



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 18, 2018 – 09:38 PM EST

PDB ID : 1GQQ
Title : MURC - Crystal structure of the apo-enzyme from Haemophilus influenzae
Authors : Skarzynski, T.; Cleasby, A.; Domenici, E.; Gevi, M.; Shaw, J.
Deposited on : 2001-12-03
Resolution : 3.10 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
Xtriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20030736

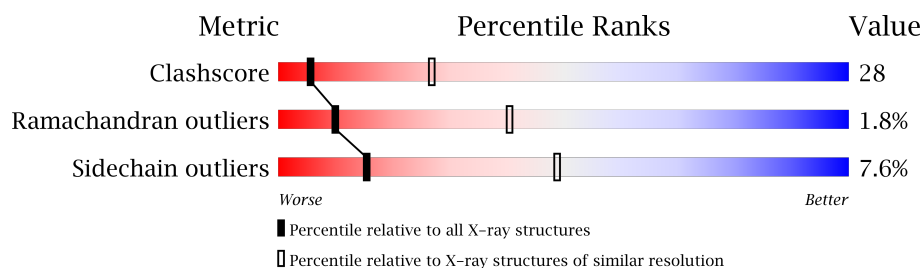
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.10 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	112137	1099 (3.12-3.08)
Ramachandran outliers	110173	1057 (3.12-3.08)
Sidechain outliers	110143	1057 (3.12-3.08)

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	475	
1	B	475	

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 6578 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 UDP-N-ACETYLMURAMATE-L-ALANINE LIGASE.

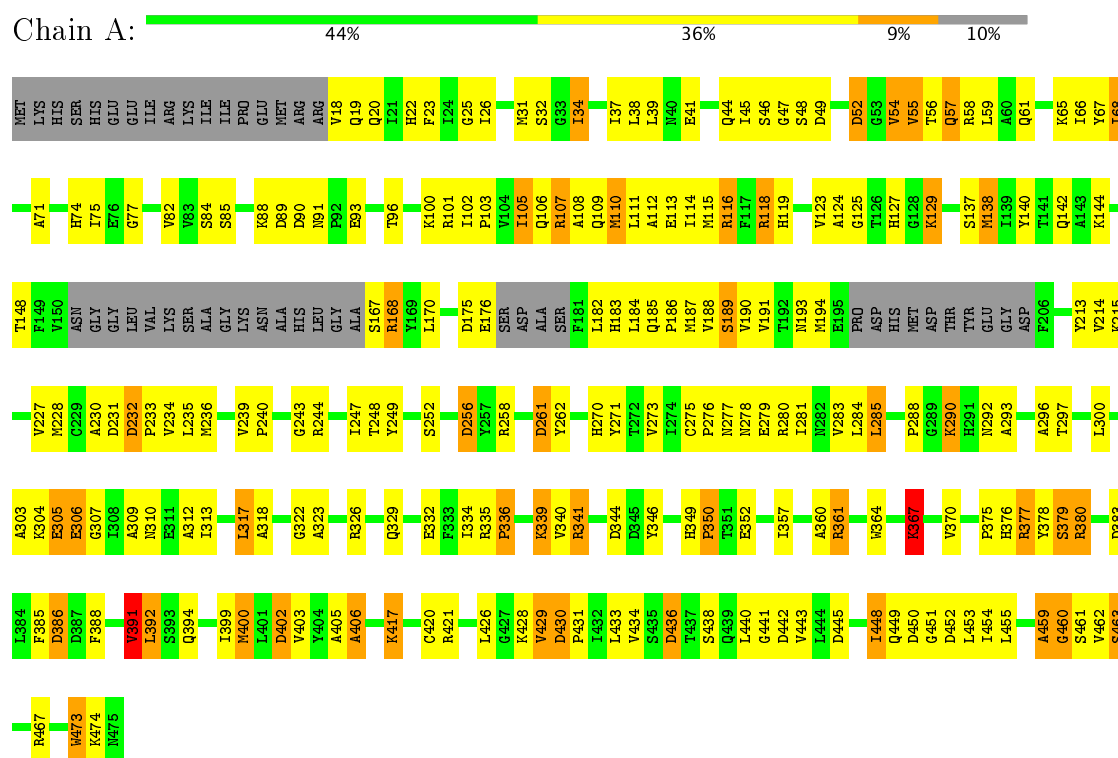
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	428	Total	C	N	O	S	0	0	0
			3292	2081	573	623	15			
1	B	427	Total	C	N	O	S	0	0	0
			3286	2078	572	621	15			

3 Residue-property plots

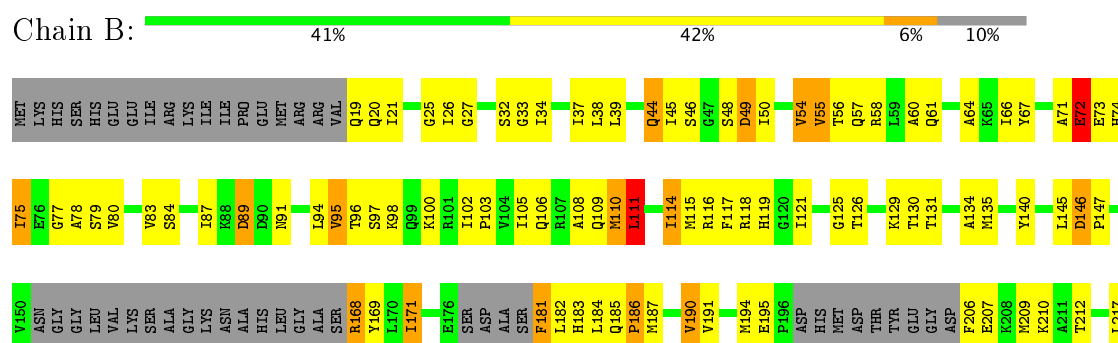
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are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

Note EDS was not executed.

