



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 07:03 PM GMT

PDB ID : 1DV2
Title : The structure of biotin carboxylase, mutant E288K, complexed with ATP
Authors : Thoden, J.B.; Blanchard, C.Z.; Holden, H.M.; Waldrop, G.L.
Deposited on : 2000-01-19
Resolution : 2.50 Å(reported)

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

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

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

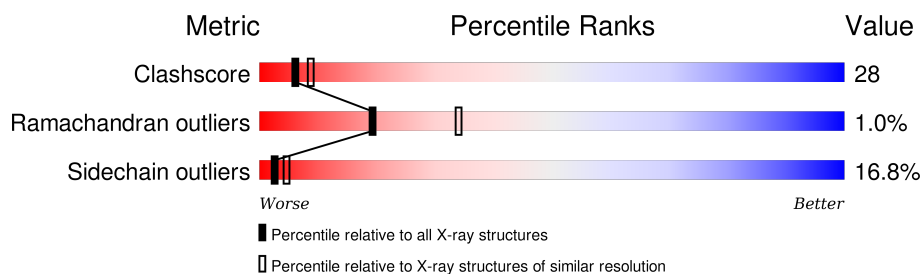
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	102246	4242 (2.50-2.50)
Ramachandran outliers	100387	4156 (2.50-2.50)
Sidechain outliers	100360	4158 (2.50-2.50)

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.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	452	
1	B	452	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	ATP	A	1000	-	-	X	-

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 7113 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.

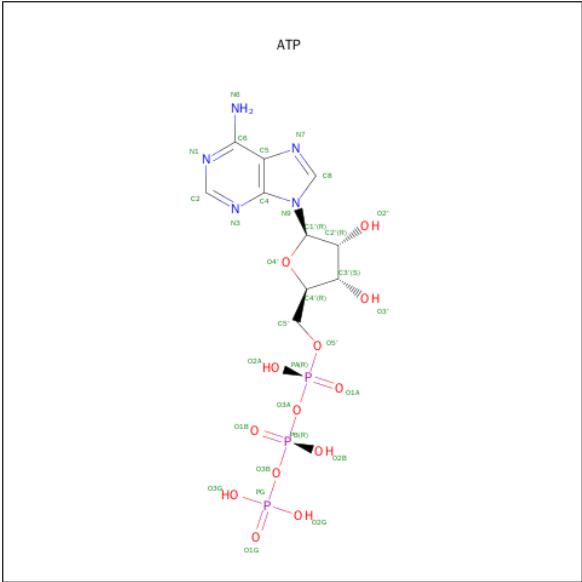
- Molecule 1 is a protein called BIOTIN CARBOXYLASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	450	Total	C	N	O	S	0	1	0
			3469	2184	624	639	22			
1	B	448	Total	C	N	O	S	0	0	0
			3452	2175	619	636	22			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1A	HIS	-	INSERTED	UNP P24182
A	1B	SER	-	INSERTED	UNP P24182
A	1C	GLY	-	INSERTED	UNP P24182
B	1A	HIS	-	INSERTED	UNP P24182
B	1B	SER	-	INSERTED	UNP P24182
B	1C	GLY	-	INSERTED	UNP P24182
A	288	LYS	GLU	MUTATION	UNP P24182
B	288	LYS	GLU	MUTATION	UNP P24182

- Molecule 2 is ADENOSINE-5'-TRIPHOSPHATE (three-letter code: ATP) (formula: C₁₀H₁₆N₅O₁₃P₃).



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

- Molecule 3 is water.

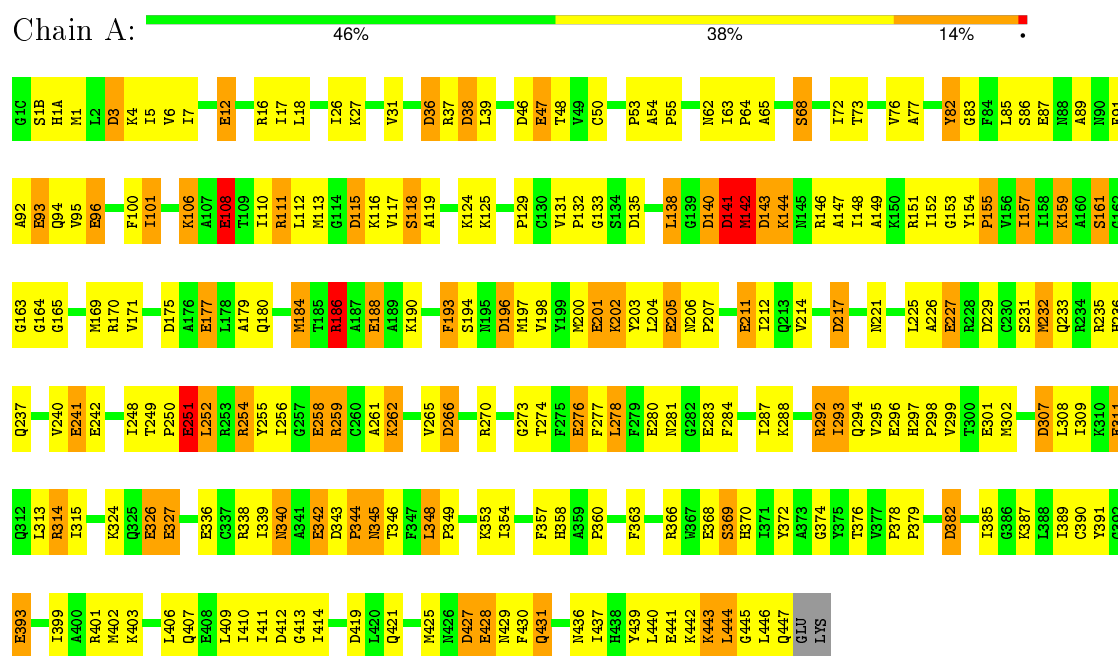
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	82	Total	O	0	0
			82	82		
3	B	48	Total	O	0	0
			48	48		

3 Residue-property plots

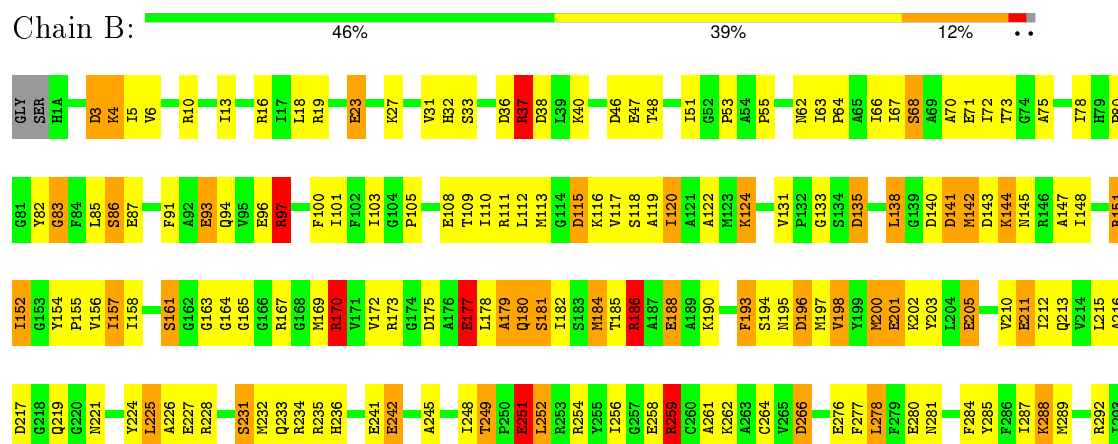
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according 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.

