



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 11:41 PM GMT

PDB ID : 1Y8R
Title : SUMO E1 ACTIVATING ENZYME SAE1-SAE2-SUMO1-MG-ATP COMPLEX
Authors : Lois, L.M.; Lima, C.D.
Deposited on : 2004-12-13
Resolution : 2.75 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

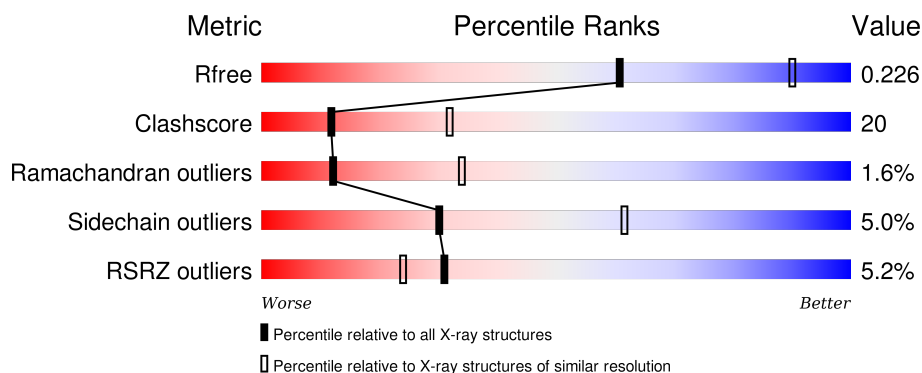
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.75 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	3340 (2.80-2.72)
Clashscore	102246	3829 (2.80-2.72)
Ramachandran outliers	100387	3767 (2.80-2.72)
Sidechain outliers	100360	3770 (2.80-2.72)
RSRZ outliers	91569	3352 (2.80-2.72)

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

Mol	Chain	Length	Quality of chain
1	A	346	<div> <div>3%</div> <div> <div></div> <div>55%</div> <div>34%</div> <div>• 9%</div> </div> </div>
1	D	346	<div> <div>•</div> <div> <div></div> <div>59%</div> <div>29%</div> <div>• 10%</div> </div> </div>
2	B	640	<div> <div>4%</div> <div> <div></div> <div>49%</div> <div>29%</div> <div>• 20%</div> </div> </div>
2	E	640	<div> <div>5%</div> <div> <div></div> <div>50%</div> <div>28%</div> <div>• 20%</div> </div> </div>
3	C	97	<div> <div>5%</div> <div> <div></div> <div>42%</div> <div>41%</div> <div>• • 13%</div> </div> </div>

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Mol	Chain	Length	Quality of chain
3	F	97	<p>22% 33% 48% 13%</p>

2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 14695 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 Ubiquitin-like 1 activating enzyme E1A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	314	Total	C	N	O	S	0	0	0
			2462	1559	418	472	13			
1	D	311	Total	C	N	O	S	0	0	0
			2437	1544	414	466	13			

- Molecule 2 is a protein called Ubiquitin-like 2 activating enzyme E1B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	512	Total	C	N	O	S	0	0	0
			4022	2556	695	752	19			
2	E	514	Total	C	N	O	S	0	0	0
			4031	2562	696	754	19			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	173	ALA	CYS	ENGINEERED	UNP Q9UBT2
E	173	ALA	CYS	ENGINEERED	UNP Q9UBT2

- Molecule 3 is a protein called Ubiquitin-like protein SMT3C.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	84	Total	C	N	O	S	0	0	0
			680	425	117	134	4			
3	F	84	Total	C	N	O	S	0	0	0
			680	425	117	134	4			

- Molecule 4 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	1	Total	Mg	0	0
			1	1		

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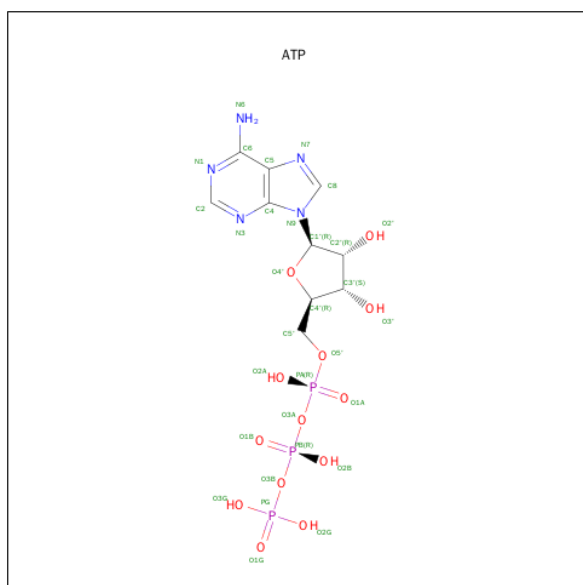
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	E	1	Total	Mg	0	0
			1	1		

- Molecule 5 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	B	1	Total	Zn	0	0
			1	1		
5	E	1	Total	Zn	0	0
			1	1		

- Molecule 6 is ADENOSINE-5'-TRIPHOSPHATE (three-letter code: ATP) (formula: C₁₀H₁₆N₅O₁₃P₃).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
6	E	1	Total	C	N	O	P	0	0
			31	10	5	13	3		
6	B	1	Total	C	N	O	P	0	0
			31	10	5	13	3		

- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	61	Total	O	0	0
			61	61		

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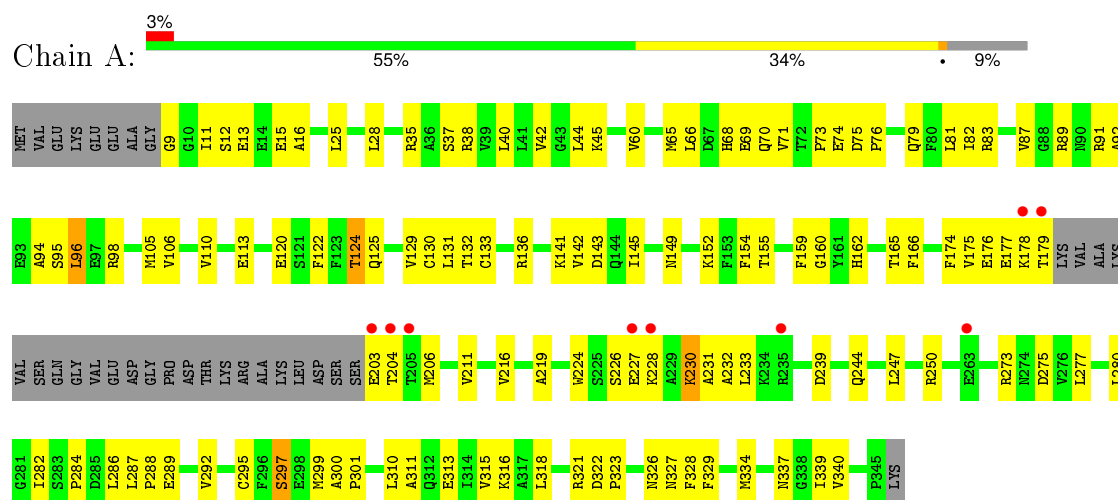
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	B	89	Total 89	O 89	0	0
7	C	13	Total 13	O 13	0	0
7	D	62	Total 62	O 62	0	0
7	E	85	Total 85	O 85	0	0
7	F	7	Total 7	O 7	0	0

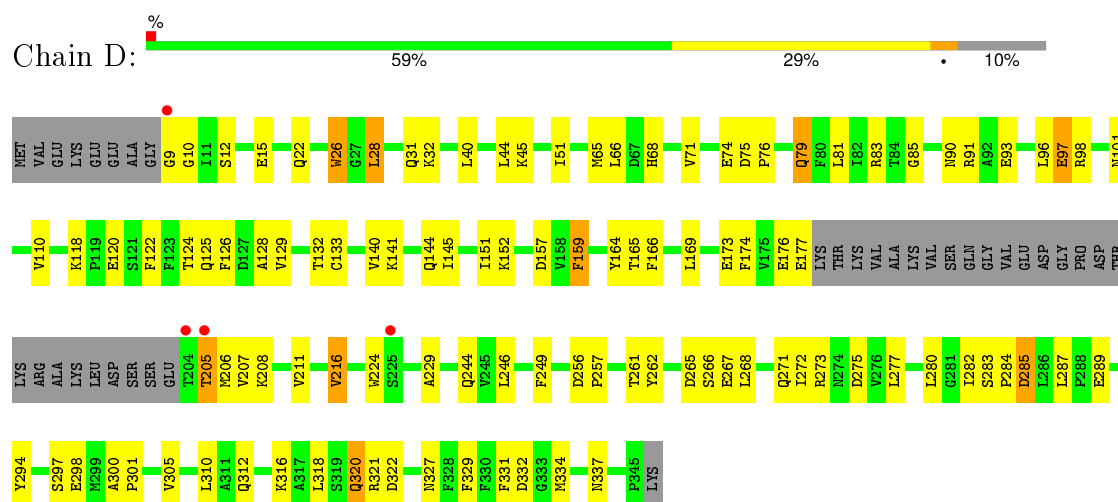
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). 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: Ubiquitin-like 1 activating enzyme E1A