• Molecule 1: UDP-N-ACETYLMURAMATE-L-ALANINE LIGASE



• Molecule 1: UDP-N-ACETYLMURAMATE-L-ALANINE LIGASE





4 Data and refinement statistics

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

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	65.51 Å 99.48 Å 180.59 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.88 – 3.10	Depositor
% Data completeness (in resolution range)	100.0 (19.88-3.10)	Depositor
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	REFMAC	Depositor
R, R_{free}	0.239 , 0.286	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	6578	wwPDB-VP
Average B, all atoms (Å ²)	37.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	1.33	17/3346 (0.5%)	1.38	35/4525 (0.8%)
1	B	1.00	2/3341 (0.1%)	1.17	22/4519 (0.5%)
All	All	1.18	19/6687 (0.3%)	1.28	57/9044 (0.6%)

All (19) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	68	ILE	CA-CB	-8.14	1.36	1.54
1	A	430	ASP	CB-CG	8.01	1.68	1.51
1	A	429	VAL	CB-CG1	-7.79	1.36	1.52
1	A	367	LYS	CE-NZ	6.82	1.66	1.49
1	B	417	LYS	CD-CE	6.52	1.67	1.51
1	A	344	ASP	CB-CG	-6.41	1.38	1.51
1	A	352	GLU	CD-OE1	6.24	1.32	1.25
1	A	429	VAL	CB-CG2	-6.22	1.39	1.52
1	A	357	ILE	CA-CB	-6.06	1.41	1.54
1	A	473	TRP	C-O	-6.03	1.11	1.23
1	A	54	VAL	CB-CG1	-5.77	1.40	1.52
1	A	400	MET	CG-SD	-5.62	1.66	1.81
1	A	463	SER	CB-OG	-5.56	1.35	1.42
1	B	462	VAL	CB-CG1	-5.45	1.41	1.52
1	A	391	VAL	CB-CG2	-5.26	1.41	1.52
1	A	107	ARG	NE-CZ	5.16	1.39	1.33
1	A	55	VAL	CB-CG1	-5.10	1.42	1.52
1	A	460	GLY	C-O	-5.09	1.15	1.23
1	A	459	ALA	CA-CB	-5.04	1.41	1.52

All (57) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	344	ASP	CB-CG-OD1	-10.40	108.94	118.30
1	A	386	ASP	CB-CG-OD2	10.04	127.34	118.30
1	A	344	ASP	CB-CG-OD2	9.77	127.10	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	382	ARG	NE-CZ-NH1	-9.39	115.61	120.30
1	A	474	LYS	CD-CE-NZ	-8.13	93.00	111.70
1	A	452	ASP	CB-CG-OD2	7.47	125.02	118.30
1	A	317	LEU	CB-CG-CD2	-7.46	98.32	111.00
1	B	344	ASP	CB-CG-OD2	7.42	124.97	118.30
1	A	232	ASP	CB-CG-OD2	7.25	124.82	118.30
1	B	402	ASP	CB-CG-OD2	7.22	124.80	118.30
1	A	383	ASP	CB-CG-OD2	7.13	124.72	118.30
1	A	285	LEU	CB-CG-CD1	-7.12	98.89	111.00
1	A	261	ASP	CB-CG-OD2	6.94	124.54	118.30
1	A	256	ASP	CB-CG-OD2	6.93	124.53	118.30
1	A	430	ASP	CB-CG-OD2	6.86	124.47	118.30
1	A	453	LEU	CB-CG-CD1	-6.58	99.82	111.00
1	B	231	ASP	CB-CG-OD2	6.37	124.03	118.30
1	B	146	ASP	CB-CG-OD2	6.33	124.00	118.30
1	A	380	ARG	NE-CZ-NH1	-6.19	117.20	120.30
1	A	361	ARG	NE-CZ-NH1	-6.16	117.22	120.30
1	B	328	ASP	CB-CG-OD2	6.15	123.84	118.30
1	A	429	VAL	CG1-CB-CG2	-6.08	101.16	110.90
1	A	52	ASP	CB-CG-OD2	6.05	123.75	118.30
1	B	49	ASP	CB-CG-OD2	6.03	123.73	118.30
1	A	380	ARG	NE-CZ-NH2	6.03	123.31	120.30
1	A	436	ASP	CB-CG-OD2	6.00	123.70	118.30
1	A	34	ILE	CG1-CB-CG2	-5.97	98.27	111.40
1	B	261	ASP	CB-CG-OD2	5.92	123.63	118.30
1	A	402	ASP	CB-CG-OD2	5.91	123.61	118.30
1	B	452	ASP	CB-CG-OD2	5.84	123.56	118.30
1	A	290	LYS	CD-CE-NZ	5.81	125.07	111.70
1	B	366	ASP	CB-CG-OD2	5.76	123.49	118.30
1	B	387	ASP	CB-CG-OD2	5.75	123.47	118.30
1	B	383	ASP	CB-CG-OD2	5.71	123.44	118.30
1	A	116	ARG	NE-CZ-NH2	5.67	123.13	120.30
1	B	370	VAL	CB-CA-C	-5.63	100.69	111.40
1	B	396	ASP	CB-CG-OD2	5.63	123.37	118.30
1	B	377	ARG	NE-CZ-NH1	-5.62	117.49	120.30
1	A	445	ASP	CB-CG-OD2	5.58	123.32	118.30
1	B	266	GLY	N-CA-C	-5.58	99.14	113.10
1	A	175	ASP	CB-CG-OD2	5.56	123.31	118.30
1	A	107	ARG	NE-CZ-NH1	5.53	123.06	120.30
1	B	111	LEU	CB-CG-CD2	-5.52	101.61	111.00
1	B	190	VAL	CB-CA-C	-5.42	101.11	111.40
1	A	68	ILE	CA-CB-CG1	-5.38	100.78	111.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	406	ALA	C-N-CA	-5.32	111.14	122.30
1	A	453	LEU	CB-CA-C	-5.30	100.13	110.20
1	B	285	LEU	CA-CB-CG	-5.29	103.14	115.30
1	A	430	ASP	OD1-CG-OD2	-5.27	113.28	123.30
1	A	326	ARG	NE-CZ-NH1	5.25	122.93	120.30
1	B	89	ASP	CB-CG-OD2	5.23	123.01	118.30
1	B	445	ASP	CB-CG-OD2	5.17	122.95	118.30
1	A	129	LYS	CD-CE-NZ	-5.17	99.82	111.70
1	A	392	LEU	CB-CG-CD1	-5.15	102.24	111.00
1	A	231	ASP	CB-CG-OD2	5.12	122.90	118.30
1	A	336	PRO	C-N-CA	-5.05	109.08	121.70
1	B	436	ASP	CB-CG-OD2	5.01	122.81	118.30