Note EDS was not executed.

• Molecule 1: BIOTIN CARBOXYLASE



• Molecule 1: BIOTIN CARBOXYLASE



S369	Q294	H370	Y295	P378	E301	D307	L308	K387	C390	D396	I399	A400	R401	K403	L409	T416	D419	L420	Q421	I422	R423	I424	M425	N426	D427	E428	M429	F430	Q431	T435	M436	L437	H438	Y439	L440	E441	K442	K443	L444	G445	L446	Q447	GLU	LYS	E368		
H371	E296	P298	Y380	Y381	I303	I309	K310	E311	Q312	L313	R314	A315	K319	P320	L321	S322	I323	K324	Q325	E326	E327	Y330	H333	A334	V335	E336	C337	R338	I339	N340	A341	E342	D343	P344	R345	T346	F347	L348	P349	S350	K353	H358	G364	V365	R366	V367	E368

4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section will therefore be incomplete.

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	81.30 Å 115.50 Å 122.40 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 2.50	Depositor
% Data completeness (in resolution range)	92.6 (30.00-2.50)	Depositor
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	TNT V. 5-E	Depositor
R, R_{free}	0.171 , 0.203	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	7113	wwPDB-VP
Average B, all atoms (Å ²)	37.0	wwPDB-VP

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: 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	1.02	27/3537 (0.8%)	1.48	49/4771 (1.0%)
1	B	0.98	27/3516 (0.8%)	1.40	32/4744 (0.7%)
All	All	1.00	54/7053 (0.8%)	1.44	81/9515 (0.9%)

All (54) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	47	GLU	CD-OE2	7.32	1.33	1.25
1	A	342	GLU	CD-OE2	7.01	1.33	1.25
1	A	211	GLU	CD-OE2	6.79	1.33	1.25
1	B	342	GLU	CD-OE2	6.69	1.33	1.25
1	B	177	GLU	CD-OE2	6.62	1.32	1.25
1	B	47	GLU	CD-OE2	6.57	1.32	1.25
1	A	326	GLU	CD-OE2	6.55	1.32	1.25
1	A	441	GLU	CD-OE2	6.49	1.32	1.25
1	A	428	GLU	CD-OE2	6.37	1.32	1.25
1	B	188	GLU	CD-OE2	6.36	1.32	1.25
1	A	188	GLU	CD-OE2	6.27	1.32	1.25
1	B	71	GLU	CD-OE2	6.26	1.32	1.25
1	A	276	GLU	CD-OE2	6.24	1.32	1.25
1	B	211	GLU	CD-OE2	6.22	1.32	1.25
1	A	201	GLU	CD-OE2	6.17	1.32	1.25
1	B	326	GLU	CD-OE2	6.16	1.32	1.25
1	B	276	GLU	CD-OE2	6.13	1.32	1.25
1	A	93	GLU	CD-OE2	6.12	1.32	1.25
1	A	205	GLU	CD-OE2	6.11	1.32	1.25
1	A	96	GLU	CD-OE2	6.08	1.32	1.25
1	B	441	GLU	CD-OE2	6.02	1.32	1.25
1	A	251	GLU	CD-OE2	6.01	1.32	1.25
1	B	251	GLU	CD-OE2	5.95	1.32	1.25
1	B	428	GLU	CD-OE2	5.92	1.32	1.25

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	12	GLU	CD-OE2	5.86	1.32	1.25
1	B	93	GLU	CD-OE2	5.83	1.32	1.25
1	B	23	GLU	CD-OE2	5.81	1.32	1.25
1	B	311	GLU	CD-OE2	5.81	1.32	1.25
1	B	296	GLU	CD-OE1	-5.79	1.19	1.25
1	B	201	GLU	CD-OE2	5.77	1.31	1.25
1	B	242	GLU	CD-OE2	5.72	1.31	1.25
1	B	296	GLU	CD-OE2	5.70	1.31	1.25
1	B	280	GLU	CD-OE2	5.66	1.31	1.25
1	A	368	GLU	CD-OE2	5.63	1.31	1.25
1	A	311	GLU	CD-OE2	5.61	1.31	1.25
1	A	258	GLU	CD-OE2	5.60	1.31	1.25
1	B	368	GLU	CD-OE2	5.58	1.31	1.25
1	A	242	GLU	CD-OE2	5.55	1.31	1.25
1	A	393	GLU	CD-OE2	5.55	1.31	1.25
1	A	177	GLU	CD-OE2	5.53	1.31	1.25
1	A	301	GLU	CD-OE2	5.50	1.31	1.25
1	B	205	GLU	CD-OE2	5.44	1.31	1.25
1	B	87	GLU	CD-OE2	5.41	1.31	1.25
1	B	241	GLU	CD-OE2	5.39	1.31	1.25
1	B	227	GLU	CD-OE2	5.38	1.31	1.25
1	A	283	GLU	CD-OE2	5.25	1.31	1.25
1	B	96	GLU	CD-OE2	5.25	1.31	1.25
1	A	108	GLU	CD-OE2	5.21	1.31	1.25
1	A	87	GLU	CD-OE2	5.17	1.31	1.25
1	B	108	GLU	CD-OE2	5.14	1.31	1.25
1	B	327	GLU	CD-OE2	5.14	1.31	1.25
1	A	327	GLU	CD-OE2	5.13	1.31	1.25
1	A	227	GLU	CD-OE2	5.03	1.31	1.25
1	A	241	GLU	CD-OE2	5.02	1.31	1.25