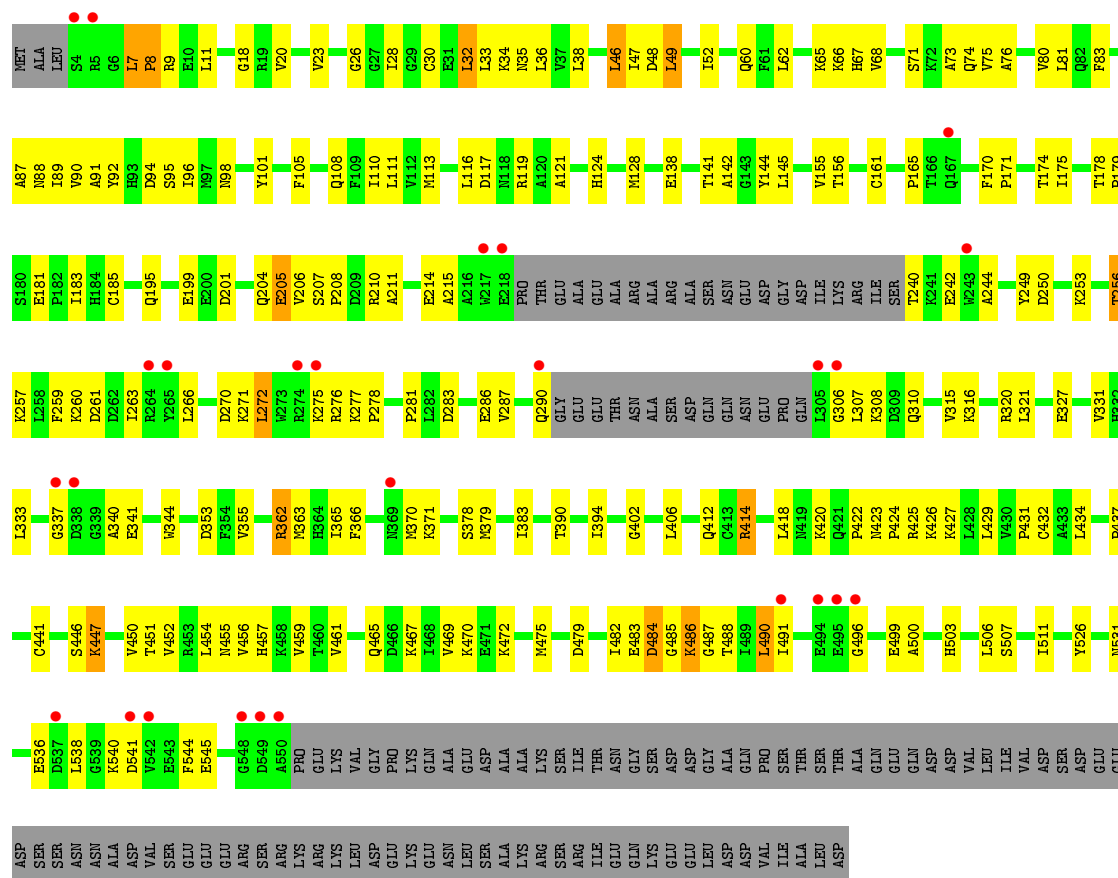


- Molecule 1: Ubiquitin-like 1 activating enzyme E1A

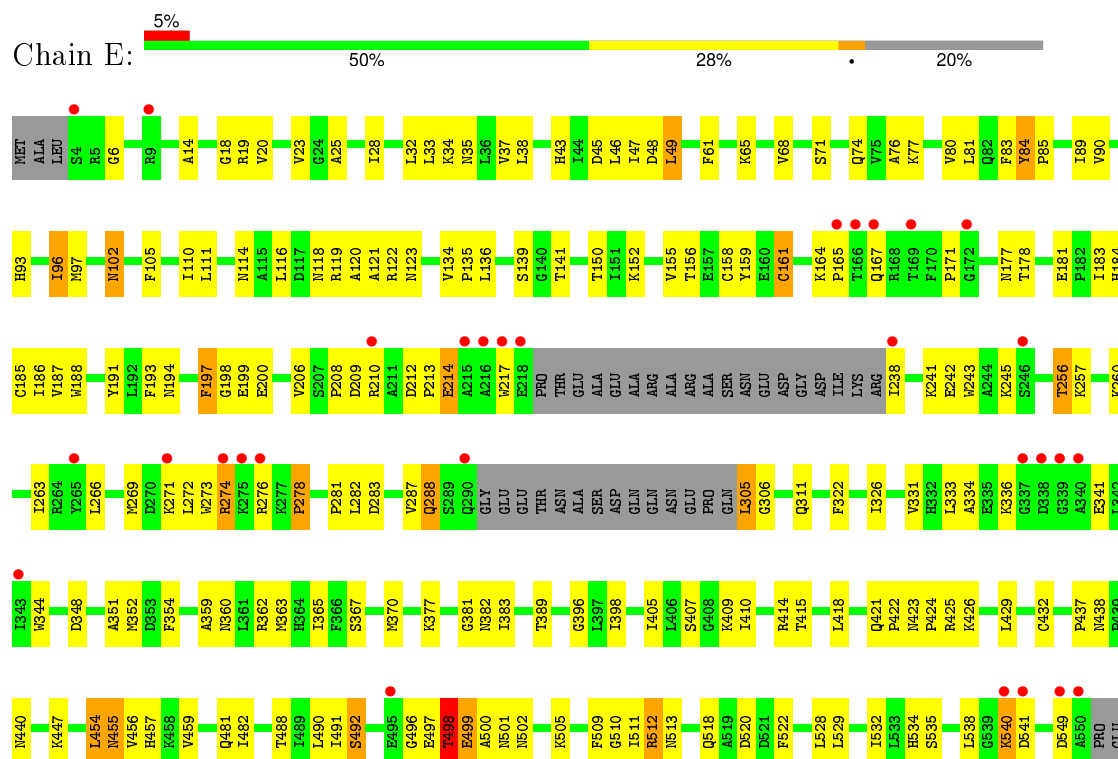


- Molecule 2: Ubiquitin-like 2 activating enzyme E1B



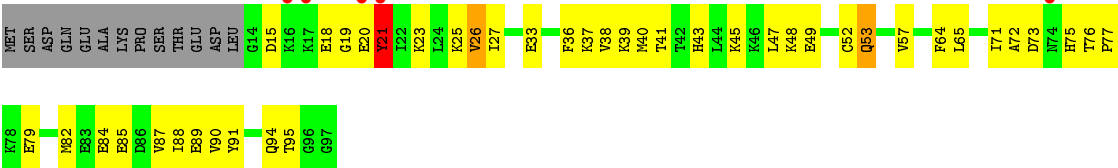


- Molecule 2: Ubiquitin-like 2 activating enzyme E1B

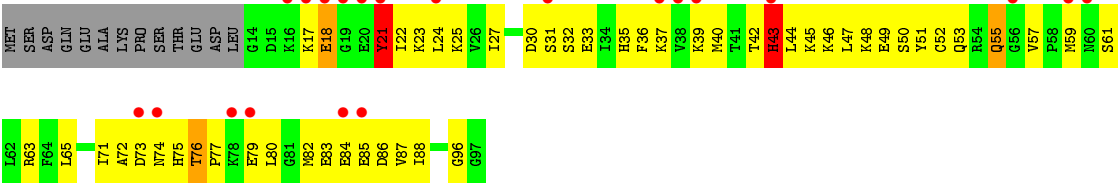


LYS	VAL	GLY	PRO	LYS	GLN	ALA	GLU	ASP	ALA	LYS	SER	ILE	THR	ASN	GLY	ASP	ALA	GLN	PRO	SER	THR	SER	THR	ALA	ALA	GLN	GLU	ASP	ASP	VAL	LEU	ILE	VAL	VAL	ASP	SER	ASP	GLU	GLU	ASP	SER	SER	ASN	ASN	ALA	ASP	VAL	SER	GLU	GLU	GLU	ARG	SER	ARG	LYS	ARG
LYS	LEU	ASP	GLU	LYS	GLU	ASN	LEU	SER	ALA	LYS	ARG	SER	ARG	ILE	THR	GLU	GLN	LYS	GLU	GLU	LEU	ASP	ASP	VAL	ILE	ALA	LEU	ASP																												

• Molecule 3: Ubiquitin-like protein SMT3C



• Molecule 3: Ubiquitin-like protein SMT3C



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	117.20Å 215.15Å 100.87Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.99 – 2.75 19.99 – 2.75	Depositor EDS
% Data completeness (in resolution range)	94.9 (19.99-2.75) 95.1 (19.99-2.75)	Depositor EDS
R_{merge}	0.15	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.25 (at 2.75Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.220 , 0.276 0.222 , 0.226	Depositor DCC
R_{free} test set	3228 reflections (5.08%)	DCC
Wilson B-factor (Å ²)	43.3	Xtriage
Anisotropy	0.114	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 59.3	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.43$, $\langle L^2 \rangle = 0.25$	Xtriage
Outliers	0 of 63862 reflections	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	14695	wwPDB-VP
Average B, all atoms (Å ²)	52.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 18.76% 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: MG, ZN, ATP

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	0/2505	0.59	0/3379
1	D	0.51	0/2480	0.61	0/3346
2	B	0.42	0/4099	0.60	0/5548
2	E	0.46	0/4108	0.61	0/5560
3	C	0.40	0/690	0.55	0/918
3	F	0.38	0/690	0.52	0/918
All	All	0.45	0/14572	0.60	0/19669

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2462	0	2451	94	0
1	D	2437	0	2425	82	0
2	B	4022	0	4058	160	0
2	E	4031	0	4067	159	0
3	C	680	0	674	39	0
3	F	680	0	674	60	0
4	B	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	E	1	0	0	0	0
5	B	1	0	0	0	0
5	E	1	0	0	0	0
6	B	31	0	12	0	0
6	E	31	0	12	1	0
7	A	61	0	0	3	0
7	B	89	0	0	6	0
7	C	13	0	0	0	0
7	D	62	0	0	4	0
7	E	85	0	0	7	0
7	F	7	0	0	0	0
All	All	14695	0	14373	577	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 20.