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	3292	0	3295	165	0
1	B	3286	0	3288	213	0
All	All	6578	0	6583	372	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 (372) 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:A:105:ILE:HD11	1:A:110:MET:HG2	1.23	1.16
1:A:417:LYS:N	1:A:417:LYS:HD3	1.66	1.08
1:B:39:LEU:HD13	1:B:45:ILE:HG12	1.42	1.02
1:B:287:VAL:HG12	1:B:288:PRO:HD2	1.39	0.99
1:B:80:VAL:HG21	1:B:105:ILE:HD12	1.44	0.98
1:A:105:ILE:HD11	1:A:110:MET:CG	1.97	0.95

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:275:CYS:SG	1:B:281:ILE:HD12	2.08	0.94
1:B:287:VAL:CG1	1:B:288:PRO:HD2	1.97	0.93
1:A:105:ILE:CD1	1:A:110:MET:HG2	1.98	0.93
1:B:368:ARG:NH2	1:B:452:ASP:OD2	2.00	0.92
1:A:417:LYS:HD3	1:A:417:LYS:H	1.31	0.91
1:A:436:ASP:OD1	1:A:438:SER:OG	1.91	0.89
1:B:265:THR:HB	1:B:270:HIS:CE1	2.07	0.88
1:B:181:PHE:N	1:B:181:PHE:CD2	2.41	0.87
1:B:255:ALA:HB3	1:B:258:ARG:HB2	1.55	0.86
1:B:135:MET:SD	1:B:296:ALA:HA	2.15	0.86
1:B:340:VAL:HG12	1:B:452:ASP:HB2	1.55	0.86
1:A:334:ILE:HG12	1:A:339:LYS:HG3	1.57	0.85
1:B:249:TYR:CZ	1:B:298:ALA:HB2	2.10	0.85
1:A:113:GLU:OE2	1:B:221:PRO:HA	1.77	0.85
1:B:108:ALA:O	1:B:109:GLN:C	2.16	0.84
1:B:19:GLN:HG3	1:B:44:GLN:HG3	1.58	0.83
1:A:317:LEU:N	1:A:317:LEU:HD23	1.91	0.82
1:A:275:CYS:HB3	1:A:276:PRO:CD	2.10	0.82
1:A:124:ALA:O	1:A:191:VAL:HA	1.81	0.81
1:B:71:ALA:O	1:B:73:GLU:N	2.14	0.80
1:B:108:ALA:O	1:B:111:LEU:N	2.14	0.80
1:B:230:ALA:HA	1:B:236:MET:SD	2.22	0.80
1:B:306:GLU:O	1:B:306:GLU:HG3	1.81	0.80
1:B:268:GLN:HE21	1:B:286:ASN:HA	1.46	0.80
1:B:252:SER:O	1:B:254:GLN:N	2.15	0.80
1:A:111:LEU:HD12	1:A:111:LEU:O	1.83	0.78
1:B:287:VAL:HG12	1:B:288:PRO:CD	2.14	0.78
1:B:181:PHE:HD2	1:B:181:PHE:N	1.79	0.77
1:B:116:ARG:HG2	1:B:117:PHE:N	2.00	0.77
1:A:402:ASP:OD1	1:A:417:LYS:NZ	2.18	0.76
1:A:275:CYS:SG	1:A:281:ILE:HD11	2.26	0.75
1:B:26:ILE:HG21	1:B:66:ILE:HD12	1.67	0.75
1:B:233:PRO:O	1:B:237:GLU:HB2	1.87	0.74
1:A:275:CYS:HB3	1:A:276:PRO:HD2	1.68	0.74
1:A:176:GLU:HG2	1:A:213:TYR:OH	1.87	0.73
1:A:436:ASP:CG	1:A:438:SER:HG	1.90	0.73
1:B:230:ALA:HB2	1:B:248:THR:HB	1.70	0.73
1:A:376:HIS:O	1:A:377:ARG:HB2	1.87	0.72
1:A:460:GLY:H	1:A:462:VAL:HG12	1.54	0.72
1:B:184:LEU:O	1:B:186:PRO:HD3	1.88	0.72
1:A:377:ARG:HH11	1:A:377:ARG:HG2	1.53	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:285:LEU:HD12	1:B:286:ASN:N	2.05	0.71
1:B:461:SER:O	1:B:465:ILE:HD12	1.91	0.71
1:B:267:PHE:CE1	1:B:363:GLY:HA3	2.26	0.71
1:A:304:LYS:NZ	1:A:310:ASN:OD1	2.22	0.71
1:A:88:LYS:O	1:A:90:ASP:N	2.22	0.71
1:B:281:ILE:HG23	1:B:314:LEU:HD11	1.74	0.70
1:B:75:ILE:O	1:B:75:ILE:HG23	1.90	0.70
1:B:341:ARG:HD2	1:B:364:TRP:CH2	2.27	0.70
1:B:72:GLU:HB3	1:B:96:THR:HG21	1.72	0.70
1:B:275:CYS:SG	1:B:281:ILE:CD1	2.79	0.69
1:B:218:HIS:O	1:B:220:LEU:N	2.25	0.69
1:B:243:GLY:C	1:B:244:ARG:HG2	2.14	0.69