All (81) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	97	ARG	NE-CZ-NH1	15.59	128.09	120.30
1	B	97	ARG	NE-CZ-NH2	-11.66	114.47	120.30
1	A	270	ARG	NE-CZ-NH1	9.95	125.27	120.30
1	A	16	ARG	NE-CZ-NH1	9.79	125.19	120.30
1	B	37	ARG	NE-CZ-NH1	9.18	124.89	120.30
1	B	175	ASP	CB-CG-OD1	8.64	126.08	118.30
1	B	175	ASP	CB-CG-OD2	-8.22	110.90	118.30
1	A	259	ARG	NE-CZ-NH1	7.87	124.23	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	16	ARG	NE-CZ-NH2	-7.83	116.39	120.30
1	A	412	ASP	CB-CG-OD2	-7.45	111.59	118.30
1	B	350	SER	N-CA-CB	7.28	121.41	110.50
1	A	46	ASP	CB-CG-OD2	-7.15	111.86	118.30
1	B	259	ARG	NE-CZ-NH1	7.11	123.86	120.30
1	A	427	ASP	CB-CG-OD1	7.10	124.69	118.30
1	A	259	ARG	NE-CZ-NH2	-7.08	116.76	120.30
1	A	266	ASP	CB-CG-OD2	-7.01	111.99	118.30
1	A	307	ASP	CB-CG-OD1	6.98	124.58	118.30
1	B	366	ARG	NE-CZ-NH2	-6.92	116.84	120.30
1	B	141	ASP	CB-CG-OD2	-6.90	112.09	118.30
1	A	382	ASP	CB-CG-OD2	-6.80	112.18	118.30
1	A	419	ASP	CB-CG-OD2	-6.71	112.26	118.30
1	A	46	ASP	CB-CG-OD1	6.65	124.28	118.30
1	B	196	ASP	CB-CG-OD2	-6.56	112.39	118.30
1	B	228	ARG	NE-CZ-NH1	6.51	123.56	120.30
1	A	135	ASP	CB-CG-OD2	-6.51	112.44	118.30
1	B	46	ASP	CB-CG-OD1	6.47	124.12	118.30
1	A	427	ASP	CB-CG-OD2	-6.45	112.49	118.30
1	A	143	ASP	CB-CG-OD2	-6.33	112.60	118.30
1	B	135	ASP	CB-CG-OD1	6.33	123.99	118.30
1	A	314	ARG	NE-CZ-NH1	6.27	123.44	120.30
1	B	115	ASP	CB-CG-OD2	-6.26	112.66	118.30
1	B	3	ASP	CB-CG-OD2	-6.25	112.67	118.30
1	B	196	ASP	CB-CG-OD1	6.24	123.92	118.30
1	A	217	ASP	CB-CG-OD2	-6.24	112.68	118.30
1	B	234	ARG	NE-CZ-NH1	6.24	123.42	120.30
1	A	343	ASP	CB-CG-OD2	-6.15	112.76	118.30
1	A	292	ARG	NE-CZ-NH1	6.03	123.32	120.30
1	A	235	ARG	NE-CZ-NH1	5.98	123.29	120.30
1	A	140	ASP	CB-CG-OD2	-5.98	112.92	118.30
1	B	396	ASP	CB-CG-OD1	5.97	123.68	118.30
1	A	175	ASP	CB-CG-OD1	5.94	123.65	118.30
1	B	266	ASP	CB-CG-OD2	-5.92	112.97	118.30
1	B	170	ARG	NE-CZ-NH2	-5.90	117.35	120.30
1	B	401	ARG	NE-CZ-NH1	5.88	123.24	120.30
1	A	3	ASP	CB-CG-OD2	-5.86	113.03	118.30
1	A	143	ASP	CB-CG-OD1	5.81	123.53	118.30
1	A	141	ASP	N-CA-CB	5.77	120.99	110.60
1	B	307	ASP	CB-CG-OD2	-5.76	113.11	118.30
1	A	307	ASP	CB-CG-OD2	-5.75	113.12	118.30
1	B	141	ASP	CB-CG-OD1	5.75	123.47	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	196	ASP	CB-CG-OD2	-5.74	113.13	118.30
1	A	36	ASP	CB-CG-OD2	-5.72	113.15	118.30
1	A	115	ASP	CB-CG-OD2	-5.70	113.17	118.30
1	A	76	VAL	CA-CB-CG2	-5.70	102.35	110.90
1	A	140	ASP	CB-CG-OD1	5.70	123.43	118.30
1	A	38	ASP	CB-CG-OD2	-5.62	113.24	118.30
1	A	186	ARG	NE-CZ-NH1	5.60	123.10	120.30
1	B	396	ASP	CB-CG-OD2	-5.59	113.27	118.30
1	A	390	CYS	N-CA-CB	5.58	120.65	110.60
1	A	382	ASP	CB-CG-OD1	5.58	123.32	118.30
1	B	143	ASP	CB-CG-OD2	-5.57	113.28	118.30
1	A	135	ASP	CB-CG-OD1	5.57	123.31	118.30
1	A	266	ASP	CB-CG-OD1	5.54	123.29	118.30
1	A	284	PHE	CB-CG-CD1	-5.54	116.92	120.80
1	A	229	ASP	CB-CG-OD1	5.53	123.28	118.30
1	A	3	ASP	CB-CG-OD1	5.50	123.25	118.30
1	B	36	ASP	CB-CG-OD2	-5.48	113.37	118.30
1	A	155	PRO	N-CA-CB	5.43	109.82	103.30
1	A	308	LEU	CB-CA-C	5.40	120.45	110.20
1	A	235	ARG	NE-CZ-NH2	-5.39	117.60	120.30
1	B	83	GLY	N-CA-C	5.29	126.31	113.10
1	A	376	THR	CA-CB-CG2	-5.25	105.04	112.40
1	B	135	ASP	CB-CG-OD2	-5.23	113.59	118.30
1	B	38	ASP	CB-CG-OD2	-5.21	113.61	118.30
1	B	10	ARG	NE-CZ-NH1	5.18	122.89	120.30
1	A	419	ASP	CB-CG-OD1	5.12	122.91	118.30
1	A	344	PRO	N-CA-CB	5.10	109.42	103.30
1	A	343	ASP	CB-CG-OD1	5.09	122.89	118.30
1	B	186	ARG	NE-CZ-NH1	5.09	122.84	120.30
1	B	419	ASP	CB-CG-OD2	-5.04	113.77	118.30
1	A	83	GLY	C-N-CA	-5.03	109.12	121.70

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3469	0	3498	188	0
1	B	3452	0	3481	207	0
2	A	31	0	12	10	0
2	B	31	0	12	8	0
3	A	82	0	0	3	0
3	B	48	0	0	4	0
All	All	7113	0	7003	394	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 28.

