	I	260/275 (94%)	0.84	33 (12%) 5 4	46, 53, 67, 73	0
1	K	260/275 (94%)	0.89	18 (6%) 20 16	46, 53, 67, 75	0
1	M	260/275 (94%)	0.79	11 (4%) 40 33	46, 53, 67, 75	0
1	O	260/275 (94%)	0.82	12 (4%) 36 30	46, 53, 67, 75	0
1	Q	260/275 (94%)	0.77	8 (3%) 52 46	46, 53, 67, 74	0
1	S	259/275 (94%)	0.91	33 (12%) 5 4	46, 53, 67, 73	0
1	U	255/275 (92%)	1.00	39 (15%) 3 2	46, 53, 67, 73	0
1	W	259/275 (94%)	0.89	24 (9%) 11 9	46, 53, 67, 75	0
2	B	241/248 (97%)	0.90	22 (9%) 11 9	46, 52, 68, 80	0
2	D	248/248 (100%)	0.84	13 (5%) 31 25	45, 52, 68, 80	0
2	F	241/248 (97%)	0.84	18 (7%) 17 14	46, 52, 68, 80	0
2	H	230/248 (92%)	1.06	48 (20%) 1 1	46, 52, 69, 80	0
2	J	241/248 (97%)	0.94	30 (12%) 5 4	46, 52, 68, 80	0
2	L	247/248 (99%)	0.82	15 (6%) 25 20	45, 52, 68, 80	0
2	N	239/248 (96%)	0.79	9 (3%) 44 37	46, 52, 69, 79	0
2	P	248/248 (100%)	0.89	13 (5%) 31 25	45, 52, 68, 80	0
2	R	248/248 (100%)	0.78	13 (5%) 31 25	45, 52, 69, 80	0
2	T	248/248 (100%)	0.82	18 (7%) 18 15	45, 52, 69, 79	0
2	V	239/248 (96%)	1.19	43 (17%) 2 1	46, 52, 68, 79	0
2	X	239/248 (96%)	0.88	32 (13%) 4 3	46, 52, 69, 79	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
All	All	6022/6276 (95%)	0.86	514 (8%) 13 10	45, 52, 68, 80	0

All (514) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	I	275	ILE	7.2
1	U	171	TYR	6.0
1	U	1	MET	6.0
2	L	248	VAL	5.3
2	D	248	VAL	5.3
2	V	55	ILE	5.2
1	S	88	VAL	5.2
1	S	90	LEU	5.1
1	S	138	TRP	5.0
2	F	248	VAL	5.0
2	B	15	ASP	4.9
2	V	132	LEU	4.8
2	V	56	ALA	4.7
2	V	123	THR	4.5
2	V	209	MET	4.5
2	B	248	VAL	4.4
1	S	167	ASN	4.4
1	U	44	LEU	4.4
2	V	53	LYS	4.3
2	V	64	MET	4.3
2	H	248	VAL	4.2
1	S	83	ASN	4.2
2	X	12	LEU	4.2
1	U	78	THR	4.2
2	N	248	VAL	4.1
1	C	12	PRO	4.1
2	H	55	ILE	4.0
2	P	248	VAL	4.0
1	U	170	VAL	4.0
2	V	133	GLN	3.9
2	X	124	ALA	3.9
2	R	248	VAL	3.9
2	V	107	ILE	3.9
1	S	166	TYR	3.9
2	X	132	LEU	3.9
1	M	6	SER	3.9
2	V	25	PRO	3.8

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Mol	Chain	Res	Type	RSRZ
1	G	233	LEU	3.7
1	U	52	GLY	3.7
2	J	248	VAL	3.7
1	W	275	ILE	3.7
2	V	128	PHE	3.6
2	V	153	ALA	3.6
2	X	161	ILE	3.6
1	W	265	LEU	3.6
1	G	56	VAL	3.6
2	H	160	LEU	3.6
2	H	80	ARG	3.5
2	J	169	ALA	3.5
1	W	58	LEU	3.5
2	X	160	LEU	3.5
2	X	172	VAL	3.5
1	W	213	PRO	3.5
1	G	131	ILE	3.5
2	H	56	ALA	3.5
2	J	70	SER	3.5
2	V	131	ILE	3.5
1	G	273	LEU	3.5
2	H	60	GLY	3.5
1	S	171	TYR	3.4
2	V	222	VAL	3.4
2	J	15	ASP	3.4
2	H	111	LEU	3.4
2	H	57	ALA	3.3
2	X	142	SER	3.3
1	K	171	TYR	3.3
2	H	26	ASP	3.3
1	G	47	ALA	3.3
1	A	173	VAL	3.3
2	X	221	ALA	3.3
2	N	247	GLY	3.3
2	V	185	GLY	3.3
1	M	37	TYR	3.3
1	S	142	LEU	3.3
2	J	162	ALA	3.3
2	J	148	LEU	3.3
1	U	157	CYS	3.3
2	X	126	ASP	3.3
1	K	37	TYR	3.3