All (577) 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:B:465:GLN:HB2	2:B:491:ILE:HD13	1.43	0.99
1:A:40:LEU:HD12	1:A:129:VAL:HG13	1.51	0.92
2:E:490:LEU:HD11	2:E:511:ILE:HD11	1.52	0.91
3:F:21:TYR:HB3	3:F:22:ILE:HD12	1.54	0.88
1:D:22:GLN:HE21	1:D:31:GLN:HE22	1.23	0.85
1:D:90:ASN:HB3	1:D:93:GLU:HB2	1.58	0.85
2:E:541:ASP:HA	7:E:833:HOH:O	1.75	0.84
3:F:75:HIS:HB3	3:F:80:LEU:HD11	1.57	0.84
1:D:40:LEU:HD12	1:D:129:VAL:HG13	1.59	0.84
1:A:124:THR:HG23	1:A:149:ASN:HD22	1.45	0.82
1:A:282:ILE:HG21	1:A:286:LEU:HD22	1.62	0.81
2:B:455:ASN:HD22	2:B:536:GLU:HA	1.47	0.80
1:A:277:LEU:HD13	1:A:284:PRO:HA	1.64	0.79
2:E:47:ILE:HD13	2:E:96:ILE:HG23	1.65	0.79
3:F:84:GLU:HG3	3:F:85:GLU:HG2	1.63	0.78
2:B:307:LEU:HB2	2:B:310:GLN:HG3	1.63	0.78
2:E:197:PHE:HB3	2:E:333:LEU:HD22	1.63	0.78
2:E:23:VAL:HG12	2:E:116:LEU:HD21	1.66	0.78
1:D:98:ARG:HH12	2:E:83:PHE:HB3	1.46	0.77
2:B:283:ASP:HB3	2:B:286:GLU:HG3	1.65	0.77
2:B:452:VAL:HG12	2:B:454:LEU:HD22	1.66	0.77
2:B:475:MET:HA	7:B:833:HOH:O	1.85	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:8:PRO:HD2	2:B:9:ARG:H	1.49	0.76
1:A:44:LEU:HD21	1:A:65:MET:HB3	1.65	0.76
2:E:491:ILE:HA	2:E:498:THR:HG21	1.66	0.76
2:B:18:GLY:HA3	2:B:110:ILE:HD13	1.67	0.76
2:B:277:LYS:HD2	2:B:278:PRO:HD2	1.66	0.76
2:E:177:ASN:HD21	2:E:209:ASP:HB3	1.50	0.75
1:D:9:GLY:N	1:D:32:LYS:HZ1	1.84	0.75
1:D:22:GLN:HE21	1:D:31:GLN:NE2	1.84	0.75
2:B:465:GLN:HB2	2:B:491:ILE:CD1	2.17	0.74
2:E:305:LEU:HD12	2:E:311:GLN:HE22	1.52	0.74
2:B:178:THR:HG21	2:B:276:ARG:HH11	1.53	0.74
3:F:43:HIS:HB2	3:F:46:LYS:HE2	1.70	0.73
2:B:271:LYS:H	2:B:271:LYS:HD2	1.52	0.73
3:C:72:ALA:H	3:C:75:HIS:HD2	1.35	0.73
3:F:25:LYS:HG3	3:F:87:VAL:HG22	1.69	0.73
2:E:171:PRO:HA	2:E:541:ASP:OD2	1.89	0.72
2:B:470:LYS:HG2	2:B:475:MET:O	1.89	0.72
1:D:83:ARG:HA	1:D:98:ARG:NH2	2.06	0.71
2:B:467:LYS:NZ	2:B:467:LYS:HB3	2.06	0.71
2:E:183:ILE:O	2:E:187:VAL:HG23	1.90	0.71
2:E:33:LEU:HD23	2:E:80:VAL:HG21	1.73	0.71
1:D:22:GLN:NE2	1:D:31:GLN:HE22	1.89	0.70
2:B:141:THR:HG22	2:B:394:ILE:HG13	1.74	0.70
2:B:111:LEU:HG	2:B:113:MET:HE2	1.74	0.69
1:A:42:VAL:HG12	1:A:66:LEU:HB3	1.74	0.69
1:A:133:CYS:HA	1:A:250:ARG:HH12	1.58	0.69
2:B:482:ILE:HD13	2:B:488:THR:HB	1.74	0.69
1:D:249:PHE:CE1	1:D:268:LEU:HD23	2.28	0.69
2:B:256:THR:O	2:B:260:LYS:HB3	1.95	0.67
1:A:311:ALA:O	1:A:315:VAL:HG23	1.95	0.67
2:E:28:ILE:HD11	2:E:141:THR:HG23	1.76	0.67
3:F:27:ILE:HG12	3:F:33:GLU:HG3	1.74	0.67
1:D:141:LYS:HE2	1:D:145:ILE:HD11	1.76	0.67
3:F:45:LYS:HA	3:F:48:LYS:HD3	1.76	0.67
2:B:454:LEU:HD12	2:B:459:VAL:HG21	1.76	0.66
2:B:423:ASN:HB2	2:B:424:PRO:HD2	1.78	0.66
3:C:76:THR:HG22	3:C:79:GLU:HG3	1.78	0.66
2:B:316:LYS:HE2	2:B:320:ARG:NH1	2.11	0.66
1:D:174:PHE:HE2	1:D:211:VAL:HG23	1.61	0.65
1:A:42:VAL:HG21	1:A:131:LEU:HG	1.78	0.65
3:F:22:ILE:HD13	3:F:40:MET:HB2	1.78	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:F:25:LYS:HD3	3:F:85:GLU:O	1.97	0.65
1:D:273:ARG:HH12	1:D:289:GLU:HG2	1.61	0.65
1:A:233:LEU:HD21	1:A:286:LEU:HD21	1.77	0.65
2:E:456:VAL:HG12	2:E:534:HIS:ND1	2.12	0.65
2:B:321:LEU:HD11	2:B:353:ASP:HB3	1.78	0.65
2:E:183:ILE:HA	2:E:186:ILE:HD12	1.79	0.65
2:B:47:ILE:HD12	2:B:92:TYR:HB2	1.78	0.65
2:E:25:ALA:HB2	2:E:46:LEU:HD11	1.79	0.64
2:B:145:LEU:HB2	3:C:94:GLN:HE21	1.62	0.64
2:B:465:GLN:HG2	2:B:465:GLN:O	1.96	0.64
2:B:155:VAL:HG12	2:B:156:THR:HG23	1.79	0.64
2:B:263:ILE:HG22	2:B:281:PRO:HG3	1.80	0.64
2:E:194:ASN:HA	2:E:198:GLY:HA3	1.80	0.64
3:F:44:LEU:HD21	3:F:77:PRO:HG3	1.80	0.63
2:E:23:VAL:CG1	2:E:96:ILE:HG12	2.28	0.63
2:E:414:ARG:NE	7:E:802:HOH:O	2.32	0.63
3:F:22:ILE:CD1	3:F:40:MET:HB2	2.29	0.63
2:E:499:GLU:HA	2:E:502:ASN:HD21	1.62	0.63
1:A:60:VAL:O	1:A:106:VAL:HG22	1.98	0.63
1:D:98:ARG:NH1	2:E:83:PHE:HB3	2.11	0.63
1:A:133:CYS:HA	1:A:250:ARG:NH1	2.13	0.63
1:D:83:ARG:HA	1:D:98:ARG:HH21	1.63	0.63
2:B:259:PHE:HB3	2:B:365:ILE:HD11	1.80	0.63
1:A:92:ALA:HB1	1:A:110:VAL:HG13	1.80	0.63
1:A:273:ARG:HG2	1:A:277:LEU:HD12	1.80	0.63
1:D:277:LEU:HD13	1:D:284:PRO:HA	1.80	0.62
2:B:145:LEU:HB2	3:C:94:GLN:NE2	2.15	0.62
1:D:152:LYS:HG2	1:D:169:LEU:HD22	1.81	0.62
2:E:421:GLN:HG3	2:E:422:PRO:HD2	1.80	0.62
2:B:156:THR:O	2:B:437:PRO:HG3	1.98	0.62
2:E:522:PHE:N	7:E:877:HOH:O	2.32	0.62
3:F:55:GLN:HB3	3:F:57:VAL:HG23	1.79	0.62
2:B:215:ALA:HB2	2:B:272:LEU:HB2	1.80	0.62
1:A:42:VAL:HG22	1:A:131:LEU:HA	1.81	0.62
2:E:134:VAL:HG13	2:E:135:PRO:HD2	1.82	0.62
2:E:156:THR:O	2:E:437:PRO:HG3	2.00	0.61
2:B:71:SER:O	2:B:75:VAL:HG23	2.00	0.61
2:B:423:ASN:HD21	2:B:425:ARG:HE	1.49	0.61
3:F:17:LYS:HG3	3:F:18:GLU:H	1.65	0.61
3:F:43:HIS:HA	3:F:76:THR:HG23	1.81	0.61
3:C:45:LYS:HD2	3:C:73:ASP:HB3	1.81	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:456:VAL:HG21	2:E:511:ILE:O	2.01	0.61
1:A:71:VAL:HG22	1:A:91:ARG:HA	1.81	0.61
3:C:52:CYS:HB2	3:C:57:VAL:O	2.00	0.61
1:A:337:ASN:HB3	1:A:339:ILE:HD11	1.81	0.61
1:D:10:GLY:H	1:D:32:LYS:HE2	1.67	0.60
1:A:42:VAL:CG2	1:A:131:LEU:HG	2.30	0.60
2:B:142:ALA:HB3	3:C:94:GLN:NE2	2.16	0.60
1:A:120:GLU:HG3	1:A:145:ILE:HG23	1.81	0.60
2:E:496:GLY:H	2:E:499:GLU:CD	2.05	0.60
2:B:23:VAL:HG12	2:B:116:LEU:HD21	1.83	0.60
2:E:97:MET:HE3	2:E:121:ALA:HA	1.84	0.60
1:A:273:ARG:HG3	1:A:287:LEU:HD23	1.83	0.60
3:F:23:LYS:HE2	3:F:37:LYS:HE2	1.83	0.59
2:E:84:TYR:N	2:E:85:PRO:HD3	2.17	0.59
1:D:205:THR:HG22	1:D:207:VAL:HG23	1.83	0.59
1:A:132:THR:HG22	1:A:133:CYS:SG	2.42	0.59
1:A:339:ILE:N	1:A:339:ILE:HD12	2.18	0.59
2:E:499:GLU:HA	2:E:502:ASN:ND2	2.18	0.59
1:A:165:THR:OG1	1:A:329:PHE:HB3	2.03	0.59
1:A:38:ARG:HH11	1:A:38:ARG:HB2	1.68	0.59
1:D:118:LYS:HG2	1:D:122:PHE:CD2	2.38	0.58
3:C:76:THR:CG2	3:C:79:GLU:HG3	2.34	0.58
2:B:371:LYS:HD3	2:B:379:MET:HE1	1.85	0.58
1:A:82:ILE:HG23	1:A:94:ALA:HB1	1.84	0.58
1:A:70:GLN:HE21	1:A:89:ARG:C	2.07	0.58
2:B:538:LEU:HD11	2:B:545:GLU:HG2	1.86	0.58
2:E:89:ILE:HD12	2:E:89:ILE:N	2.19	0.58
1:A:131:LEU:N	1:A:131:LEU:HD12	2.19	0.57
2:B:73:ALA:HB1	2:B:91:ALA:HB1	1.87	0.57
1:A:131:LEU:HD21	1:A:142:VAL:HG21	1.85	0.57
2:B:215:ALA:HB1	2:B:271:LYS:HD3	1.86	0.57
3:C:39:LYS:HE2	3:C:41:THR:O	2.05	0.57
1:D:165:THR:HG23	1:D:310:LEU:HD13	1.86	0.57
1:A:11:ILE:HG22	1:A:35:ARG:CZ	2.35	0.57
1:D:312:GLN:O	1:D:316:LYS:HG3	2.05	0.57
3:F:63:ARG:HG2	3:F:65:LEU:CD1	2.34	0.57
2:B:420:LYS:HB3	2:B:420:LYS:HZ3	1.70	0.57
3:F:45:LYS:HD2	3:F:73:ASP:HB3	1.87	0.57
2:B:8:PRO:HD2	2:B:9:ARG:N	2.20	0.56