All (394) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:179:ALA:HB3	1:B:180:GLN:HE21	1.19	1.00
1:B:440:LEU:HG	1:B:444:LEU:HD22	1.40	0.97
1:B:131:VAL:HG22	1:B:285:TYR:HB3	1.45	0.95
1:A:117:VAL:HG21	1:A:197:MET:HE3	1.48	0.95
1:B:278:LEU:HD22	1:B:287:ILE:HD11	1.51	0.93
1:B:278:LEU:HD13	1:B:287:ILE:HD11	1.52	0.91
1:A:54:ALA:HB3	1:A:55:PRO:HD3	1.54	0.89
1:A:133:GLY:HA2	1:A:152:ILE:HD11	1.55	0.87
1:B:236:HIS:CE1	2:B:1001:ATP:H5'2	2.11	0.85
1:B:72:ILE:HD12	1:B:73:THR:HG23	1.58	0.84
1:B:154:TYR:HE1	1:B:172:VAL:HG12	1.41	0.84
1:B:72:ILE:CD1	1:B:73:THR:HG23	2.06	0.84
1:B:133:GLY:HA2	1:B:152:ILE:HD11	1.60	0.84
1:A:72:ILE:CD1	1:A:73:THR:HG23	2.09	0.83
1:A:72:ILE:HD12	1:A:73:THR:N	1.94	0.83
1:B:440:LEU:HG	1:B:444:LEU:CD2	2.07	0.83
1:B:419:ASP:HB3	1:B:423:ARG:NH1	1.94	0.82
1:B:142:MET:HA	1:B:145:ASN:HB2	1.62	0.82
1:B:154:TYR:CE1	1:B:172:VAL:HG12	2.16	0.81
1:B:340:ASN:HD22	1:B:384:MET:HA	1.44	0.81
1:A:133:GLY:HA2	1:A:152:ILE:CD1	2.12	0.79
1:B:297:HIS:CG	1:B:298:PRO:HD3	2.17	0.79
1:B:323:ILE:HD12	1:B:323:ILE:H	1.48	0.78
1:B:179:ALA:HB3	1:B:180:GLN:NE2	1.96	0.77
1:B:369:SER:OG	1:B:371:ILE:HG12	1.84	0.77
1:B:249:THR:OG1	1:B:251:GLU:HG2	1.85	0.76
1:B:151:ARG:HG2	1:B:152:ILE:N	1.99	0.76
1:B:236:HIS:HE1	2:B:1001:ATP:H5'2	1.48	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:278:LEU:CD2	1:B:287:ILE:HD11	2.16	0.75
1:A:117:VAL:CG2	1:A:197:MET:HE3	2.16	0.75
1:A:298:PRO:O	1:A:302:MET:HG2	1.88	0.74
1:B:278:LEU:HD13	1:B:287:ILE:CD1	2.17	0.73
1:A:91:PHE:O	1:A:95:VAL:HG23	1.88	0.73
1:B:278:LEU:CD1	1:B:287:ILE:HD11	2.18	0.72
1:B:278:LEU:HD22	1:B:287:ILE:CD1	2.19	0.72
1:A:309:ILE:O	1:A:313:LEU:HG	1.89	0.72
1:B:217:ASP:OD2	1:B:221:ASN:HB2	1.90	0.71
1:A:250:PRO:O	1:A:254:ARG:HD3	1.89	0.71
1:A:370:HIS:H	1:A:370:HIS:CD2	2.07	0.71
1:B:37:ARG:HG3	1:B:37:ARG:HH11	1.55	0.70
1:B:441:GLU:HG2	1:B:446:LEU:HD13	1.73	0.70
1:A:72:ILE:HD12	1:A:73:THR:HG23	1.72	0.70
1:A:324:LYS:HB2	1:A:327:GLU:OE2	1.92	0.69
1:A:36:ASP:HB3	1:A:39:LEU:CD1	2.22	0.69
1:A:372:TYR:HB3	1:B:358:HIS:CE1	2.27	0.69
1:A:112:LEU:HG	1:A:113:MET:CE	2.22	0.69
1:A:345:ASN:HD22	1:A:345:ASN:N	1.89	0.69
1:A:295:VAL:O	1:A:387:LYS:HE3	1.91	0.69
1:B:435:THR:HB	3:B:1316:HOH:O	1.92	0.69
1:B:72:ILE:HD12	1:B:73:THR:N	2.09	0.68
1:B:346:THR:OG1	1:B:348:LEU:HD12	1.94	0.67
1:B:419:ASP:O	1:B:423:ARG:HD2	1.94	0.67
1:B:323:ILE:HD12	1:B:323:ILE:N	2.09	0.67
1:A:278:LEU:N	1:A:287:ILE:HD11	2.10	0.66
1:B:252:LEU:HD22	1:B:284:PHE:HE1	1.59	0.66
1:A:427:ASP:OD2	1:A:429:ASN:HB2	1.96	0.66
1:B:256:ILE:HD11	1:B:277:PHE:CE2	2.31	0.65
1:A:440:LEU:HG	1:A:444:LEU:HD22	1.78	0.65
1:B:184:MET:O	1:B:188:GLU:HG3	1.96	0.65
1:A:82:TYR:CZ	1:A:295:VAL:HG22	2.32	0.65
1:A:93:GLU:OE1	1:A:111:ARG:NH1	2.29	0.65
1:A:138:LEU:HD21	1:A:200:MET:HB2	1.79	0.64
1:A:63:ILE:HB	1:A:64:PRO:HD3	1.78	0.64
1:B:217:ASP:CG	1:B:221:ASN:HB2	2.18	0.64
1:B:288:LYS:NZ	2:B:1001:ATP:O3G	2.31	0.64
1:A:403:LYS:O	1:A:407:GLN:HG3	1.98	0.64
1:B:112:LEU:HG	1:B:113:MET:CE	2.27	0.64
1:A:231:SER:O	1:A:437:ILE:HA	1.96	0.64
1:B:80:PRO:HB2	1:B:86:SER:HA	1.80	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:142:MET:HE3	1:A:179:ALA:HA	1.80	0.63
1:A:274:THR:CB	1:A:294:GLN:HE21	2.10	0.63
1:B:112:LEU:HG	1:B:113:MET:HE2	1.78	0.63
1:B:113:MET:CE	1:B:119:ALA:HA	2.29	0.62
1:B:133:GLY:CA	1:B:152:ILE:HD11	2.29	0.62
1:B:116:LYS:O	1:B:120:ILE:HG13	1.99	0.62
1:A:311:GLU:OE2	1:A:314:ARG:NH1	2.33	0.61
1:A:207:PRO:CA	1:A:280:GLU:HG3	2.29	0.61
1:B:259:ARG:HG3	1:B:259:ARG:HH11	1.65	0.61
1:B:138:LEU:HD23	1:B:182:ILE:HG12	1.82	0.61
1:B:242:GLU:OE2	1:B:333:HIS:NE2	2.32	0.61
1:B:4:LYS:HB2	1:B:27:LYS:HB2	1.82	0.61
1:B:53:PRO:HB2	1:B:55:PRO:HD2	1.83	0.61
1:A:12:GLU:OE2	1:A:387:LYS:NZ	2.34	0.61
1:B:186:ARG:HG2	1:B:198:VAL:HG13	1.83	0.60
1:A:36:ASP:HB3	1:A:39:LEU:HD12	1.83	0.60
1:B:427:ASP:OD1	1:B:443:LYS:HE2	2.01	0.60
1:A:184:MET:O	1:A:188:GLU:HG3	2.02	0.60
1:B:212:ILE:N	1:B:212:ILE:HD12	2.17	0.60
1:A:115:ASP:HB3	1:A:118:SER:OG	2.02	0.60
1:B:245:ALA:HB3	1:B:248:ILE:HG13	1.83	0.60
1:A:206:ASN:HD22	1:A:436:ASN:ND2	2.00	0.60
1:A:190:LYS:O	1:A:194:SER:HA	2.00	0.60
1:A:288:LYS:NZ	2:A:1000:ATP:O3G	2.31	0.60
1:B:154:TYR:HE1	1:B:172:VAL:CG1	2.14	0.59
1:B:19:ARG:HD2	3:B:1307:HOH:O	2.01	0.59
1:B:298:PRO:O	1:B:302:MET:HG2	2.03	0.59
1:A:169:MET:HE3	2:A:1000:ATP:H5'1	1.84	0.59
1:A:112:LEU:CD2	1:A:113:MET:HE3	2.31	0.59
1:A:5:ILE:HG23	1:A:26:ILE:CG2	2.32	0.59
1:B:200:MET:HG3	1:B:201:GLU:N	2.17	0.59
1:B:425:MET:O	1:B:431:GLN:NE2	2.36	0.59
1:B:427:ASP:OD2	1:B:429:ASN:HB2	2.03	0.59
1:B:441:GLU:O	1:B:446:LEU:HB2	2.02	0.58
1:B:232:MET:HE2	3:B:1316:HOH:O	2.03	0.58
1:B:115:ASP:HB3	1:B:118:SER:HB2	1.84	0.58
1:A:249:THR:OG1	1:A:251:GLU:HG2	2.03	0.58
1:A:254:ARG:O	1:A:258:GLU:HG3	2.04	0.58
1:A:358:HIS:O	1:A:409:LEU:HD12	2.04	0.58
1:A:164:GLY:CA	1:A:193:PHE:HE2	2.17	0.58
1:A:379:PRO:HD3	3:A:1228:HOH:O	2.03	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:344:PRO:HG3	1:B:416:THR:O	2.04	0.58
1:B:145:ASN:HD22	1:B:182:ILE:HD13	1.67	0.58
1:B:346:THR:CB	1:B:348:LEU:HD12	2.34	0.58
1:A:154:TYR:HB3	1:A:155:PRO:HA	1.85	0.58
1:B:148:ILE:HA	1:B:151:ARG:HD2	1.86	0.58
1:A:164:GLY:HA3	1:A:193:PHE:CE2	2.39	0.58
1:B:172:VAL:HG13	1:B:177:GLU:HB2	1.85	0.57
1:B:145:ASN:ND2	1:B:182:ILE:HD13	2.18	0.57
1:A:63:ILE:CB	1:A:64:PRO:HD3	2.34	0.57
1:A:236:HIS:NE2	2:A:1000:ATP:O2G	2.37	0.57
1:B:256:ILE:HD11	1:B:277:PHE:CZ	2.39	0.57
1:A:148:ILE:O	1:A:151:ARG:HB3	2.02	0.57
1:A:214:VAL:HG22	1:A:273:GLY:O	2.04	0.57
1:B:133:GLY:HA2	1:B:152:ILE:CD1	2.32	0.57
1:B:259:ARG:HH11	1:B:259:ARG:CG	2.16	0.57
1:B:370:HIS:CD2	1:B:370:HIS:H	2.22	0.57
1:A:149:ALA:O	1:A:153:GLY:N	2.34	0.57
1:A:53:PRO:HB2	1:A:55:PRO:HD2	1.87	0.57
1:A:164:GLY:N	1:A:193:PHE:HE2	2.03	0.57
1:A:203:TYR:C	1:A:204:LEU:HD12	2.25	0.57
1:A:141:ASP:O	1:A:144:LYS:HD2	2.05	0.57