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Mol	Chain	Res	Type	RSRZ
2	H	23	ARG	3.3
1	S	37	TYR	3.3
1	I	248	LEU	3.3
2	V	170	ASP	3.2
2	D	145	ALA	3.2
2	H	100	GLU	3.2
2	T	248	VAL	3.2
1	I	124	LEU	3.2
1	S	89	GLU	3.2
1	U	42	ILE	3.2
1	U	225	ILE	3.2
2	N	15	ASP	3.2
1	W	80	ASN	3.1
1	I	37	TYR	3.1
2	F	120	PHE	3.1
1	I	154	LEU	3.1
1	A	37	TYR	3.1
2	V	204	GLN	3.1
1	G	136	SER	3.1
2	V	116	LEU	3.1
2	X	47	PHE	3.1
2	X	46	ILE	3.1
2	V	201	THR	3.1
2	J	18	LYS	3.0
2	V	166	VAL	3.0
1	G	29	GLN	3.0
2	H	120	PHE	3.0
1	C	37	TYR	3.0
1	K	149	TYR	3.0
2	P	48	GLU	3.0
1	S	53	SER	3.0
1	S	144	VAL	3.0
1	U	43	THR	3.0
2	X	141	VAL	3.0
2	N	156	PRO	3.0
2	F	175	LEU	3.0
2	J	120	PHE	3.0
2	D	161	ILE	3.0
2	V	199	GLN	2.9
1	G	14	ILE	2.9
1	G	71	ILE	2.9
1	A	161	SER	2.9

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Mol	Chain	Res	Type	RSRZ
2	H	112	GLU	2.9
2	J	79	VAL	2.9
2	T	125	ILE	2.9
2	X	69	LEU	2.9
2	J	224	GLY	2.9
1	U	56	VAL	2.9
2	H	209	MET	2.9
2	H	164	VAL	2.9
2	T	162	ALA	2.9
1	G	129	LEU	2.9
1	E	196	PRO	2.9
2	L	162	ALA	2.9
1	W	191	LEU	2.9
1	C	11	ILE	2.8
1	S	225	ILE	2.8
2	L	161	ILE	2.8
1	S	248	LEU	2.8
1	U	196	PRO	2.8
2	D	160	LEU	2.8
2	H	132	LEU	2.8
1	I	88	VAL	2.8
1	W	67	THR	2.8
2	B	17	GLY	2.8
1	I	140	VAL	2.8
2	N	239	LYS	2.8
1	G	171	TYR	2.8
2	B	125	ILE	2.8
1	E	124	LEU	2.8
2	R	128	PHE	2.8
1	I	158	THR	2.8
1	U	195	TYR	2.8
2	J	14	LEU	2.8
2	J	223	LYS	2.8
2	D	141	VAL	2.8
1	U	12	PRO	2.8
2	F	247	GLY	2.8
1	G	40	LEU	2.8
1	K	63	VAL	2.8
1	O	63	VAL	2.8
2	J	188	ASP	2.8
1	W	71	ILE	2.8
1	U	165	LEU	2.8

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Mol	Chain	Res	Type	RSRZ
2	L	240	TYR	2.8
1	U	28	ARG	2.8
1	I	35	THR	2.8
1	I	90	LEU	2.8
2	B	55	ILE	2.8
1	K	209	LEU	2.7
1	U	235	ILE	2.7
2	X	45	ALA	2.7
2	J	231	LEU	2.7
2	N	191	ILE	2.7
2	B	188	ASP	2.7
2	J	163	GLY	2.7
1	E	171	TYR	2.7
2	V	84	THR	2.7
2	X	192	ALA	2.7
1	I	171	TYR	2.7
1	M	230	THR	2.7
1	E	173	VAL	2.7
2	V	126	ASP	2.7
1	W	129	LEU	2.7
1	I	66	GLY	2.7
1	S	173	VAL	2.7
2	V	165	ALA	2.7
1	I	74	PRO	2.7
2	F	165	ALA	2.7
2	X	16	ASP	2.7
2	V	138	SER	2.7
1	G	248	LEU	2.7
1	U	269	LEU	2.7
2	F	60	GLY	2.7
2	J	110	ALA	2.7
2	X	232	GLU	2.7
1	M	63	VAL	2.7
1	U	53	SER	2.7
1	W	75	TYR	2.7
1	U	47	ALA	2.7
1	K	13	ILE	2.7
2	J	227	ILE	2.7
1	S	213	PRO	2.7
2	B	57	ALA	2.6
2	X	54	ALA	2.6
1	S	187	VAL	2.6