2:B:526:TYR:HA	7:B:855:HOH:O	2.04	0.56
3:C:64:PHE:HB3	3:C:71:ILE:HD12	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:141:THR:CG2	2:B:394:ILE:HG13	2.34	0.56
1:D:45:LYS:HE3	1:D:91:ARG:HH12	1.70	0.56
2:B:215:ALA:HA	2:B:271:LYS:HB2	1.87	0.56
2:E:418:LEU:HD13	2:E:429:LEU:HD21	1.87	0.56
2:B:467:LYS:HZ3	2:B:467:LYS:HB3	1.70	0.56
2:E:360:ASN:HA	2:E:363:MET:HE3	1.87	0.56
1:A:224:TRP:HE1	1:A:280:LEU:HD23	1.70	0.56
3:F:21:TYR:HB2	3:F:39:LYS:HA	1.87	0.56
1:D:273:ARG:NH1	1:D:289:GLU:HG2	2.19	0.56
1:D:176:GLU:O	1:D:206:MET:HA	2.05	0.56
3:F:72:ALA:H	3:F:75:HIS:CG	2.23	0.55
3:F:44:LEU:HG	3:F:77:PRO:HD3	1.88	0.55
2:B:425:ARG:O	2:B:426:LYS:HB2	2.06	0.55
1:A:71:VAL:HG23	1:A:89:ARG:O	2.06	0.55
1:A:179:THR:HG21	1:A:203:GLU:HG3	1.88	0.55
2:B:461:VAL:HG12	7:B:887:HOH:O	2.06	0.55
1:A:226:SER:O	1:A:230:LYS:HG2	2.07	0.55
1:A:299:MET:CE	2:B:7:LEU:HD11	2.35	0.55
3:C:72:ALA:H	3:C:75:HIS:CD2	2.21	0.55
1:A:300:ALA:HB3	1:A:301:PRO:HD3	1.89	0.55
2:E:188:TRP:NE1	2:E:362:ARG:NH2	2.55	0.55
2:E:243:TRP:CH2	2:E:257:LYS:HG3	2.41	0.55
2:B:450:VAL:HG22	2:B:451:THR:N	2.20	0.55
1:D:157:ASP:HB2	1:D:164:TYR:HE2	1.71	0.55
1:D:273:ARG:HG3	1:D:287:LEU:HD23	1.89	0.55
3:C:19:GLY:H	3:C:39:LYS:HB2	1.71	0.55
2:B:65:LYS:O	2:B:68:VAL:HG23	2.07	0.55
2:E:77:LYS:HG3	2:E:89:ILE:HB	1.88	0.54
1:D:165:THR:HB	1:D:329:PHE:HB3	1.90	0.54
3:F:72:ALA:O	3:F:75:HIS:HB2	2.07	0.54
2:B:316:LYS:HG2	2:B:320:ARG:CZ	2.37	0.54
1:D:45:LYS:HE3	1:D:91:ARG:NH1	2.23	0.54
2:B:484:ASP:OD1	2:B:486:LYS:HD2	2.06	0.54
2:E:23:VAL:HG13	2:E:96:ILE:HG12	1.90	0.54
1:A:141:LYS:HE2	1:A:145:ILE:HD11	1.90	0.54
2:E:455:ASN:C	2:E:455:ASN:HD22	2.11	0.54
1:A:124:THR:HG23	1:A:149:ASN:ND2	2.18	0.54
1:D:9:GLY:HA3	2:E:306:GLY:O	2.08	0.54
1:D:177:GLU:HA	1:D:206:MET:H	1.72	0.54
2:B:244:ALA:HB1	2:B:249:TYR:CE1	2.43	0.54
2:E:273:TRP:HA	2:E:276:ARG:CG	2.37	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:42:VAL:CG2	1:A:131:LEU:HA	2.38	0.54
3:C:20:GLU:OE1	3:C:37:LYS:HB3	2.07	0.54
2:B:240:THR:HA	2:B:242:GLU:OE2	2.07	0.54
2:E:283:ASP:O	2:E:287:VAL:HG23	2.07	0.54
1:A:66:LEU:HD21	1:A:113:GLU:O	2.08	0.54
1:D:68:HIS:HB3	7:D:381:HOH:O	2.07	0.54
2:E:65:LYS:O	2:E:68:VAL:HG23	2.08	0.54
2:E:19:ARG:HH21	2:E:90:VAL:HG21	1.73	0.54
1:A:44:LEU:CD2	1:A:65:MET:HB3	2.38	0.53
1:A:68:HIS:HB2	7:A:376:HOH:O	2.08	0.53
1:D:173:GLU:HG2	1:D:208:LYS:HE2	1.91	0.53
2:E:181:GLU:HB2	2:E:184:HIS:CE1	2.42	0.53
2:B:47:ILE:CD1	2:B:92:TYR:HB2	2.39	0.53
2:E:257:LYS:HD3	2:E:257:LYS:O	2.08	0.53
3:C:84:GLU:HG3	3:C:85:GLU:HG2	1.90	0.53
3:F:49:GLU:O	3:F:53:GLN:HB2	2.09	0.53
2:B:181:GLU:HB2	2:B:183:ILE:HG22	1.90	0.53
3:F:40:MET:HA	3:F:77:PRO:HB2	1.91	0.53
2:E:188:TRP:HE1	2:E:362:ARG:HH21	1.56	0.53
2:B:456:VAL:HG11	2:B:511:ILE:O	2.08	0.53
2:E:141:THR:O	3:F:96:GLY:HA3	2.09	0.53
2:E:37:VAL:HG23	2:E:38:LEU:N	2.23	0.53
2:B:500:ALA:HA	2:B:503:HIS:HE1	1.74	0.53
2:B:412:GLN:O	2:B:414:ARG:HD2	2.08	0.53
3:F:24:LEU:HD13	3:F:88:ILE:HD11	1.91	0.53
2:B:459:VAL:O	2:B:506:LEU:HG	2.08	0.53
1:D:165:THR:HG22	7:D:373:HOH:O	2.08	0.53
2:E:243:TRP:CZ3	2:E:257:LYS:HG3	2.43	0.53
3:C:49:GLU:O	3:C:53:GLN:HB2	2.09	0.53
2:E:454:LEU:HD21	2:E:532:ILE:HG23	1.91	0.53
1:A:334:MET:CE	1:A:334:MET:HA	2.39	0.53
1:D:280:LEU:O	1:D:282:ILE:HG13	2.08	0.53
2:B:81:LEU:HD23	2:B:87:ALA:HB3	1.89	0.53
1:D:176:GLU:HG2	1:D:177:GLU:H	1.73	0.52
3:F:25:LYS:HB3	3:F:35:HIS:CD2	2.44	0.52
2:B:28:ILE:HD11	2:B:141:THR:HG23	1.92	0.52
2:E:102:ASN:O	2:E:105:PHE:HB3	2.09	0.52
2:B:201:ASP:HB3	2:B:204:GLN:HB2	1.92	0.52
2:E:210:ARG:CZ	2:E:210:ARG:HA	2.39	0.52
2:E:158:CYS:O	2:E:161:CYS:HB2	2.09	0.52
2:E:457:HIS:O	2:E:505:LYS:HG2	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:20:VAL:HG13	2:B:113:MET:HE3	1.92	0.52
3:F:23:LYS:HG2	3:F:24:LEU:N	2.25	0.52
2:B:420:LYS:NZ	2:B:420:LYS:HB3	2.25	0.52
2:B:199:GLU:HA	2:B:341:GLU:OE2	2.09	0.52
3:F:75:HIS:CB	3:F:80:LEU:HD11	2.34	0.52
2:B:540:LYS:HA	7:B:807:HOH:O	2.09	0.52
2:E:365:ILE:HG22	2:E:365:ILE:O	2.08	0.52
1:D:321:ARG:O	1:D:322:ASP:HB2	2.09	0.51
1:A:313:GLU:OE2	1:A:316:LYS:HE2	2.10	0.51
2:B:33:LEU:HD11	2:B:46:LEU:CD1	2.41	0.51
2:E:498:THR:C	2:E:500:ALA:H	2.13	0.51
2:E:97:MET:CE	2:E:121:ALA:HA	2.40	0.51
1:D:75:ASP:N	1:D:76:PRO:HD2	2.25	0.51
1:A:136:ARG:HG3	1:A:247:LEU:HD13	1.92	0.51
2:B:470:LYS:HA	2:B:475:MET:O	2.09	0.51
2:B:423:ASN:OD1	2:B:427:LYS:HB2	2.09	0.51
3:C:26:VAL:HG12	3:C:90:VAL:HG23	1.91	0.51
1:A:179:THR:HG21	1:A:203:GLU:O	2.10	0.51
2:E:273:TRP:HB3	2:E:278:PRO:HG3	1.93	0.51
1:A:176:GLU:HG3	1:A:323:PRO:HD3	1.91	0.51
2:E:482:ILE:HD12	2:E:488:THR:HB	1.92	0.51
2:E:348:ASP:HB3	2:E:351:ALA:HB3	1.93	0.51
3:F:43:HIS:CD2	3:F:74:ASN:HA	2.46	0.51
1:D:268:LEU:O	1:D:271:GLN:HB3	2.11	0.51
2:E:71:SER:HB3	2:E:74:GLN:HB2	1.93	0.51
1:D:71:VAL:HG22	1:D:91:ARG:HA	1.93	0.51
3:F:76:THR:OG1	3:F:79:GLU:HB2	2.11	0.50
3:C:19:GLY:O	3:C:20:GLU:HG2	2.10	0.50
2:E:102:ASN:HD22	2:E:102:ASN:H	1.59	0.50
1:D:74:GLU:N	1:D:74:GLU:OE2	2.43	0.50
2:B:8:PRO:CD	2:B:9:ARG:H	2.21	0.50
2:E:288:GLN:N	2:E:288:GLN:HE21	2.09	0.50
2:E:37:VAL:HG23	2:E:38:LEU:H	1.76	0.50
1:A:340:VAL:HG21	2:B:422:PRO:HG3	1.93	0.50
2:B:257:LYS:HA	2:B:261:ASP:HB2	1.92	0.50
2:E:49:LEU:C	2:E:49:LEU:HD12	2.32	0.50
3:F:52:CYS:HB2	3:F:57:VAL:O	2.11	0.50
2:E:260:LYS:HB2	2:E:282:LEU:O	2.12	0.50
1:A:143:ASP:OD1	1:A:216:VAL:HG12	2.12	0.50
3:C:27:ILE:HG12	3:C:33:GLU:HG2	1.93	0.50
1:A:179:THR:OG1	1:A:204:THR:HA	2.10	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:310:LEU:O	1:D:310:LEU:HD12	2.12	0.50
3:F:63:ARG:HG2	3:F:65:LEU:HD11	1.93	0.50
2:B:240:THR:HG23	2:B:242:GLU:OE1	2.11	0.50
2:E:352:MET:SD	2:E:377:LYS:HG3	2.52	0.50
2:E:164:LYS:HB3	2:E:165:PRO:HD2	1.94	0.50
1:A:162:HIS:HD2	1:A:239:ASP:OD2	1.95	0.49
2:E:212:ASP:O	2:E:214:GLU:N	2.45	0.49
2:B:30:CYS:SG	2:B:62:LEU:HD12	2.51	0.49
2:B:482:ILE:N	2:B:482:ILE:HD12	2.28	0.49
1:D:332:ASP:OD1	1:D:334:MET:HB2	2.12	0.49
2:B:482:ILE:O	2:B:487:GLY:HA2	2.12	0.49
3:C:45:LYS:HA	3:C:48:LYS:HD3	1.94	0.49
2:E:492:SER:N	2:E:498:THR:HG21	2.27	0.49
2:E:497:GLU:O	2:E:498:THR:HG23	2.13	0.49
1:A:175:VAL:CG2	1:A:206:MET:HB2	2.43	0.49
1:D:166:PHE:CE2	1:D:216:VAL:HG22	2.48	0.49
2:B:344:TRP:NE1	2:B:355:VAL:HG21	2.28	0.49
3:F:72:ALA:HB3	3:F:75:HIS:ND1	2.27	0.49
7:D:402:HOH:O	2:E:389:THR:HG23	2.12	0.49
2:B:283:ASP:O	2:B:287:VAL:HG23	2.12	0.49