1:B:185:THR:O	1:B:188:GLU:N	2.38	0.57
1:A:348:LEU:HD12	1:A:349:PRO:HD2	1.87	0.57
1:A:296:GLU:N	1:A:296:GLU:OE2	2.37	0.56
1:B:147:ALA:O	1:B:151:ARG:HB3	2.06	0.56
1:B:37:ARG:CG	1:B:37:ARG:HH11	2.18	0.56
1:B:340:ASN:HD22	1:B:384:MET:CA	2.15	0.56
1:A:112:LEU:HG	1:A:113:MET:HE3	1.85	0.56
1:B:210:VAL:O	1:B:277:PHE:HB2	2.06	0.56
1:A:207:PRO:HB3	1:A:280:GLU:HG3	1.88	0.56
1:B:278:LEU:HD22	1:B:287:ILE:CG1	2.35	0.55
1:A:112:LEU:HG	1:A:113:MET:HE2	1.88	0.55
1:A:421:GLN:HA	1:A:421:GLN:OE1	2.06	0.55
1:A:336:GLU:HB2	1:A:389:ILE:HG12	1.89	0.55
1:B:170:ARG:HE	1:B:181:SER:HA	1.71	0.55
1:B:216:ALA:O	1:B:315:ILE:HD13	2.07	0.55
1:B:63:ILE:HB	1:B:64:PRO:HD3	1.87	0.55
1:A:207:PRO:HA	1:A:280:GLU:HG3	1.88	0.55
1:B:141:ASP:OD1	1:B:144:LYS:HD2	2.08	0.55
1:B:105:PRO:HG2	1:B:110:ILE:CG1	2.37	0.54
1:B:164:GLY:N	1:B:193:PHE:HE2	2.05	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:274:THR:HG21	1:A:294:GLN:NE2	2.22	0.54
1:A:112:LEU:HD23	1:A:113:MET:HE3	1.89	0.54
1:A:212:ILE:HD13	1:A:277:PHE:CD1	2.43	0.54
1:B:186:ARG:HG2	1:B:198:VAL:CG1	2.37	0.54
1:A:369:SER:HB2	1:A:385:ILE:O	2.07	0.54
1:B:75:ALA:O	1:B:100:PHE:HE1	1.91	0.54
1:A:236:HIS:CE1	2:A:1000:ATP:H5'2	2.42	0.54
1:A:54:ALA:HB3	1:A:55:PRO:CD	2.33	0.54
1:A:339:ILE:C	1:A:340:ASN:HD22	2.11	0.54
1:A:38:ASP:HB2	3:A:1327:HOH:O	2.08	0.54
1:B:165:GLY:HA2	2:B:1001:ATP:O3B	2.08	0.53
1:B:62:ASN:OD1	1:B:64:PRO:HD2	2.08	0.53
1:A:106:LYS:HB2	1:A:108:GLU:HG3	1.90	0.53
1:A:357:PHE:HA	1:A:410:ILE:O	2.08	0.53
1:B:278:LEU:CG	1:B:287:ILE:HD11	2.38	0.53
1:A:276:GLU:OE1	1:A:288:LYS:HE3	2.07	0.53
1:A:252:LEU:O	1:A:255:TYR:HB3	2.09	0.53
1:A:346:THR:HB	1:A:348:LEU:HB2	1.89	0.53
1:B:190:LYS:O	1:B:194:SER:HA	2.08	0.53
1:A:402:MET:O	1:A:406:LEU:HG	2.09	0.53
1:B:152:ILE:CD1	1:B:200:MET:HG2	2.38	0.53
1:A:261:ALA:O	1:A:265:VAL:HG23	2.09	0.53
1:A:129:PRO:HG2	1:A:256:ILE:CD1	2.39	0.52
1:A:143:ASP:OD2	1:A:146:ARG:NH1	2.43	0.52
1:B:72:ILE:C	1:B:72:ILE:HD12	2.30	0.52
1:A:193:PHE:CD1	1:A:193:PHE:N	2.76	0.52
1:B:169:MET:CE	2:B:1001:ATP:H5'1	2.40	0.52
1:B:19:ARG:O	1:B:23:GLU:HG3	2.10	0.52
1:B:231:SER:HB3	1:B:437:ILE:HG22	1.90	0.52
1:A:425:MET:O	1:A:431:GLN:NE2	2.43	0.52
1:B:93:GLU:O	1:B:97:ARG:HB2	2.09	0.52
1:A:68:SER:O	1:A:72:ILE:HG13	2.08	0.52
1:B:346:THR:HB	1:B:348:LEU:HD12	1.91	0.52
1:A:165:GLY:N	2:A:1000:ATP:O1B	2.43	0.52
1:B:145:ASN:HD22	1:B:182:ILE:CD1	2.22	0.52
1:A:421:GLN:O	1:A:425:MET:HG2	2.10	0.52
1:A:411:ILE:HG22	1:A:411:ILE:O	2.10	0.52
1:B:441:GLU:CG	1:B:446:LEU:HD13	2.40	0.52
1:A:413:GLY:O	1:A:414:ILE:HG23	2.10	0.52
1:A:206:ASN:N	1:A:280:GLU:OE2	2.43	0.52
1:B:314:ARG:O	1:B:319:GLN:HB2	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:261:ALA:O	1:B:264:CYS:HB2	2.09	0.52
1:B:101:ILE:O	1:B:101:ILE:HG22	2.09	0.51
1:B:109:THR:O	1:B:112:LEU:HB3	2.11	0.51
1:B:113:MET:HE1	1:B:119:ALA:HA	1.93	0.51
1:B:85:LEU:HB3	1:B:91:PHE:CD1	2.45	0.51
1:A:133:GLY:HA3	1:A:200:MET:O	2.11	0.51
1:B:297:HIS:CD2	1:B:298:PRO:HD3	2.44	0.51
1:A:360:PRO:HD3	1:A:409:LEU:HD13	1.92	0.51
1:B:164:GLY:HA3	1:B:193:PHE:CE2	2.46	0.51
1:A:353:LYS:HE3	1:A:374:GLY:HA2	1.93	0.51
1:B:346:THR:HB	1:B:348:LEU:CD1	2.41	0.51
1:A:427:ASP:OD1	1:A:439:TYR:OH	2.28	0.51
1:A:277:PHE:C	1:A:287:ILE:HD11	2.32	0.50
1:A:164:GLY:HA3	1:A:193:PHE:HE2	1.76	0.50
1:A:112:LEU:CG	1:A:113:MET:HE3	2.41	0.50
1:B:440:LEU:O	1:B:444:LEU:HD22	2.12	0.50
1:A:204:LEU:HD12	1:A:204:LEU:N	2.25	0.50
1:B:4:LYS:HD2	1:B:75:ALA:HA	1.93	0.50
1:B:6:VAL:HB	1:B:78:ILE:HG12	1.93	0.50
1:B:297:HIS:N	1:B:298:PRO:HD2	2.27	0.50
1:A:399:ILE:HD13	1:A:430:PHE:CE1	2.47	0.50
1:A:391:TYR:O	1:A:401:ARG:NH1	2.41	0.50
1:B:148:ILE:HG22	1:B:152:ILE:HD12	1.93	0.49
1:A:72:ILE:C	1:A:72:ILE:HD12	2.32	0.49
1:B:343:ASP:O	1:B:347:PHE:N	2.45	0.49
1:A:203:TYR:CD1	2:A:1000:ATP:C2	3.00	0.49
1:A:340:ASN:N	1:A:340:ASN:HD22	2.08	0.49
1:A:164:GLY:CA	1:A:193:PHE:CE2	2.95	0.49
1:B:323:ILE:HG22	1:B:324:LYS:N	2.27	0.49
1:B:427:ASP:OD2	1:B:429:ASN:N	2.44	0.49
1:B:163:GLY:C	1:B:193:PHE:HE2	2.15	0.49
1:B:419:ASP:HB3	1:B:423:ARG:HH11	1.76	0.49
1:B:346:THR:O	1:B:347:PHE:HB2	2.13	0.49
1:B:105:PRO:HG2	1:B:110:ILE:HG13	1.94	0.49
1:B:325:GLN:O	1:B:327:GLU:N	2.46	0.49
1:A:207:PRO:CB	1:A:280:GLU:HG3	2.43	0.49
1:A:201:GLU:OE2	2:A:1000:ATP:N6	2.38	0.49
1:B:358:HIS:O	1:B:409:LEU:HA	2.13	0.49
1:B:211:GLU:C	1:B:212:ILE:HD12	2.33	0.49
1:A:249:THR:HG23	1:A:252:LEU:HD12	1.95	0.49
1:A:370:HIS:N	1:A:370:HIS:CD2	2.80	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:399:ILE:HD13	1:A:430:PHE:HE1	1.78	0.49
1:A:443:LYS:C	1:A:445:GLY:H	2.15	0.48
1:A:241:GLU:OE1	1:A:338:ARG:NE	2.41	0.48
1:B:297:HIS:ND1	1:B:298:PRO:HD3	2.28	0.48
1:A:236:HIS:HE2	2:A:1000:ATP:PG	2.37	0.48
1:A:196:ASP:O	1:A:198:VAL:HG13	2.14	0.48
1:B:233:GLN:O	1:B:440:LEU:HB3	2.13	0.48
1:A:217:ASP:OD1	1:A:221:ASN:HB2	2.14	0.48
1:B:62:ASN:O	1:B:66:ILE:HG13	2.14	0.48
1:B:13:ILE:HD12	1:B:13:ILE:HA	1.63	0.48
1:A:204:LEU:CD1	1:A:204:LEU:N	2.76	0.47
1:A:17:ILE:O	1:A:17:ILE:HG22	2.15	0.47
1:A:62:ASN:ND2	1:A:65:ALA:HB2	2.29	0.47
1:A:186:ARG:HG2	1:A:196:ASP:O	2.14	0.47
1:A:133:GLY:HA2	1:A:152:ILE:HD13	1.95	0.47
1:B:200:MET:HB2	1:B:200:MET:HE2	1.56	0.47
1:B:16:ARG:HA	3:B:1307:HOH:O	2.14	0.47
1:B:301:GLU:CG	1:B:308:LEU:HD12	2.45	0.47
1:B:156:VAL:HG13	1:B:157:ILE:N	2.29	0.47
1:B:16:ARG:CZ	1:B:309:ILE:HG13	2.45	0.47
1:B:37:ARG:CG	1:B:37:ARG:NH1	2.78	0.47
1:B:64:PRO:O	1:B:68:SER:HB2	2.15	0.47
1:B:133:GLY:HA2	1:B:201:GLU:HA	1.97	0.46
1:B:297:HIS:N	1:B:298:PRO:CD	2.79	0.46
1:B:195:ASN:C	1:B:197:MET:H	2.16	0.46
1:B:252:LEU:HD22	1:B:284:PHE:CE1	2.46	0.46
1:A:206:ASN:HD22	1:A:436:ASN:HD21	1.61	0.46
1:A:227:GLU:CD	1:A:227:GLU:H	2.18	0.46
1:B:249:THR:HG1	1:B:251:GLU:HG2	1.77	0.46
1:B:440:LEU:O	1:B:444:LEU:HB2	2.15	0.46
1:A:95:VAL:HG13	1:A:100:PHE:HB2	1.96	0.46
1:A:92:ALA:O	1:A:96:GLU:HG3	2.15	0.46