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Mol	Chain	Res	Type	RSRZ
1	W	130	VAL	2.6
1	G	169	LYS	2.6
2	P	178	ASN	2.6
1	I	89	GLU	2.6
2	H	232	GLU	2.6
1	G	275	ILE	2.6
1	M	11	ILE	2.6
1	U	146	VAL	2.6
2	H	192	ALA	2.6
2	P	57	ALA	2.6
1	W	4	THR	2.6
2	V	20	THR	2.6
1	I	62	MET	2.6
2	T	67	ARG	2.6
1	S	69	LEU	2.6
2	H	107	ILE	2.6
1	I	146	VAL	2.6
2	F	79	VAL	2.6
2	V	57	ALA	2.6
1	U	155	ASP	2.6
2	R	126	ASP	2.6
1	U	55	LEU	2.6
1	C	131	ILE	2.6
1	S	220	ILE	2.6
2	X	107	ILE	2.6
2	J	193	MET	2.6
1	I	14	ILE	2.6
1	Q	54	ALA	2.6
1	S	182	VAL	2.6
1	E	272	HIS	2.6
1	K	157	CYS	2.6
1	A	136	SER	2.6
1	A	171	TYR	2.6
2	V	169	ALA	2.6
1	S	140	VAL	2.6
1	U	202	VAL	2.6
2	F	202	LEU	2.5
2	H	175	LEU	2.5
2	X	202	LEU	2.5
1	U	137	VAL	2.5
2	H	79	VAL	2.5
2	H	127	VAL	2.5

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Mol	Chain	Res	Type	RSRZ
2	T	148	LEU	2.5
1	I	11	ILE	2.5
1	W	81	GLN	2.5
2	B	187	ALA	2.5
2	B	120	PHE	2.5
1	G	63	VAL	2.5
2	V	75	ALA	2.5
1	W	124	LEU	2.5
1	G	12	PRO	2.5
2	V	144	MET	2.5
1	Q	65	ALA	2.5
2	T	226	ASN	2.5
1	S	146	VAL	2.5
1	S	191	LEU	2.5
2	J	11	LYS	2.5
1	Q	213	PRO	2.5
2	V	208	SER	2.5
2	J	86	PHE	2.5
1	C	153	VAL	2.5
1	W	168	THR	2.5
1	E	46	TYR	2.5
2	X	229	TYR	2.5
1	A	275	ILE	2.5
2	H	168	LYS	2.5
1	C	138	TRP	2.5
2	H	247	GLY	2.5
2	V	17	GLY	2.5
1	C	14	ILE	2.5
1	I	12	PRO	2.5
1	M	159	LEU	2.5
1	U	272	HIS	2.5
1	I	251	ILE	2.5
1	S	202	VAL	2.5
2	D	231	LEU	2.5
2	V	54	ALA	2.5
2	H	43	GLY	2.5
2	T	201	THR	2.5
2	B	132	LEU	2.5
2	D	58	VAL	2.5
2	H	239	LYS	2.5
1	E	11	ILE	2.4
2	B	209	MET	2.4