2:B:111:LEU:CG	2:B:113:MET:HE2	2.42	0.49
3:C:20:GLU:OE1	3:C:37:LYS:HD3	2.13	0.49
2:B:26:GLY:O	2:B:60:GLN:HG2	2.13	0.49
2:E:122:ARG:HD3	2:E:159:TYR:CZ	2.47	0.49
1:A:130:CYS:HA	1:A:154:PHE:O	2.13	0.49
3:F:43:HIS:HA	3:F:76:THR:CG2	2.43	0.49
2:B:210:ARG:HG3	2:B:211:ALA:N	2.27	0.49
2:B:450:VAL:CG2	2:B:451:THR:N	2.76	0.49
2:B:34:LYS:HD2	2:B:35:ASN:OD1	2.13	0.49
2:E:241:LYS:O	2:E:245:LYS:HG2	2.13	0.49
1:A:224:TRP:NE1	1:A:280:LEU:HD23	2.28	0.48
2:B:208:PRO:HB3	2:B:266:LEU:HD13	1.94	0.48
2:B:98:ASN:HB3	2:B:101:TYR:CE1	2.47	0.48
2:E:271:LYS:O	2:E:274:ARG:HB2	2.13	0.48
1:D:132:THR:HG22	1:D:133:CYS:SG	2.53	0.48
2:B:18:GLY:CA	2:B:110:ILE:HD13	2.41	0.48
2:E:256:THR:O	2:E:260:LYS:HB3	2.12	0.48
2:B:263:ILE:HD12	2:B:263:ILE:N	2.28	0.48
2:E:193:PHE:CD2	2:E:344:TRP:HB2	2.48	0.48
3:F:22:ILE:HG12	3:F:40:MET:CE	2.43	0.48
1:A:321:ARG:O	1:A:322:ASP:HB2	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:305:VAL:HG23	2:E:396:GLY:HA3	1.94	0.48
2:B:179:PRO:HD2	2:B:366:PHE:CE2	2.48	0.48
2:B:418:LEU:HA	2:B:429:LEU:HD23	1.95	0.48
2:E:118:ASN:C	2:E:118:ASN:ND2	2.65	0.48
2:B:98:ASN:HB3	2:B:101:TYR:CD1	2.49	0.48
2:B:429:LEU:O	2:B:431:PRO:HD3	2.13	0.48
2:B:455:ASN:ND2	2:B:536:GLU:HA	2.21	0.48
3:F:22:ILE:N	3:F:22:ILE:HD12	2.29	0.48
2:E:492:SER:H	2:E:498:THR:HG21	1.79	0.48
1:A:96:LEU:HD13	1:A:110:VAL:HG23	1.96	0.48
2:E:257:LYS:HD3	2:E:257:LYS:C	2.34	0.48
1:A:81:LEU:O	1:A:95:SER:HA	2.13	0.48
2:B:76:ALA:O	2:B:80:VAL:HG23	2.13	0.47
2:B:469:VAL:O	2:B:475:MET:HB2	2.14	0.47
2:B:7:LEU:H	2:B:8:PRO:HA	1.79	0.47
3:F:36:PHE:HZ	3:F:51:TYR:HA	1.79	0.47
2:E:77:LYS:O	2:E:81:LEU:HB2	2.15	0.47
2:B:33:LEU:HD11	2:B:46:LEU:HD11	1.96	0.47
1:D:10:GLY:H	1:D:32:LYS:CE	2.26	0.47
2:B:71:SER:HB3	2:B:74:GLN:HB2	1.96	0.47
2:E:418:LEU:HD13	2:E:429:LEU:CD2	2.45	0.47
2:B:315:VAL:HG22	2:B:370:MET:HE1	1.95	0.47
1:A:178:LYS:HG3	1:A:178:LYS:O	2.14	0.47
3:F:75:HIS:CD2	3:F:80:LEU:HD21	2.50	0.47
2:E:188:TRP:HE1	2:E:362:ARG:NH2	2.12	0.47
2:E:197:PHE:CD1	2:E:197:PHE:N	2.83	0.47
2:B:454:LEU:N	2:B:454:LEU:HD23	2.29	0.47
2:B:33:LEU:HD13	2:B:80:VAL:HG21	1.96	0.47
2:E:415:THR:HB	7:E:834:HOH:O	2.15	0.47
2:B:327:GLU:O	2:B:331:VAL:HG23	2.13	0.47
2:E:242:GLU:HA	2:E:245:LYS:HB2	1.97	0.47
2:B:333:LEU:HD11	2:B:340:ALA:O	2.15	0.47
2:E:134:VAL:CG1	2:E:135:PRO:HD2	2.45	0.47
3:C:64:PHE:CD2	3:C:90:VAL:HG22	2.50	0.46
1:A:174:PHE:HE2	1:A:211:VAL:HG23	1.80	0.46
3:F:22:ILE:HG22	3:F:23:LYS:N	2.30	0.46
2:B:250:ASP:HB3	2:B:253:LYS:HB2	1.96	0.46
3:F:71:ILE:HA	3:F:75:HIS:CD2	2.51	0.46
3:C:26:VAL:HG13	3:C:88:ILE:HB	1.97	0.46
1:D:128:ALA:HB2	1:D:318:LEU:HD21	1.96	0.46
2:E:208:PRO:HG3	2:E:266:LEU:HD13	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:150:THR:CG2	2:E:405:ILE:HD11	2.46	0.46
2:E:322:PHE:CE1	2:E:326:ILE:HD11	2.51	0.46
2:B:362:ARG:HG2	2:B:362:ARG:HH11	1.80	0.46
2:B:105:PHE:O	2:B:108:GLN:HG3	2.15	0.46
2:B:414:ARG:HB2	2:B:432:CYS:O	2.14	0.46
2:B:52:ILE:H	2:B:52:ILE:HD12	1.80	0.46
3:F:47:LEU:HA	3:F:50:SER:HB3	1.98	0.46
2:B:455:ASN:OD1	2:B:457:HIS:HB2	2.16	0.46
2:B:214:GLU:HB3	2:B:272:LEU:HG	1.97	0.46
3:F:45:LYS:HB2	3:F:73:ASP:CA	2.46	0.46
2:B:263:ILE:CG2	2:B:281:PRO:HG3	2.44	0.46
3:C:26:VAL:HG12	3:C:90:VAL:CG2	2.46	0.46
1:D:265:ASP:O	1:D:266:SER:C	2.52	0.46
2:B:124:HIS:O	2:B:128:MET:HG2	2.16	0.46
2:E:425:ARG:O	2:E:426:LYS:HB2	2.16	0.46
2:B:49:LEU:HD23	2:B:95:SER:HB2	1.97	0.46
2:E:161:CYS:SG	2:E:438:ASN:HB3	2.57	0.45
2:B:170:PHE:CB	2:B:175:ILE:HD11	2.46	0.45
1:D:244:GLN:HA	1:D:244:GLN:HE21	1.81	0.45
3:F:39:LYS:HB3	3:F:42:THR:OG1	2.17	0.45
1:D:97:GLU:O	1:D:98:ARG:C	2.55	0.45
3:C:25:LYS:HG3	3:C:87:VAL:HG22	1.97	0.45
2:E:510:GLY:O	2:E:512:ARG:HD3	2.16	0.45
2:B:308:LYS:NZ	2:B:308:LYS:HB3	2.31	0.45
2:E:34:LYS:HD3	2:E:61:PHE:CZ	2.51	0.45
3:C:38:VAL:HG21	3:C:47:LEU:HD12	1.99	0.45
1:A:11:ILE:HA	1:A:35:ARG:HH12	1.82	0.45
1:A:73:PRO:HG3	1:A:87:VAL:HG11	1.98	0.45
2:B:496:GLY:H	2:B:499:GLU:CD	2.20	0.45
1:D:44:LEU:HD21	1:D:65:MET:HB3	1.96	0.45
1:A:230:LYS:NZ	1:A:230:LYS:HB3	2.32	0.45
2:B:446:SER:O	2:B:447:LYS:HD2	2.16	0.45
2:E:407:SER:HB3	2:E:409:LYS:HE3	1.99	0.45
2:E:23:VAL:CG1	2:E:116:LEU:HD21	2.42	0.45
2:B:482:ILE:H	2:B:482:ILE:HD12	1.82	0.45
3:C:89:GLU:OE1	3:C:91:TYR:OH	2.31	0.45
1:D:334:MET:HE3	1:D:334:MET:HA	1.98	0.45
2:B:94:ASP:OD2	2:B:98:ASN:ND2	2.50	0.45
3:F:75:HIS:CD2	3:F:80:LEU:HD11	2.51	0.45
1:A:230:LYS:NZ	1:A:230:LYS:CB	2.80	0.45
2:E:188:TRP:O	2:E:191:TYR:HB2	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:19:ARG:NH2	2:E:90:VAL:HG21	2.32	0.45
3:F:21:TYR:HB3	3:F:22:ILE:CD1	2.37	0.45
2:B:116:LEU:HD13	2:B:121:ALA:CB	2.47	0.45
1:A:154:PHE:HB3	1:A:310:LEU:HD11	1.98	0.45
2:B:34:LYS:O	2:B:38:LEU:HG	2.16	0.45
2:E:34:LYS:HE2	2:E:34:LYS:HB3	1.77	0.45
1:D:224:TRP:HA	1:D:229:ALA:HB1	1.98	0.45
2:B:195:GLN:NE2	2:B:201:ASP:H	2.15	0.45
2:E:535:SER:HB3	2:E:538:LEU:HD21	1.98	0.45
2:E:76:ALA:O	2:E:80:VAL:HG23	2.17	0.45
2:E:276:ARG:O	2:E:278:PRO:HD3	2.17	0.45
2:B:418:LEU:HD13	2:B:429:LEU:HD21	1.99	0.45
1:A:73:PRO:O	1:A:74:GLU:HB2	2.17	0.45
1:A:228:LYS:HD2	1:A:228:LYS:N	2.32	0.45
3:C:64:PHE:O	3:C:65:LEU:HD12	2.16	0.44
2:E:178:THR:HG21	2:E:276:ARG:CZ	2.47	0.44
2:E:447:LYS:HD3	2:E:447:LYS:HA	1.75	0.44
1:A:244:GLN:NE2	7:A:354:HOH:O	2.49	0.44
3:F:44:LEU:CD2	3:F:77:PRO:HG3	2.46	0.44
1:A:28:LEU:HD23	2:B:306:GLY:HA2	2.00	0.44
1:A:9:GLY:HA2	2:B:306:GLY:O	2.17	0.44
2:B:67:HIS:CD2	2:B:75:VAL:HG13	2.53	0.44
2:B:451:THR:HA	2:B:531:ASN:HB2	1.98	0.44
2:B:207:SER:HB3	2:B:208:PRO:HD2	2.00	0.44
2:E:415:THR:O	2:E:432:CYS:N	2.50	0.44
3:C:23:LYS:HA	3:C:36:PHE:O	2.17	0.44
2:E:491:ILE:CA	2:E:498:THR:HG21	2.43	0.44
3:C:77:PRO:HA	3:C:82:MET:HG3	1.98	0.44
2:E:421:GLN:CG	2:E:422:PRO:HD2	2.47	0.44
2:E:119:ARG:O	2:E:123:ASN:ND2	2.51	0.44
1:A:122:PHE:O	1:A:125:GLN:HG2	2.17	0.44
1:D:79:GLN:OE1	1:D:81:LEU:HB2	2.17	0.44
2:E:454:LEU:O	2:E:534:HIS:HA	2.18	0.44
3:F:23:LYS:HD2	3:F:85:GLU:OE1	2.17	0.44
3:F:27:ILE:HD12	3:F:87:VAL:HG11	1.99	0.44
3:C:19:GLY:N	3:C:39:LYS:HB2	2.32	0.44
2:E:438:ASN:OD1	2:E:440:ASN:N	2.47	0.44
2:E:238:ILE:HG23	7:E:870:HOH:O	2.17	0.44
2:E:263:ILE:CG2	2:E:281:PRO:HG3	2.48	0.44
2:E:199:GLU:HA	2:E:341:GLU:OE2	2.18	0.44
3:F:27:ILE:HG23	3:F:32:SER:O	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:102:ASN:O	2:E:105:PHE:N	2.47	0.44
2:E:139:SER:OG	2:E:398:ILE:HD11	2.17	0.44
1:A:175:VAL:HG21	1:A:206:MET:HB2	2.00	0.44