1:A:196:ASP:N	1:A:196:ASP:OD2	2.46	0.46
1:B:380:TYR:HB2	1:B:381:TYR:CE1	2.51	0.46
1:B:63:ILE:N	1:B:64:PRO:CD	2.79	0.46
1:B:180:GLN:HB3	1:B:184:MET:SD	2.56	0.46
1:A:85:LEU:HB3	1:A:91:PHE:CD1	2.51	0.46
1:A:399:ILE:CD1	1:A:430:PHE:CE1	2.98	0.46
1:A:159:LYS:HE3	2:A:1000:ATP:N7	2.31	0.46
1:A:4:LYS:HE2	1:A:47:GLU:OE2	2.16	0.46
1:B:152:ILE:HG21	1:B:156:VAL:HG22	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:232:MET:CB	1:A:240:VAL:HB	2.46	0.46
1:B:295:VAL:HG11	1:B:338:ARG:CZ	2.46	0.46
1:A:131:VAL:HG12	1:A:132:PRO:N	2.31	0.46
1:A:117:VAL:HG23	1:A:161:SER:OG	2.17	0.45
1:A:297:HIS:N	1:A:298:PRO:CD	2.79	0.45
1:A:225:LEU:O	1:A:226:ALA:HB3	2.14	0.45
1:A:193:PHE:HD1	1:A:193:PHE:H	1.63	0.45
1:A:378:PRO:HA	1:A:379:PRO:HD3	1.82	0.45
1:A:62:ASN:HB3	1:A:65:ALA:HB3	1.98	0.45
1:B:224:TYR:C	1:B:225:LEU:HG	2.36	0.45
1:B:335:VAL:HG12	1:B:336:GLU:N	2.31	0.45
1:A:142:MET:CE	1:A:179:ALA:HA	2.47	0.45
1:B:309:ILE:O	1:B:312:GLN:HB2	2.17	0.45
1:A:212:ILE:HD13	1:A:277:PHE:CE1	2.51	0.45
1:B:113:MET:HE2	1:B:119:ALA:HA	1.98	0.45
1:A:5:ILE:HG23	1:A:26:ILE:HG21	1.97	0.45
1:A:37:ARG:NH2	1:A:50:CYS:SG	2.89	0.45
1:A:138:LEU:HA	1:A:138:LEU:HD12	1.46	0.45
1:B:152:ILE:HG21	1:B:156:VAL:CG2	2.46	0.45
1:A:274:THR:CB	1:A:294:GLN:NE2	2.79	0.45
1:A:292:ARG:HG3	1:A:293:ILE:O	2.17	0.45
1:B:165:GLY:N	2:B:1001:ATP:O1B	2.48	0.45
1:B:301:GLU:HG3	1:B:308:LEU:HD12	1.98	0.45
1:A:348:LEU:HD12	1:A:348:LEU:HA	1.79	0.45
1:B:303:ILE:HD12	1:B:330:VAL:HG22	1.99	0.45
1:B:138:LEU:HA	1:B:138:LEU:HD12	1.75	0.45
1:B:142:MET:SD	1:B:142:MET:N	2.90	0.44
1:B:399:ILE:HG22	1:B:403:LYS:HD2	1.99	0.44
1:B:156:VAL:CG1	1:B:157:ILE:N	2.80	0.44
1:B:113:MET:HE1	1:B:122:ALA:HB3	1.99	0.44
1:A:251:GLU:H	1:A:251:GLU:CD	2.20	0.44
1:B:307:ASP:O	1:B:311:GLU:HG2	2.18	0.44
1:B:259:ARG:NH1	1:B:259:ARG:CG	2.78	0.44
1:B:315:ILE:HD11	1:B:321:LEU:HD21	1.99	0.44
1:B:200:MET:CG	1:B:201:GLU:N	2.80	0.44
1:A:89:ALA:O	1:A:93:GLU:HB2	2.18	0.44
1:B:164:GLY:CA	1:B:193:PHE:CE2	3.00	0.44
1:A:363:PHE:O	1:A:401:ARG:HD3	2.16	0.44
1:A:77:ALA:HB2	1:A:101:ILE:HB	2.00	0.44
1:B:378:PRO:HA	1:B:379:PRO:HD3	1.77	0.44
1:A:307:ASP:O	1:A:311:GLU:HG2	2.16	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:278:LEU:HD22	1:A:287:ILE:HG12	1.99	0.44
1:A:233:GLN:O	1:A:440:LEU:HB3	2.18	0.44
1:A:169:MET:CE	2:A:1000:ATP:H5'1	2.48	0.44
1:B:32:HIS:HE1	1:B:37:ARG:HH11	1.66	0.44
1:B:154:TYR:HA	1:B:155:PRO:C	2.39	0.43
1:B:427:ASP:OD1	1:B:439:TYR:OH	2.30	0.43
1:A:144:LYS:O	1:A:147:ALA:HB3	2.18	0.43
1:B:421:GLN:O	1:B:425:MET:HG2	2.19	0.43
1:B:403:LYS:HG3	1:B:425:MET:HB3	2.00	0.43
1:B:193:PHE:O	1:B:194:SER:HB2	2.18	0.43
1:A:212:ILE:N	1:A:212:ILE:HD12	2.32	0.43
1:A:427:ASP:HB3	1:A:430:PHE:CB	2.49	0.43
1:A:278:LEU:HA	1:A:278:LEU:HD12	1.83	0.43
1:B:195:ASN:OD1	1:B:197:MET:HB2	2.18	0.43
1:A:116:LYS:O	1:A:119:ALA:HB3	2.19	0.43
1:B:133:GLY:C	1:B:152:ILE:HD11	2.39	0.43
1:A:444:LEU:HD12	1:A:444:LEU:HA	1.40	0.43
1:B:156:VAL:HG11	1:B:200:MET:SD	2.58	0.43
1:A:440:LEU:HA	1:A:440:LEU:HD12	1.78	0.43
1:A:348:LEU:HA	1:A:349:PRO:HD2	1.76	0.43
1:B:164:GLY:CA	1:B:193:PHE:HE2	2.31	0.43
1:A:108:GLU:HG2	1:A:108:GLU:H	1.21	0.43
1:A:110:ILE:HD13	1:A:110:ILE:HG21	1.73	0.43
1:A:232:MET:CG	1:A:240:VAL:HB	2.49	0.42
1:B:124:LYS:NZ	1:B:135:ASP:OD2	2.29	0.42
1:A:217:ASP:HA	1:A:315:ILE:HG12	2.00	0.42
1:B:212:ILE:CD1	1:B:212:ILE:N	2.82	0.42
1:B:67:ILE:O	1:B:70:ALA:HB3	2.19	0.42
1:A:298:PRO:HB3	1:A:366:ARG:CZ	2.49	0.42
1:B:294:GLN:HE21	1:B:294:GLN:HB3	1.49	0.42
1:B:117:VAL:HG23	1:B:161:SER:OG	2.18	0.42
1:B:169:MET:HE3	2:B:1001:ATP:H5'1	2.01	0.42
1:B:157:ILE:HB	1:B:203:TYR:HB2	2.02	0.42
1:A:280:GLU:O	1:A:281:ASN:HB2	2.20	0.42
1:A:298:PRO:HB3	1:A:366:ARG:NH1	2.34	0.42
1:B:252:LEU:HD23	1:B:252:LEU:HA	1.80	0.42
1:B:40:LYS:HA	1:B:40:LYS:HD3	1.81	0.42
1:B:256:ILE:HD13	1:B:284:PHE:CG	2.54	0.42
1:B:33:SER:HB2	1:B:53:PRO:O	2.19	0.42
1:A:342:GLU:O	1:A:344:PRO:HD3	2.20	0.42
1:A:1(A):HIS:HA	3:A:1239:HOH:O	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:31:VAL:HG23	1:A:31:VAL:O	2.18	0.42
1:B:133:GLY:HA3	1:B:200:MET:O	2.20	0.41
1:B:213:GLN:O	1:B:225:LEU:HD12	2.19	0.41
1:A:211:GLU:C	1:A:212:ILE:HD12	2.40	0.41
1:B:112:LEU:HG	1:B:113:MET:HE3	2.01	0.41
1:B:364:GLY:O	1:B:390:CYS:HA	2.20	0.41
1:B:236:HIS:HE2	2:B:1001:ATP:PG	2.44	0.41
1:B:101:ILE:HD13	1:B:101:ILE:HG21	1.80	0.41
1:A:354:ILE:O	1:A:374:GLY:N	2.47	0.41
1:A:410:ILE:O	1:A:410:ILE:HG22	2.12	0.41
1:B:116:LYS:O	1:B:119:ALA:HB3	2.20	0.41
1:B:368:GLU:HB2	1:B:387:LYS:HB2	2.03	0.41
1:B:424:ILE:C	1:B:426:ASN:N	2.74	0.41
1:B:419:ASP:HB3	1:B:423:ARG:HH12	1.81	0.41
1:B:31:VAL:HB	1:B:51:ILE:CG2	2.51	0.41
1:A:6:VAL:HG12	1:A:7:ILE:N	2.34	0.41
1:B:217:ASP:OD1	1:B:221:ASN:HB2	2.21	0.41
1:A:163:GLY:C	1:A:193:PHE:HE2	2.24	0.41
1:A:443:LYS:C	1:A:445:GLY:N	2.73	0.41
1:A:152:ILE:HD13	1:A:152:ILE:HG21	1.62	0.41
1:B:18:LEU:C	1:B:18:LEU:HD23	2.40	0.41
1:A:262:LYS:HE2	1:A:266:ASP:OD1	2.21	0.41
1:A:63:ILE:CB	1:A:64:PRO:CD	2.99	0.41
1:A:296:GLU:O	1:A:299:VAL:HG22	2.20	0.41
1:B:215:LEU:HD23	1:B:215:LEU:HA	1.91	0.41
1:A:393:GLU:OE2	1:A:393:GLU:N	2.43	0.41
1:A:157:ILE:HG13	1:A:171:VAL:HG22	2.03	0.41
1:A:427:ASP:HB3	1:A:430:PHE:HB3	2.01	0.41
1:B:23:GLU:OE1	1:B:310:LYS:HE3	2.20	0.40
1:A:129:PRO:HG2	1:A:256:ILE:HD11	2.03	0.40
1:B:152:ILE:CG2	1:B:156:VAL:CG2	2.99	0.40
1:B:443:LYS:C	1:B:445:GLY:H	2.24	0.40
1:A:152:ILE:CG2	1:A:202:LYS:HB2	2.52	0.40
1:B:343:ASP:O	1:B:347:PHE:HA	2.22	0.40
1:A:193:PHE:O	1:A:194:SER:HB2	2.21	0.40
1:A:54:ALA:CB	1:A:55:PRO:HD3	2.36	0.40
1:B:323:ILE:H	1:B:323:ILE:CD1	2.25	0.40
1:B:254:ARG:O	1:B:258:GLU:HB2	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	449/452 (99%)	406 (90%)	41 (9%)	2 (0%)	39	61
1	B	446/452 (99%)	407 (91%)	32 (7%)	7 (2%)	12	21
All	All	895/904 (99%)	813 (91%)	73 (8%)	9 (1%)	19	34