1:A:370:VAL:O	1:A:454:ILE:HA	1.93	0.68
1:B:80:VAL:CG2	1:B:105:ILE:HD12	2.22	0.68
1:B:116:ARG:HB2	1:B:185:GLN:OE1	1.93	0.68
1:B:287:VAL:CG1	1:B:288:PRO:CD	2.70	0.68
1:A:275:CYS:SG	1:A:281:ILE:CD1	2.82	0.68
1:A:230:ALA:HB2	1:A:248:THR:HB	1.76	0.68
1:A:417:LYS:HD2	1:A:433:LEU:HD21	1.74	0.67
1:A:243:GLY:O	1:A:244:ARG:HD3	1.94	0.67
1:B:33:GLY:O	1:B:37:ILE:HG13	1.94	0.67
1:A:375:PRO:HB2	1:A:403:VAL:HG22	1.77	0.66
1:A:391:VAL:CG1	1:A:392:LEU:N	2.58	0.66
1:B:285:LEU:HD12	1:B:286:ASN:H	1.61	0.66
1:B:364:TRP:CD1	1:B:367:LYS:HB2	2.30	0.66
1:B:140:TYR:HB3	1:B:147:PRO:HG3	1.77	0.66
1:B:308:ILE:HG22	1:B:309:ALA:N	2.11	0.65
1:B:209:MET:O	1:B:212:THR:N	2.28	0.65
1:B:21:ILE:HD13	1:B:38:LEU:HD13	1.78	0.65
1:B:109:GLN:OE1	1:B:183:HIS:NE2	2.30	0.65
1:A:405:ALA:O	1:A:406:ALA:HB3	1.96	0.64
1:B:67:TYR:HB3	1:B:74:HIS:CE1	2.32	0.64
1:B:67:TYR:CD2	1:B:74:HIS:HB3	2.33	0.64
1:B:207:GLU:OE1	1:B:210:LYS:HD3	1.96	0.64
1:A:417:LYS:N	1:A:417:LYS:CD	2.52	0.63
1:A:71:ALA:HB3	1:A:74:HIS:CE1	2.34	0.63
1:A:247:ILE:HG13	1:A:305:GLU:OE1	1.98	0.62
1:A:176:GLU:CD	1:A:176:GLU:H	2.04	0.62
1:B:20:GLN:HB3	1:B:78:ALA:HA	1.80	0.62
1:A:232:ASP:OD2	1:A:234:VAL:HB	2.01	0.61
1:A:391:VAL:HG13	1:A:392:LEU:N	2.13	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:126:THR:OG1	1:B:194:MET:HA	1.99	0.61
1:B:449:GLN:O	1:B:450:ASP:C	2.37	0.61
1:B:27:GLY:HA3	1:B:49:ASP:OD2	2.01	0.60
1:A:239:VAL:HB	1:A:240:PRO:HD3	1.83	0.60
1:B:56:THR:HB	1:B:66:ILE:HG21	1.82	0.60
1:B:265:THR:HB	1:B:270:HIS:HE1	1.64	0.60
1:B:135:MET:SD	1:B:296:ALA:CA	2.88	0.60
1:A:417:LYS:O	1:A:421:ARG:HG3	2.01	0.60
1:B:247:ILE:HD12	1:B:257:TYR:HE1	1.67	0.60
1:B:275:CYS:HG	1:B:281:ILE:HD12	1.66	0.59
1:A:244:ARG:HH22	1:B:109:GLN:NE2	2.00	0.59
1:B:19:GLN:N	1:B:79:SER:HG	2.00	0.59
1:A:167:SER:OG	1:A:168:ARG:N	2.32	0.59
1:A:400:MET:O	1:A:433:LEU:HD12	2.02	0.59
1:A:417:LYS:HD2	1:A:433:LEU:CD2	2.31	0.59
1:A:335:ARG:HB3	1:A:336:PRO:HD2	1.85	0.58
1:A:335:ARG:HD3	1:A:473:TRP:CD2	2.38	0.58
1:B:281:ILE:CG2	1:B:314:LEU:HD21	2.33	0.58
1:A:185:GLN:HB3	1:B:116:ARG:HH22	1.69	0.58
1:B:121:ILE:HD12	1:B:171:ILE:HD13	1.85	0.58
1:A:34:ILE:HD11	1:A:111:LEU:HB2	1.85	0.58
1:B:105:ILE:HG21	1:B:110:MET:HG2	1.86	0.58
1:B:385:PHE:O	1:B:389:VAL:HG23	2.03	0.58
1:A:113:GLU:OE2	1:B:221:PRO:CA	2.51	0.58
1:A:258:ARG:O	1:A:273:VAL:HA	2.04	0.57
1:A:39:LEU:CD1	1:A:45:ILE:HB	2.34	0.57
1:B:262:TYR:CD2	1:B:262:TYR:C	2.77	0.57
1:B:265:THR:CB	1:B:270:HIS:CE1	2.83	0.57
1:A:460:GLY:N	1:A:462:VAL:HG12	2.19	0.57
1:B:75:ILE:HD11	1:B:97:SER:OG	2.05	0.57
1:B:108:ALA:O	1:B:110:MET:N	2.38	0.56
1:B:243:GLY:O	1:B:244:ARG:HG2	2.04	0.56
1:A:385:PHE:O	1:A:386:ASP:C	2.43	0.56
1:B:119:HIS:ND1	1:B:119:HIS:O	2.38	0.56
1:B:146:ASP:N	1:B:147:PRO:HD3	2.20	0.56
1:B:434:VAL:HG12	1:B:434:VAL:O	2.03	0.56