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Mol	Chain	Res	Type	RSRZ
2	P	221	ALA	2.4
2	T	60	GLY	2.4
2	F	193	MET	2.4
1	Q	266	LEU	2.4
1	U	173	VAL	2.4
2	R	79	VAL	2.4
1	W	152	ASN	2.4
1	I	18	SER	2.4
1	S	200	ILE	2.4
2	H	62	LYS	2.4
1	E	248	LEU	2.4
2	X	11	LYS	2.4
2	P	136	ALA	2.4
2	L	191	ILE	2.4
2	F	47	PHE	2.4
2	T	160	LEU	2.4
2	R	165	ALA	2.4
2	V	189	MET	2.4
2	H	142	SER	2.4
2	R	218	PHE	2.4
2	X	166	VAL	2.4
1	A	134	GLY	2.3
2	X	101	ILE	2.3
1	I	169	LYS	2.3
2	J	61	PRO	2.3
1	O	65	ALA	2.3
2	V	231	LEU	2.3
2	X	127	VAL	2.3
2	X	248	VAL	2.3
1	O	149	TYR	2.3
2	V	202	LEU	2.3
2	X	128	PHE	2.3
2	D	37	VAL	2.3
1	G	170	VAL	2.3
1	I	197	VAL	2.3
1	K	138	TRP	2.3
1	E	1	MET	2.3
2	L	221	ALA	2.3
1	U	67	THR	2.3
2	P	142	SER	2.3
2	T	17	GLY	2.3
1	M	64	LEU	2.3

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Mol	Chain	Res	Type	RSRZ
2	L	88	THR	2.3
2	J	125	ILE	2.3
2	F	246	GLU	2.3
1	W	61	THR	2.3
2	J	208	SER	2.3
1	I	246	MET	2.3
1	O	82	GLY	2.3
2	F	161	ILE	2.3
2	H	241	VAL	2.3
2	T	165	ALA	2.3
2	B	176	ASP	2.3
1	I	147	LEU	2.3
1	W	248	LEU	2.3
2	D	177	LEU	2.3
1	C	198	VAL	2.3
1	I	170	VAL	2.3
1	S	14	ILE	2.3
2	T	79	VAL	2.3
2	V	112	GLU	2.2
1	G	145	TYR	2.2
1	G	91	LEU	2.2
2	R	247	GLY	2.2
1	E	225	ILE	2.2
2	H	235	ALA	2.2
2	P	217	ALA	2.2
1	K	190	LYS	2.2
1	M	149	TYR	2.2
1	S	66	GLY	2.2
1	W	196	PRO	2.2
2	F	148	LEU	2.2
1	I	273	LEU	2.2
2	V	77	LEU	2.2
2	F	131	ILE	2.2
2	H	145	ALA	2.2
2	H	240	TYR	2.2
2	J	81	TYR	2.2
2	L	160	LEU	2.2
1	K	108	ILE	2.2
1	Q	246	MET	2.2
1	K	60	THR	2.2
1	U	126	LEU	2.2
2	F	35	LEU	2.2

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Mol	Chain	Res	Type	RSRZ
2	V	247	GLY	2.2
1	E	14	ILE	2.2
1	S	198	VAL	2.2
2	L	33	ILE	2.2
1	S	65	ALA	2.2
2	F	162	ALA	2.2
2	T	192	ALA	2.2
1	G	269	LEU	2.2
1	U	63	VAL	2.2
1	U	144	VAL	2.2
2	B	228	ILE	2.2
2	H	51	ASN	2.2
2	N	85	PRO	2.2
2	H	228	ILE	2.2
2	L	46	ILE	2.2
2	P	76	VAL	2.2
2	X	201	THR	2.2
1	O	248	LEU	2.2
2	H	116	LEU	2.2
2	V	35	LEU	2.2
1	E	220	ILE	2.2
2	H	225	ILE	2.2
2	D	142	SER	2.2
2	V	85	PRO	2.2
1	U	227	PHE	2.2
2	P	164	VAL	2.2
2	B	130	GLU	2.2
1	W	269	LEU	2.2
2	H	128	PHE	2.2
2	J	220	LEU	2.2
2	D	79	VAL	2.2
2	P	225	ILE	2.2
2	H	45	ALA	2.2
2	H	156	PRO	2.2
2	J	129	THR	2.2
2	R	148	LEU	2.2
2	H	21	ASP	2.2
2	T	159	ASP	2.2
1	U	25	LYS	2.1
2	R	81	TYR	2.1
1	W	118	LEU	2.1
2	J	123	THR	2.1