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	142	MET
1	B	181	SER
1	B	179	ALA
1	B	196	ASP
1	B	226	ALA
1	A	382	ASP
1	B	326	GLU
1	B	444	LEU
1	B	83	GLY

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	362/363 (100%)	307 (85%)	55 (15%)	3	6
1	B	360/363 (99%)	294 (82%)	66 (18%)	2	3
All	All	722/726 (99%)	601 (83%)	121 (17%)	2	4

All (121) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1(B)	SER
1	A	1	MET
1	A	3	ASP
1	A	18	LEU
1	A	27	LYS
1	A	48	THR
1	A	68	SER
1	A	82	TYR
1	A	86	SER
1	A	94	GLN
1	A	101	ILE
1	A	106	LYS
1	A	108	GLU
1	A	111	ARG
1	A	118	SER
1	A	124	LYS
1	A	125	LYS
1	A	138	LEU
1	A	140	ASP
1	A	141	ASP
1	A	142	MET
1	A	144	LYS
1	A	157	ILE
1	A	159	LYS
1	A	161	SER
1	A	170	ARG
1	A	177	GLU
1	A	180	GLN
1	A	184	MET
1	A	186	ARG
1	A	193	PHE
1	A	202	LYS
1	A	205	GLU
1	A	232	MET
1	A	237	GLN
1	A	248	ILE
1	A	251	GLU
1	A	252	LEU
1	A	254	ARG
1	A	259	ARG
1	A	262	LYS
1	A	278	LEU