1:A:26:ILE:HG21	1:A:66:ILE:HD13	1.86	0.56
1:A:332:GLU:HG2	1:A:341:ARG:HG3	1.86	0.56
1:A:434:VAL:O	1:A:434:VAL:HG12	2.05	0.56
1:B:242:VAL:HG12	1:B:244:ARG:N	2.20	0.56
1:A:18:VAL:HG21	1:B:222:PHE:HE1	1.71	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:39:LEU:HD13	1:B:45:ILE:CG1	2.27	0.55
1:A:176:GLU:CG	1:A:213:TYR:OH	2.54	0.55
1:B:83:VAL:HG12	1:B:84:SER:O	2.06	0.55
1:B:357:ILE:O	1:B:358:LYS:C	2.41	0.55
1:A:288:PRO:O	1:A:292:ASN:ND2	2.40	0.55
1:B:415:ASP:C	1:B:415:ASP:OD1	2.44	0.55
1:A:84:SER:OG	1:A:85:SER:N	2.40	0.55
1:A:243:GLY:C	1:B:103:PRO:HB3	2.28	0.54
1:A:312:ALA:O	1:A:313:ILE:C	2.43	0.54
1:A:82:VAL:HA	1:A:105:ILE:O	2.08	0.54
1:B:105:ILE:HG22	1:B:106:GLN:O	2.07	0.54
1:B:249:TYR:CE1	1:B:298:ALA:HB2	2.42	0.54
1:B:126:THR:HG21	1:B:195:GLU:O	2.07	0.54
1:B:19:GLN:NE2	1:B:44:GLN:OE1	2.40	0.53
1:B:20:GLN:NE2	1:B:77:GLY:O	2.40	0.53
1:B:341:ARG:HH11	1:B:364:TRP:HH2	1.54	0.53
1:A:429:VAL:HG22	1:A:430:ASP:N	2.24	0.53
1:B:83:VAL:HG13	1:B:87:ILE:HG13	1.90	0.53
1:B:335:ARG:HB3	1:B:336:PRO:HD2	1.90	0.53
1:A:127:HIS:O	1:A:193:ASN:ND2	2.39	0.53
1:B:125:GLY:O	1:B:129:LYS:NZ	2.32	0.53
1:B:72:GLU:HB3	1:B:96:THR:CG2	2.38	0.53
1:B:75:ILE:O	1:B:75:ILE:CG2	2.56	0.53
1:B:25:GLY:N	1:B:48:SER:O	2.42	0.52
1:B:308:ILE:CG2	1:B:309:ALA:N	2.72	0.52
1:A:429:VAL:O	1:A:431:PRO:HD3	2.10	0.52
1:A:350:PRO:HD3	1:A:388:PHE:CZ	2.45	0.52
1:A:100:LYS:O	1:A:101:ARG:CB	2.58	0.52
1:A:71:ALA:HB3	1:A:74:HIS:NE2	2.25	0.52
1:A:49:ASP:O	1:A:68:ILE:HA	2.10	0.52
1:A:22:HIS:HA	1:A:46:SER:O	2.11	0.51
1:B:190:VAL:HG12	1:B:191:VAL:N	2.24	0.51
1:A:41:GLU:OE1	1:A:118:ARG:NH2	2.43	0.51
1:A:96:THR:HG22	1:A:100:LYS:HD2	1.93	0.51
1:A:148:THR:HB	1:A:170:LEU:HD12	1.91	0.51
1:B:228:MET:HE2	1:B:235:LEU:HD22	1.93	0.51
1:B:287:VAL:HG21	1:B:320:PHE:HD2	1.75	0.51
1:B:67:TYR:CG	1:B:74:HIS:CG	2.99	0.51
1:A:304:LYS:HD3	1:A:313:ILE:HD12	1.93	0.51
1:B:108:ALA:HA	1:B:111:LEU:HB3	1.93	0.51
1:B:140:TYR:CB	1:B:147:PRO:HG3	2.41	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:287:VAL:HG13	1:B:288:PRO:HD2	1.87	0.51
1:B:264:GLN:NE2	1:B:267:PHE:HD1	2.08	0.50
1:B:340:VAL:CG1	1:B:452:ASP:HB2	2.34	0.50
1:A:340:VAL:HG11	1:A:448:ILE:HD13	1.94	0.50
1:B:109:GLN:HG3	1:B:183:HIS:CD2	2.46	0.50
1:B:218:HIS:C	1:B:220:LEU:N	2.64	0.50
1:B:355:VAL:CG2	1:B:356:THR:N	2.75	0.50
1:B:248:THR:N	1:B:256:ASP:OD1	2.38	0.50
1:B:67:TYR:CD1	1:B:74:HIS:CD2	3.00	0.50
1:A:142:GLN:C	1:A:144:LYS:H	2.15	0.49
1:A:37:ILE:HG21	1:A:114:ILE:HD13	1.94	0.49
1:B:184:LEU:C	1:B:186:PRO:HD3	2.32	0.49
1:A:377:ARG:HH11	1:A:377:ARG:CG	2.19	0.49
1:B:242:VAL:HG12	1:B:244:ARG:H	1.77	0.49
1:B:34:ILE:HD11	1:B:111:LEU:HB2	1.93	0.49
1:B:94:LEU:O	1:B:94:LEU:HD12	2.12	0.49
1:A:349:HIS:O	1:A:350:PRO:C	2.51	0.49
1:A:243:GLY:C	1:A:244:ARG:HG2	2.32	0.49
1:A:262:TYR:HA	1:A:271:TYR:HB3	1.94	0.49
1:A:52:ASP:HA	1:A:56:THR:OG1	2.13	0.49