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Mol	Chain	Res	Type	RSRZ
1	K	275	ILE	2.1
1	A	47	ALA	2.1
1	Q	209	LEU	2.1
2	B	28	LEU	2.1
1	O	169	LYS	2.1
2	X	76	VAL	2.1
1	O	138	TRP	2.1
1	Q	129	LEU	2.1
1	U	191	LEU	2.1
1	E	2	SER	2.1
1	K	218	GLU	2.1
2	L	32	LYS	2.1
2	H	173	ILE	2.1
1	U	152	ASN	2.1
2	B	111	LEU	2.1
2	L	218	PHE	2.1
2	X	231	LEU	2.1
2	J	217	ALA	2.1
1	I	225	ILE	2.1
1	K	14	ILE	2.1
1	K	251	ILE	2.1
1	S	268	GLU	2.1
2	T	141	VAL	2.1
1	A	181	SER	2.1
2	H	159	ASP	2.1
2	R	202	LEU	2.1
2	V	119	LEU	2.1
1	C	157	CYS	2.1
1	S	223	ALA	2.1
1	S	56	VAL	2.1
2	X	222	VAL	2.1
2	R	156	PRO	2.1
2	B	12	LEU	2.1
2	H	167	GLY	2.1
2	L	145	ALA	2.1
1	U	141	TRP	2.1
2	B	133	GLN	2.1
1	W	14	ILE	2.1
1	M	91	LEU	2.1
2	B	24	LYS	2.1
2	H	190	PRO	2.1
1	E	63	VAL	2.1

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Mol	Chain	Res	Type	RSRZ
1	Q	63	VAL	2.1
2	B	127	VAL	2.1
2	V	127	VAL	2.1
1	A	251	ILE	2.1
1	M	251	ILE	2.1
1	U	58	LEU	2.1
1	W	171	TYR	2.1
2	D	221	ALA	2.1
2	J	57	ALA	2.1
2	T	232	GLU	2.1
1	M	225	ILE	2.1
2	T	227	ILE	2.1
1	G	124	LEU	2.1
1	I	209	LEU	2.1
2	F	156	PRO	2.1
2	R	193	MET	2.1
1	K	201	SER	2.1
1	O	198	VAL	2.1
1	S	63	VAL	2.1
1	K	142	LEU	2.1
2	H	202	LEU	2.1
2	T	47	PHE	2.1
1	I	203	ALA	2.1
2	F	117	VAL	2.1
2	H	54	ALA	2.1
2	J	213	GLU	2.1
2	B	126	ASP	2.1
1	O	142	LEU	2.1
1	E	145	TYR	2.1
2	X	48	GLU	2.1
1	I	71	ILE	2.0
2	B	116	LEU	2.0
1	I	144	VAL	2.0
2	N	172	VAL	2.0
1	O	131	ILE	2.0
1	K	265	LEU	2.0
1	G	199	THR	2.0
2	P	201	THR	2.0
1	U	54	ALA	2.0
1	W	56	VAL	2.0
2	N	209	MET	2.0
1	U	257	THR	2.0

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Mol	Chain	Res	Type	RSRZ
1	E	65	ALA	2.0
1	E	144	VAL	2.0
2	L	31	ILE	2.0
2	L	136	ALA	2.0
1	C	105	GLU	2.0
2	R	60	GLY	2.0
1	A	183	ASN	2.0
2	H	20	THR	2.0
1	I	133	PRO	2.0
1	G	70	GLU	2.0
1	O	134	GLY	2.0
1	O	250	ASP	2.0
2	H	222	VAL	2.0
2	D	129	THR	2.0
2	P	13	ILE	2.0

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

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

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å ²)	Q<0.9
3	ADP	R	404	27/27	0.94	0.24	-0.47	47,55,58,58	0
3	ADP	T	404	27/27	0.95	0.25	-0.50	55,60,63,63	0
3	ADP	V	404	17/27	0.84	0.28	-0.51	90,93,95,95	0
3	ADP	H	404	27/27	0.83	0.24	-0.59	116,117,119,119	0
3	ADP	N	404	27/27	0.92	0.25	-0.67	59,62,64,64	0
3	ADP	L	404	27/27	0.93	0.25	-0.75	52,54,56,58	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
3	ADP	D	404	27/27	0.94	0.25	-0.90	48,50,51,51	0
3	ADP	P	404	27/27	0.95	0.23	-0.96	33,39,41,42	0
3	ADP	F	404	17/27	0.86	0.24	-1.07	91,94,95,95	0
3	ADP	X	404	17/27	0.83	0.21	-1.31	86,87,89,89	0
3	ADP	B	404	27/27	0.91	0.20	-1.38	79,90,95,95	0
3	ADP	J	404	9/27	0.92	0.14	-2.25	100,100,101,101	0

6.5 Other polymers [i](#)

There are no such residues in this entry.