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Mol	Chain	Res	Type
1	A	293	ILE
1	A	326	GLU
1	A	340	ASN
1	A	345	ASN
1	A	348	LEU
1	A	369	SER
1	A	428	GLU
1	A	431	GLN
1	A	442	LYS
1	A	443	LYS
1	A	444	LEU
1	A	446	LEU
1	A	447	GLN
1	B	3	ASP
1	B	4	LYS
1	B	5	ILE
1	B	37	ARG
1	B	48	THR
1	B	68	SER
1	B	82	TYR
1	B	86	SER
1	B	94	GLN
1	B	97	ARG
1	B	103	ILE
1	B	111	ARG
1	B	120	ILE
1	B	124	LYS
1	B	138	LEU
1	B	140	ASP
1	B	142	MET
1	B	144	LYS
1	B	151	ARG
1	B	152	ILE
1	B	157	ILE
1	B	158	ILE
1	B	161	SER
1	B	167	ARG
1	B	170	ARG
1	B	173	ARG
1	B	177	GLU
1	B	178	LEU
1	B	180	GLN

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Mol	Chain	Res	Type
1	B	184	MET
1	B	186	ARG
1	B	193	PHE
1	B	198	VAL
1	B	200	MET
1	B	202	LYS
1	B	205	GLU
1	B	219	GLN
1	B	225	LEU
1	B	231	SER
1	B	235	ARG
1	B	249	THR
1	B	251	GLU
1	B	252	LEU
1	B	259	ARG
1	B	262	LYS
1	B	266	ASP
1	B	278	LEU
1	B	281	ASN
1	B	288	LYS
1	B	289	MET
1	B	292	ARG
1	B	294	GLN
1	B	308	LEU
1	B	310	LYS
1	B	322	SER
1	B	323	ILE
1	B	324	LYS
1	B	326	GLU
1	B	353	LYS
1	B	399	ILE
1	B	423	ARG
1	B	431	GLN
1	B	435	THR
1	B	443	LYS
1	B	444	LEU
1	B	447	GLN

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	1(A)	HIS

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Mol	Chain	Res	Type
1	A	206	ASN
1	A	294	GLN
1	A	319	GLN
1	A	340	ASN
1	A	345	ASN
1	A	370	HIS
1	A	447	GLN
1	B	145	ASN
1	B	180	GLN
1	B	209	HIS
1	B	294	GLN
1	B	340	ASN
1	B	345	ASN
1	B	358	HIS
1	B	370	HIS
1	B	404	ASN
1	B	426	ASN
1	B	431	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](#)

2 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	$\# Z > 2$
2	ATP	A	1000	-	24,33,33	1.96	1 (4%)	31,52,52	1.20	3 (9%)
2	ATP	B	1001	-	24,33,33	1.85	1 (4%)	31,52,52	1.25	4 (12%)

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
2	ATP	A	1000	-	-	0/18/38/38	0/3/3/3
2	ATP	B	1001	-	-	0/18/38/38	0/3/3/3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1000	ATP	C2'-C3'	-8.57	1.30	1.53
2	B	1001	ATP	C2'-C3'	-8.05	1.31	1.53

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1000	ATP	O3A-PA-O5'	-3.02	94.91	102.94
2	B	1001	ATP	O3A-PA-O5'	-2.78	95.55	102.94
2	B	1001	ATP	C1'-N9-C4	-2.58	123.04	126.94
2	A	1000	ATP	PA-O3A-PB	-2.38	126.05	132.73
2	A	1000	ATP	O4'-C4'-C3'	-2.18	100.75	105.15
2	B	1001	ATP	O4'-C1'-N9	2.19	112.69	108.10
2	B	1001	ATP	C2'-C3'-C4'	3.03	108.85	102.61

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 18 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1000	ATP	10	0
2	B	1001	ATP	8	0

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

EDS was not executed - this section will therefore be empty.

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

EDS was not executed - this section will therefore be empty.

6.3 Carbohydrates

EDS was not executed - this section will therefore be empty.

6.4 Ligands

EDS was not executed - this section will therefore be empty.

6.5 Other polymers

EDS was not executed - this section will therefore be empty.