2:B:48:ASP:HB3	7:B:856:HOH:O	2.16	0.44
1:D:283:SER:HB2	1:D:285:ASP:OD1	2.17	0.44
3:F:25:LYS:O	3:F:87:VAL:HA	2.17	0.44
2:E:14:ALA:O	2:E:18:GLY:N	2.51	0.44
2:E:423:ASN:HB2	2:E:424:PRO:CD	2.48	0.44
1:A:337:ASN:HB3	1:A:339:ILE:CD1	2.47	0.44
2:B:171:PRO:HG2	2:B:174:THR:OG1	2.18	0.44
2:B:8:PRO:CD	2:B:9:ARG:N	2.79	0.43
2:E:77:LYS:HG3	2:E:89:ILE:CG2	2.48	0.43
1:A:233:LEU:CD2	1:A:286:LEU:HD21	2.46	0.43
1:A:299:MET:HE1	2:B:7:LEU:HD11	2.00	0.43
1:D:120:GLU:HG3	1:D:145:ILE:HG23	2.00	0.43
2:B:461:VAL:CG1	2:B:490:LEU:HD22	2.48	0.43
2:E:185:CYS:O	2:E:188:TRP:HB3	2.18	0.43
2:E:377:LYS:HG2	2:E:383:ILE:HD11	2.00	0.43
1:A:155:THR:HG22	1:A:166:PHE:HB3	1.98	0.43
2:E:150:THR:HG23	2:E:405:ILE:HD11	2.00	0.43
1:D:96:LEU:HB2	1:D:110:VAL:HG11	2.00	0.43
1:A:12:SER:HB3	1:A:15:GLU:CG	2.48	0.43
3:F:30:ASP:OD1	3:F:32:SER:HB2	2.18	0.43
3:F:42:THR:O	3:F:77:PRO:HD2	2.19	0.43
1:D:98:ARG:O	1:D:101:ASN:HB2	2.18	0.43
1:D:272:ILE:HA	1:D:275:ASP:OD1	2.19	0.43
2:E:152:LYS:HB3	2:E:155:VAL:HB	2.00	0.43
1:A:326:ASN:HA	1:A:327:ASN:HA	1.79	0.43
3:F:44:LEU:HD11	3:F:82:MET:SD	2.57	0.43
3:F:75:HIS:HB3	3:F:80:LEU:CD1	2.40	0.43
2:E:23:VAL:HG11	2:E:96:ILE:HG12	2.00	0.43
1:D:273:ARG:HG2	1:D:277:LEU:HD12	2.01	0.43
3:C:84:GLU:O	3:C:85:GLU:HB2	2.18	0.43
2:E:167:GLN:CD	2:E:167:GLN:H	2.22	0.43
2:B:96:ILE:O	2:B:96:ILE:HG13	2.19	0.43
1:D:300:ALA:HB3	1:D:301:PRO:HD3	2.00	0.43
1:D:12:SER:OG	1:D:15:GLU:HG3	2.19	0.43
3:C:64:PHE:CB	3:C:71:ILE:HD12	2.48	0.43
1:A:28:LEU:HD22	2:B:307:LEU:HG	2.00	0.43
2:E:421:GLN:HB3	3:F:31:SER:HB2	2.00	0.43
2:E:6:GLY:HA3	7:E:844:HOH:O	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:131:LEU:CD1	1:A:131:LEU:N	2.82	0.43
1:A:224:TRP:CD1	1:A:282:ILE:HD11	2.54	0.43
2:B:7:LEU:N	2:B:8:PRO:HA	2.34	0.43
2:E:214:GLU:HB3	2:E:272:LEU:HD23	2.00	0.43
1:A:289:GLU:O	1:A:292:VAL:HG22	2.19	0.43
2:B:32:LEU:HD22	2:B:36:LEU:HG	2.01	0.43
2:E:114:ASN:OD1	2:E:136:LEU:HD11	2.19	0.43
1:D:256:ASP:HB3	1:D:257:PRO:HD2	2.01	0.43
1:D:177:GLU:HA	1:D:205:THR:HB	2.01	0.42
2:E:19:ARG:HG3	2:E:43:HIS:HB3	2.01	0.42
2:B:456:VAL:O	2:B:507:SER:HB3	2.19	0.42
2:B:378:SER:HA	2:B:383:ILE:HD12	2.01	0.42
2:B:81:LEU:CD2	2:B:87:ALA:HB3	2.50	0.42
1:A:75:ASP:N	1:A:76:PRO:CD	2.81	0.42
1:D:51:ILE:HD11	1:D:310:LEU:HD23	2.01	0.42
2:E:360:ASN:HB3	2:E:370:MET:SD	2.59	0.42
1:D:85:GLY:HA2	7:D:386:HOH:O	2.20	0.42
1:A:287:LEU:HA	1:A:288:PRO:HD2	1.87	0.42
2:E:118:ASN:ND2	2:E:120:ALA:H	2.17	0.42
3:C:38:VAL:HG12	3:C:39:LYS:N	2.34	0.42
2:E:34:LYS:HE3	2:E:35:ASN:OD1	2.19	0.42
3:F:42:THR:O	3:F:76:THR:HG22	2.20	0.42
2:B:461:VAL:HG13	2:B:490:LEU:HD22	2.01	0.42
2:E:423:ASN:C	2:E:423:ASN:OD1	2.56	0.42
2:E:540:LYS:HE2	2:E:540:LYS:HB3	1.92	0.42
1:A:227:GLU:O	1:A:231:ALA:HB3	2.20	0.42
3:C:76:THR:OG1	3:C:77:PRO:HD2	2.20	0.42
1:A:230:LYS:HZ3	1:A:230:LYS:HB3	1.84	0.42
1:A:162:HIS:CE1	7:A:396:HOH:O	2.72	0.42
3:F:45:LYS:HB2	3:F:73:ASP:HB3	2.02	0.42
1:A:160:GLY:HA3	1:A:295:CYS:HA	2.01	0.42
1:D:207:VAL:HG12	1:D:208:LYS:N	2.35	0.42
2:B:32:LEU:CD2	2:B:36:LEU:HG	2.50	0.42
1:D:140:VAL:O	1:D:144:GLN:HG3	2.20	0.42
1:D:297:SER:OG	1:D:298:GLU:N	2.52	0.42
1:D:122:PHE:O	1:D:125:GLN:HG2	2.20	0.42
1:D:157:ASP:HB2	1:D:164:TYR:CE2	2.52	0.42
1:A:334:MET:HE2	1:A:334:MET:HA	2.02	0.42
1:A:129:VAL:HG12	1:A:131:LEU:CD1	2.49	0.42
2:E:513:ASN:HB2	2:E:534:HIS:HB3	2.01	0.42
3:F:22:ILE:HD11	3:F:40:MET:HB2	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:28:LEU:O	1:D:31:GLN:HB3	2.20	0.42
2:E:23:VAL:HA	2:E:47:ILE:CG2	2.50	0.42
2:E:97:MET:HE1	2:E:120:ALA:C	2.40	0.42
2:E:81:LEU:HA	2:E:81:LEU:HD12	1.81	0.42
1:D:166:PHE:HE1	1:D:327:ASN:ND2	2.18	0.42
2:B:49:LEU:CD1	2:B:49:LEU:C	2.88	0.42
2:E:334:ALA:C	2:E:336:LYS:H	2.24	0.42
2:B:89:ILE:HG22	2:B:90:VAL:N	2.35	0.42
2:E:48:ASP:OD2	6:E:801:ATP:O2'	2.36	0.42
2:E:454:LEU:HD12	2:E:459:VAL:HG21	2.01	0.41
1:A:233:LEU:HD11	1:A:282:ILE:HD13	2.01	0.41
2:E:33:LEU:CD2	2:E:80:VAL:HG21	2.45	0.41
1:A:37:SER:HB3	1:A:318:LEU:HD22	2.02	0.41
2:E:46:LEU:HD13	2:E:47:ILE:N	2.35	0.41
2:E:491:ILE:HA	2:E:498:THR:CG2	2.42	0.41
2:B:178:THR:HG21	2:B:276:ARG:NH1	2.27	0.41
2:B:92:TYR:N	2:B:92:TYR:CD1	2.88	0.41
3:F:76:THR:HA	3:F:77:PRO:HD3	1.94	0.41
2:B:467:LYS:HZ2	2:B:544:PHE:HE2	1.68	0.41
2:B:484:ASP:OD1	2:B:485:GLY:N	2.54	0.41
2:E:528:LEU:HD12	2:E:529:LEU:H	1.85	0.41
1:D:244:GLN:HA	1:D:244:GLN:NE2	2.35	0.41
1:A:219:ALA:HB1	1:A:328:PHE:HE1	1.86	0.41
2:B:402:GLY:O	2:B:406:LEU:HG	2.21	0.41
1:D:40:LEU:HB2	1:D:126:PHE:CG	2.55	0.41
2:B:47:ILE:HD12	2:B:92:TYR:O	2.20	0.41
2:E:81:LEU:HD13	2:E:89:ILE:HD13	2.01	0.41
1:A:13:GLU:O	1:A:16:ALA:HB3	2.20	0.41
1:A:98:ARG:HH12	2:B:83:PHE:HB3	1.85	0.41
3:C:76:THR:HG23	3:C:79:GLU:H	1.85	0.41
2:E:359:ALA:O	2:E:363:MET:HG3	2.20	0.41
2:E:273:TRP:HA	2:E:276:ARG:HG3	2.02	0.41
2:B:165:PRO:HA	7:B:849:HOH:O	2.21	0.41
2:B:144:TYR:HA	2:B:390:THR:HG1	1.86	0.41
2:E:381:GLY:O	2:E:382:ASN:C	2.58	0.41
1:D:26:TRP:HE1	1:D:31:GLN:HE21	1.68	0.41
2:E:322:PHE:HE1	2:E:354:PHE:CE1	2.38	0.41
2:E:331:VAL:HG12	2:E:331:VAL:O	2.21	0.41
2:B:117:ASP:HA	3:C:95:THR:O	2.21	0.41
2:B:465:GLN:OE1	2:B:491:ILE:HG23	2.20	0.41
2:E:118:ASN:ND2	2:E:119:ARG:N	2.69	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:71:ILE:HD11	3:C:88:ILE:HG23	2.02	0.41
2:B:81:LEU:HD23	2:B:81:LEU:HA	1.90	0.41
2:B:185:CYS:SG	2:B:363:MET:HG2	2.60	0.41
1:A:152:LYS:HG2	1:A:152:LYS:H	1.64	0.41
3:C:18:GLU:HA	3:C:18:GLU:OE2	2.19	0.41
2:B:161:CYS:HA	2:B:441:CYS:SG	2.60	0.41
2:E:110:ILE:HG22	7:E:861:HOH:O	2.21	0.41
1:D:334:MET:HA	1:D:334:MET:CE	2.51	0.41
2:E:405:ILE:HG12	2:E:410:ILE:HD13	2.03	0.41
1:D:124:THR:HA	1:D:151:ILE:HD11	2.03	0.41
1:D:159:PHE:CG	1:D:246:LEU:HD13	2.56	0.41
2:E:20:VAL:HG12	2:E:111:LEU:HB3	2.03	0.41
2:E:119:ARG:HG3	2:E:120:ALA:N	2.36	0.40
1:D:66:LEU:C	1:D:66:LEU:HD23	2.42	0.40
2:B:414:ARG:HA	2:B:434:LEU:HG	2.04	0.40
3:F:22:ILE:O	3:F:37:LYS:HA	2.20	0.40
2:E:518:GLN:HG3	2:E:529:LEU:CD2	2.52	0.40
2:E:501:ASN:HB3	2:E:509:PHE:CZ	2.56	0.40
1:D:320:GLN:HE21	1:D:320:GLN:HB2	1.59	0.40
3:C:21:TYR:HA	3:C:21:TYR:HD2	1.81	0.40
2:B:170:PHE:HB3	2:B:175:ILE:HD11	2.02	0.40
1:D:331:PHE:HA	1:D:337:ASN:O	2.22	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	310/346 (90%)	264 (85%)	43 (14%)	3 (1%)	19	48
1	D	307/346 (89%)	264 (86%)	40 (13%)	3 (1%)	19	48
2	B	506/640 (79%)	433 (86%)	67 (13%)	6 (1%)	16	43