1:B:270:HIS:ND1	1:B:270:HIS:N	2.60	0.49
1:B:57:GLN:O	1:B:61:GLN:HG3	2.12	0.49
1:A:190:VAL:HG22	1:A:227:VAL:HB	1.95	0.49
1:A:22:HIS:CE1	1:A:47:GLY:HA2	2.48	0.49
1:B:287:VAL:HG21	1:B:320:PHE:CD2	2.47	0.49
1:B:72:GLU:CB	1:B:96:THR:HG21	2.43	0.49
1:B:243:GLY:O	1:B:244:ARG:NH1	2.28	0.48
1:B:207:GLU:HA	1:B:207:GLU:OE1	2.12	0.48
1:B:26:ILE:HG21	1:B:66:ILE:CD1	2.40	0.48
1:B:338:GLY:CA	1:B:450:ASP:HA	2.43	0.48
1:A:112:ALA:HB2	1:A:183:HIS:HB3	1.95	0.48
1:B:109:GLN:OE1	1:B:183:HIS:CD2	2.66	0.48
1:B:114:ILE:HG22	1:B:115:MET:N	2.28	0.48
1:B:258:ARG:HD3	1:B:260:GLU:OE2	2.14	0.48
1:B:306:GLU:O	1:B:306:GLU:CG	2.58	0.48
1:A:140:TYR:N	1:A:140:TYR:CD1	2.81	0.48
1:A:194:MET:HE3	1:A:235:LEU:HD23	1.94	0.48
1:A:300:LEU:C	1:A:300:LEU:HD23	2.33	0.48
1:A:364:TRP:CD1	1:A:367:LYS:HD2	2.49	0.48
1:B:21:ILE:HB	1:B:45:ILE:HD12	1.96	0.48
1:B:244:ARG:O	1:B:246:VAL:HG23	2.13	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:31:MET:O	1:A:32:SER:C	2.49	0.47
1:A:335:ARG:HD3	1:A:473:TRP:CE2	2.49	0.47
1:A:360:ALA:O	1:A:361:ARG:C	2.49	0.47
1:A:106:GLN:O	1:A:107:ARG:C	2.49	0.47
1:B:218:HIS:C	1:B:220:LEU:H	2.17	0.47
1:B:249:TYR:CE2	1:B:298:ALA:HB2	2.50	0.47
1:A:115:MET:O	1:A:118:ARG:N	2.40	0.47
1:A:334:ILE:HG12	1:A:339:LYS:CG	2.38	0.47
1:A:303:ALA:O	1:A:304:LYS:C	2.52	0.46
1:B:346:TYR:CE1	1:B:348:HIS:HE1	2.34	0.46
1:A:39:LEU:HD13	1:A:45:ILE:HB	1.97	0.46
1:B:235:LEU:C	1:B:237:GLU:H	2.18	0.46
1:B:243:GLY:O	1:B:244:ARG:HD3	2.16	0.46
1:B:274:ILE:HG22	1:B:274:ILE:O	2.15	0.46
1:B:284:LEU:O	1:B:318:ALA:HA	2.15	0.46
1:B:20:GLN:HB3	1:B:77:GLY:O	2.15	0.46
1:B:304:LYS:HD2	1:B:304:LYS:HA	1.76	0.46
1:B:71:ALA:C	1:B:73:GLU:H	2.15	0.46
1:A:119:HIS:HD2	1:A:187:MET:HB2	1.80	0.46
1:A:88:LYS:C	1:A:90:ASP:H	2.19	0.46
1:A:23:PHE:HB2	1:A:26:ILE:HD12	1.98	0.46
1:B:228:MET:CE	1:B:235:LEU:HD22	2.45	0.46
1:A:100:LYS:O	1:A:101:ARG:HB2	2.15	0.46
1:B:294:LEU:HA	1:B:294:LEU:HD23	1.66	0.46
1:B:346:TYR:O	1:B:347:GLY:C	2.55	0.46
1:B:20:GLN:NE2	1:B:77:GLY:C	2.69	0.46
1:B:83:VAL:HG13	1:B:87:ILE:CG1	2.45	0.46
1:B:341:ARG:HD2	1:B:364:TRP:HH2	1.78	0.45
1:A:296:ALA:HB1	1:A:317:LEU:HD13	1.98	0.45
1:A:20:GLN:HE22	1:A:77:GLY:HA3	1.81	0.45
1:B:239:VAL:HB	1:B:240:PRO:HD3	1.98	0.45
1:B:355:VAL:O	1:B:356:THR:C	2.53	0.45
1:A:233:PRO:O	1:A:234:VAL:C	2.53	0.45
1:A:322:GLY:O	1:A:323:ALA:HB3	2.16	0.45
1:A:346:TYR:CZ	1:A:459:ALA:HB1	2.51	0.45
1:A:52:ASP:OD1	1:A:57:GLN:NE2	2.40	0.45
1:B:432:ILE:HD13	1:B:432:ILE:HG21	1.74	0.45
1:B:38:LEU:HA	1:B:38:LEU:HD23	1.69	0.45
1:A:249:TYR:HB2	1:A:297:THR:HG22	1.98	0.45
1:B:403:VAL:CG1	1:B:404:TYR:N	2.74	0.45
1:A:111:LEU:HD12	1:A:111:LEU:C	2.36	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:277:ASN:O	1:A:278:ASN:HB2	2.16	0.45
1:A:285:LEU:HA	1:A:285:LEU:HD12	1.58	0.45
1:B:252:SER:O	1:B:255:ALA:N	2.45	0.45