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	E	508/640 (79%)	452 (89%)	46 (9%)	10 (2%)	9	27
3	C	82/97 (84%)	70 (85%)	9 (11%)	3 (4%)	4	12
3	F	82/97 (84%)	68 (83%)	10 (12%)	4 (5%)	3	7
All	All	1795/2166 (83%)	1551 (86%)	215 (12%)	29 (2%)	12	34

All (29) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	8	PRO
1	D	205	THR
2	B	7	LEU
2	B	205	GLU
2	B	206	VAL
3	C	15	ASP
3	C	21	TYR
1	D	97	GLU
2	E	214	GLU
2	E	217	TRP
2	E	498	THR
2	E	549	ASP
3	F	21	TYR
3	F	61	SER
3	F	83	GLU
1	A	96	LEU
2	E	278	PRO
3	F	43	HIS
1	A	297	SER
2	E	540	LYS
1	A	232	ALA
1	D	262	TYR
2	E	367	SER
2	B	472	LYS
3	C	40	MET
2	E	84	TYR
2	E	213	PRO
2	E	499	GLU
2	B	337	GLY

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	270/296 (91%)	258 (96%)	12 (4%)	35	67
1	D	267/296 (90%)	257 (96%)	10 (4%)	41	74
2	B	442/551 (80%)	419 (95%)	23 (5%)	29	60
2	E	443/551 (80%)	421 (95%)	22 (5%)	30	61
3	C	75/87 (86%)	71 (95%)	4 (5%)	28	58
3	F	75/87 (86%)	68 (91%)	7 (9%)	11	29
All	All	1572/1868 (84%)	1494 (95%)	78 (5%)	30	61

All (78) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	25	LEU
1	A	45	LYS
1	A	69	GLU
1	A	79	GLN
1	A	83	ARG
1	A	105	MET
1	A	124	THR
1	A	159	PHE
1	A	177	GLU
1	A	230	LYS
1	A	275	ASP
1	A	297	SER
2	B	11	LEU
2	B	32	LEU
2	B	46	LEU
2	B	49	LEU
2	B	66	LYS
2	B	88	ASN
2	B	119	ARG
2	B	138	GLU
2	B	205	GLU
2	B	256	THR

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Mol	Chain	Res	Type
2	B	270	ASP
2	B	272	LEU
2	B	275	LYS
2	B	290	GLN
2	B	362	ARG
2	B	414	ARG
2	B	447	LYS
2	B	479	ASP
2	B	483	GLU
2	B	484	ASP
2	B	486	LYS
2	B	490	LEU
2	B	541	ASP
3	C	21	TYR
3	C	26	VAL
3	C	43	HIS
3	C	53	GLN
1	D	26	TRP
1	D	28	LEU
1	D	79	GLN
1	D	159	PHE
1	D	216	VAL
1	D	261	THR
1	D	267	GLU
1	D	285	ASP
1	D	294	TYR
1	D	320	GLN
2	E	32	LEU
2	E	45	ASP
2	E	49	LEU
2	E	93	HIS
2	E	96	ILE
2	E	102	ASN
2	E	161	CYS
2	E	197	PHE
2	E	200	GLU
2	E	206	VAL
2	E	256	THR
2	E	269	MET
2	E	274	ARG
2	E	288	GLN
2	E	305	LEU

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Mol	Chain	Res	Type
2	E	454	LEU
2	E	455	ASN
2	E	481	GLN
2	E	492	SER
2	E	498	THR
2	E	512	ARG
2	E	520	ASP
3	F	18	GLU
3	F	21	TYR
3	F	43	HIS
3	F	55	GLN
3	F	59	MET
3	F	76	THR
3	F	86	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (42) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	70	GLN
1	A	149	ASN
1	A	162	HIS
1	A	244	GLN
2	B	56	ASN
2	B	64	GLN
2	B	67	HIS
2	B	88	ASN
2	B	123	ASN
2	B	167	GLN
2	B	194	ASN
2	B	195	GLN
2	B	204	GLN
2	B	288	GLN
2	B	311	GLN
2	B	412	GLN
2	B	457	HIS
3	C	55	GLN
3	C	74	ASN
3	C	75	HIS
3	C	94	GLN
1	D	31	GLN
1	D	101	ASN
1	D	244	GLN

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Mol	Chain	Res	Type
1	D	320	GLN
2	E	43	HIS
2	E	102	ASN
2	E	118	ASN
2	E	204	GLN
2	E	288	GLN
2	E	311	GLN
2	E	421	GLN
2	E	455	ASN
2	E	457	HIS
2	E	502	ASN
3	F	35	HIS
3	F	43	HIS
3	F	55	GLN
3	F	60	ASN
3	F	69	GLN
3	F	92	GLN
3	F	94	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 6 ligands modelled in this entry, 4 are monoatomic - leaving 2 for Mogul analysis.

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	$\# Z > 2$
6	ATP	B	802	4	24,33,33	1.28	3 (12%)	31,52,52	2.62	7 (22%)
6	ATP	E	801	4	24,33,33	1.18	2 (8%)	31,52,52	2.67	7 (22%)

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
6	ATP	B	802	4	-	0/18/38/38	0/3/3/3
6	ATP	E	801	4	-	0/18/38/38	0/3/3/3

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	E	801	ATP	C2-N1	2.02	1.37	1.33
6	B	802	ATP	C4-N3	2.38	1.39	1.35
6	B	802	ATP	C2-N1	2.59	1.38	1.33
6	E	801	ATP	C2-N3	3.60	1.38	1.32
6	B	802	ATP	C2-N3	3.76	1.38	1.32

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	B	802	ATP	N3-C2-N1	-11.69	119.94	128.89
6	E	801	ATP	N3-C2-N1	-11.61	120.00	128.89
6	B	802	ATP	C4-C5-N7	-4.70	105.16	109.48
6	E	801	ATP	C4-C5-N7	-4.51	105.33	109.48
6	B	802	ATP	PB-O3B-PG	-3.19	121.96	132.67
6	E	801	ATP	C4'-O4'-C1'	-3.02	106.40	109.72
6	E	801	ATP	O4'-C1'-N9	-2.60	102.66	108.10
6	B	802	ATP	C4'-O4'-C1'	-2.28	107.22	109.72
6	B	802	ATP	O4'-C1'-N9	-2.20	103.49	108.10
6	E	801	ATP	PB-O3B-PG	-2.17	125.38	132.67
6	E	801	ATP	N6-C6-N1	-2.05	114.81	119.20
6	B	802	ATP	O2'-C2'-C3'	2.34	119.43	111.83
6	B	802	ATP	C2'-C1'-N9	2.48	118.08	114.29
6	E	801	ATP	C2'-C1'-N9	4.40	121.02	114.29

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	E	801	ATP	1	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	314/346 (90%)	-0.20	9 (2%)	55 48	13, 41, 82, 112	0
1	D	311/346 (89%)	-0.28	4 (1%)	79 75	11, 39, 73, 94	0
2	B	512/640 (80%)	-0.00	26 (5%)	32 24	17, 53, 101, 131	0
2	E	514/640 (80%)	-0.01	30 (5%)	26 20	15, 44, 102, 133	0
3	C	84/97 (86%)	0.17	5 (5%)	25 19	26, 63, 91, 101	0
3	F	84/97 (86%)	1.14	21 (25%)	1 0	29, 86, 107, 115	0
All	All	1819/2166 (83%)	-0.02	95 (5%)	31 24	11, 46, 97, 133	0

All (95) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	F	19	GLY	6.5
3	F	20	GLU	5.9
2	B	217	TRP	5.4
2	E	290	GLN	5.1
1	A	204	THR	4.9
1	D	204	THR	4.9
3	F	16	LYS	4.6
2	E	550	ALA	4.6
2	B	5	ARG	4.6
3	F	21	TYR	4.5
2	E	217	TRP	4.5
2	B	494	GLU	4.5
2	E	216	ALA	4.3
2	B	549	ASP	4.3
2	B	495	GLU	4.3
2	B	305	LEU	4.1
2	E	166	THR	4.0
2	E	274	ARG	3.9
3	F	18	GLU	3.9

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Mol	Chain	Res	Type	RSRZ
2	B	550	ALA	3.8
2	B	496	GLY	3.8
2	B	541	ASP	3.8
3	F	56	GLY	3.7
2	B	218	GLU	3.7
2	E	218	GLU	3.7
1	A	203	GLU	3.6
2	E	275	LYS	3.6
2	B	542	VAL	3.6
2	B	548	GLY	3.5
3	F	74	ASN	3.5
2	B	537	ASP	3.4
2	B	274	ARG	3.4
2	E	541	ASP	3.3
2	E	167	GLN	3.3
3	F	59	MET	3.2
2	E	165	PRO	3.2
2	E	215	ALA	3.2
2	E	238	ILE	3.2
3	F	78	LYS	3.1
2	E	540	LYS	3.1
2	E	210	ARG	3.1
3	F	39	LYS	3.1
3	F	31	SER	3.1
1	D	205	THR	3.0
1	A	205	THR	3.0
2	E	339	GLY	2.9
2	E	271	LYS	2.9
1	A	179	THR	2.9
2	E	343	ILE	2.9
3	F	60	ASN	2.9
2	E	276	ARG	2.8
1	A	228	LYS	2.8
3	C	16	LYS	2.8
2	E	265	TYR	2.8
3	C	21	TYR	2.8
3	C	17	LYS	2.7
3	C	20	GLU	2.7
2	B	491	ILE	2.7
2	B	338	ASP	2.6
2	E	9	ARG	2.5
2	E	340	ALA	2.5

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Mol	Chain	Res	Type	RSRZ
2	B	275	LYS	2.5
1	A	178	LYS	2.5
2	B	369	ASN	2.5
2	E	246	SER	2.5
3	F	79	GLU	2.5
1	D	9	GLY	2.4
3	F	85	GLU	2.4
2	E	169	THR	2.4
2	B	290	GLN	2.4
1	D	225	SER	2.3
3	F	43	HIS	2.3
2	B	337	GLY	2.3
2	B	306	GLY	2.3
2	B	167	GLN	2.3
3	F	17	LYS	2.3
3	C	74	ASN	2.3
2	E	549	ASP	2.3
2	B	4	SER	2.2
2	B	243	TRP	2.2
2	E	495	GLU	2.2
3	F	84	GLU	2.2
2	E	338	ASP	2.2
2	E	4	SER	2.2
3	F	37	LYS	2.2
2	B	265	TYR	2.1
2	B	264	ARG	2.1
1	A	263	GLU	2.1
2	E	172	GLY	2.1
3	F	38	VAL	2.1
1	A	227	GLU	2.1
1	A	235	ARG	2.1
3	F	24	LEU	2.0
3	F	73	ASP	2.0
2	E	337	GLY	2.0

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

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(\AA^2)	Q<0.9
6	ATP	B	802	31/31	0.98	0.10	-1.19	19,28,34,35	0
6	ATP	E	801	31/31	0.99	0.10	-1.35	20,26,29,32	0
5	ZN	B	642	1/1	0.99	0.07	-2.13	37,37,37,37	0
5	ZN	E	642	1/1	0.99	0.04	-2.43	31,31,31,31	0
4	MG	B	641	1/1	0.96	0.04	-	16,16,16,16	0
4	MG	E	641	1/1	0.99	0.10	-	31,31,31,31	0

6.5 Other polymers [i](#)

There are no such residues in this entry.