1:A:23:PHE:O	1:A:47:GLY:CA	2.65	0.44
1:A:280:ARG:C	1:A:281:ILE:HG13	2.37	0.44
1:B:274:ILE:N	1:B:274:ILE:HD12	2.31	0.44
1:B:110:MET:SD	1:B:110:MET:O	2.75	0.44
1:B:209:MET:O	1:B:210:LYS:C	2.54	0.44
1:A:283:VAL:HG12	1:A:284:LEU:N	2.31	0.44
1:A:440:LEU:O	1:A:441:GLY:C	2.52	0.44
1:A:44:GLN:O	1:A:45:ILE:HD13	2.17	0.44
1:A:25:GLY:N	1:A:48:SER:O	2.44	0.44
1:B:464:LYS:O	1:B:467:ARG:HG2	2.18	0.44
1:A:137:SER:O	1:A:138:MET:C	2.55	0.44
1:B:60:ALA:HA	1:B:64:ALA:O	2.17	0.44
1:A:38:LEU:HG	1:A:114:ILE:HD11	1.99	0.44
1:B:102:ILE:HA	1:B:103:PRO:HD3	1.88	0.44
1:B:447:ILE:HD13	1:B:447:ILE:HG21	1.69	0.44
1:A:304:LYS:O	1:A:307:GLY:N	2.32	0.44
1:A:61:GLN:HA	1:A:61:GLN:NE2	2.32	0.44
1:B:283:VAL:HG12	1:B:284:LEU:N	2.33	0.44
1:B:21:ILE:HB	1:B:45:ILE:CD1	2.48	0.44
1:A:420:CYS:SG	1:A:431:PRO:HB2	2.58	0.43
1:A:90:ASP:OD1	1:A:90:ASP:O	2.36	0.43
1:B:116:ARG:HD3	1:B:117:PHE:CE1	2.53	0.43
1:B:244:ARG:HG2	1:B:244:ARG:HH11	1.83	0.43
1:B:429:VAL:O	1:B:429:VAL:HG13	2.18	0.43
1:B:285:LEU:HA	1:B:285:LEU:HD12	1.35	0.43
1:B:375:PRO:HB2	1:B:403:VAL:HG22	2.00	0.43
1:A:194:MET:CE	1:A:235:LEU:HD23	2.48	0.43
1:A:428:LYS:HB3	1:A:428:LYS:HE2	1.69	0.43
1:B:243:GLY:O	1:B:244:ARG:CG	2.66	0.43
1:B:277:ASN:C	1:B:279:GLU:H	2.20	0.43
1:A:123:VAL:HG12	1:A:129:LYS:HA	1.99	0.43
1:A:140:TYR:N	1:A:140:TYR:HD1	2.17	0.43
1:A:184:LEU:C	1:A:186:PRO:HD3	2.39	0.43
1:A:214:VAL:O	1:A:215:LYS:C	2.53	0.43
1:A:377:ARG:NH1	1:A:377:ARG:CG	2.79	0.43
1:A:380:ARG:HD3	1:A:380:ARG:HH11	1.54	0.43
1:B:55:VAL:HB	1:B:56:THR:H	1.65	0.43
1:B:168:ARG:O	1:B:168:ARG:CG	2.67	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:376:HIS:O	1:B:377:ARG:HB2	2.19	0.43
1:A:335:ARG:HB3	1:A:336:PRO:CD	2.49	0.43
1:A:102:ILE:HA	1:A:103:PRO:HD2	1.87	0.43
1:A:108:ALA:O	1:A:109:GLN:C	2.56	0.43
1:A:455:LEU:HD23	1:A:455:LEU:HA	1.68	0.43
1:B:206:PHE:O	1:B:207:GLU:C	2.57	0.43
1:B:252:SER:O	1:B:253:GLU:C	2.57	0.43
1:B:270:HIS:O	1:B:271:TYR:HB3	2.19	0.43
1:A:442:ASP:O	1:A:443:VAL:C	2.57	0.43
1:A:58:ARG:O	1:A:59:LEU:C	2.54	0.43
1:B:147:PRO:HB3	1:B:169:TYR:HB2	2.01	0.43
1:A:182:LEU:HD23	1:A:182:LEU:HA	1.77	0.42
1:B:119:HIS:HA	1:B:187:MET:HG3	2.00	0.42
1:B:426:LEU:HA	1:B:426:LEU:HD23	1.67	0.42
1:A:142:GLN:C	1:A:144:LYS:N	2.72	0.42
1:B:19:GLN:HG3	1:B:44:GLN:CG	2.40	0.42
1:B:255:ALA:HB3	1:B:258:ARG:CB	2.39	0.42
1:A:228:MET:O	1:A:248:THR:HA	2.19	0.42
1:B:217:LEU:HA	1:B:217:LEU:HD23	1.49	0.42
1:B:235:LEU:C	1:B:237:GLU:N	2.70	0.42
1:B:55:VAL:O	1:B:58:ARG:N	2.53	0.42
1:A:125:GLY:O	1:A:129:LYS:NZ	2.41	0.42
1:A:129:LYS:HE2	1:A:129:LYS:HB2	1.77	0.42
1:B:145:LEU:HA	1:B:145:LEU:HD23	1.80	0.42
1:B:244:ARG:O	1:B:245:GLN:C	2.57	0.42
1:B:338:GLY:HA3	1:B:450:ASP:HA	2.02	0.42
1:A:19:GLN:O	1:A:44:GLN:HB2	2.20	0.42
1:B:232:ASP:HA	1:B:233:PRO:HD3	1.88	0.42
1:B:398:LEU:HA	1:B:398:LEU:HD12	1.77	0.42
1:B:421:ARG:O	1:B:422:SER:C	2.58	0.42
1:A:304:LYS:O	1:A:306:GLU:N	2.52	0.42
1:A:309:ALA:O	1:A:310:ASN:C	2.56	0.42
1:B:45:ILE:HG22	1:B:46:SER:N	2.34	0.42
1:B:134:ALA:O	1:B:135:MET:C	2.56	0.42
1:A:194:MET:CE	1:A:235:LEU:CD2	2.98	0.41
1:A:364:TRP:CG	1:A:367:LYS:HD2	2.55	0.41
1:B:291:HIS:CG	1:B:292:ASN:N	2.88	0.41
1:B:315:GLU:O	1:B:319:ASP:HB3	2.20	0.41
1:A:34:ILE:HG21	1:A:34:ILE:HD13	1.65	0.41
1:B:190:VAL:HA	1:B:227:VAL:O	2.20	0.41
1:B:235:LEU:HA	1:B:235:LEU:HD23	1.75	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:424:ARG:O	1:B:427:GLY:N	2.53	0.41
1:B:94:LEU:O	1:B:98:LYS:HG3	2.20	0.41
1:A:67:TYR:C	1:A:68:ILE:HG13	2.40	0.41
1:B:455:LEU:HA	1:B:455:LEU:HD23	1.88	0.41
1:A:378:TYR:O	1:A:379:SER:C	2.58	0.41
1:B:114:ILE:CG2	1:B:115:MET:N	2.81	0.41
1:B:277:ASN:C	1:B:279:GLU:N	2.73	0.41
1:A:317:LEU:O	1:A:318:ALA:C	2.57	0.41
1:A:367:LYS:HG3	1:A:451:GLY:O	2.20	0.41
1:A:399:ILE:HD13	1:A:399:ILE:HG21	1.83	0.41
1:A:436:ASP:CG	1:A:438:SER:OG	2.51	0.41
1:A:127:HIS:HB2	1:A:193:ASN:HD21	1.84	0.41
1:A:188:VAL:HG12	1:A:189:SER:N	2.36	0.41
1:B:182:LEU:O	1:B:219:ASN:ND2	2.52	0.41
1:A:449:GLN:O	1:A:450:ASP:C	2.57	0.41
1:A:248:THR:O	1:A:256:ASP:HB2	2.20	0.41
1:A:91:ASN:OD1	1:A:93:GLU:N	2.47	0.41
1:B:91:ASN:O	1:B:95:VAL:HG12	2.21	0.41
1:B:335:ARG:HH11	1:B:335:ARG:HD2	1.72	0.41
1:B:39:LEU:HA	1:B:39:LEU:HD12	1.74	0.41
1:B:96:THR:O	1:B:100:LYS:N	2.53	0.41
1:A:262:TYR:HA	1:A:270:HIS:O	2.21	0.41
1:B:267:PHE:CE1	1:B:363:GLY:CA	3.00	0.41
1:B:270:HIS:HD1	1:B:270:HIS:N	2.19	0.41
1:A:391:VAL:O	1:A:394:GLN:HB2	2.21	0.40
1:A:65:LYS:HE2	1:A:67:TYR:OH	2.20	0.40
1:B:264:GLN:NE2	1:B:267:PHE:CD1	2.89	0.40
1:B:436:ASP:OD1	1:B:436:ASP:C	2.59	0.40
1:A:75:ILE:CG2	1:A:102:ILE:HD12	2.52	0.40
1:B:129:LYS:O	1:B:130:THR:C	2.57	0.40
1:B:411:ILE:O	1:B:412:VAL:C	2.58	0.40
1:A:232:ASP:O	1:A:236:MET:HG2	2.22	0.40
1:A:275:CYS:HG	1:A:281:ILE:HD11	1.86	0.40
1:B:429:VAL:HG22	1:B:430:ASP:N	2.36	0.40
1:B:96:THR:O	1:B:97:SER:C	2.60	0.40
1:A:290:LYS:O	1:A:293:ALA:N	2.55	0.40
1:B:313:ILE:O	1:B:316:ALA:HB3	2.22	0.40
1:B:353:VAL:O	1:B:356:THR:HB	2.21	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	420/475 (88%)	384 (91%)	30 (7%)	6 (1%)	13	47
1	B	419/475 (88%)	376 (90%)	34 (8%)	9 (2%)	8	36
All	All	839/950 (88%)	760 (91%)	64 (8%)	15 (2%)	10	40

All (15) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	89	ASP
1	B	55	VAL
1	B	72	GLU
1	B	253	GLU
1	B	219	ASN
1	A	116	ARG
1	A	305	GLU
1	B	89	ASP
1	B	278	ASN
1	B	365	GLY
1	A	54	VAL
1	A	377	ARG
1	B	347	GLY
1	A	55	VAL
1	B	54	VAL

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	349/387 (90%)	325 (93%)	24 (7%)	18	53
1	B	348/387 (90%)	319 (92%)	29 (8%)	13	45
All	All	697/774 (90%)	644 (92%)	53 (8%)	15	49

All (53) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	57	GLN
1	A	105	ILE
1	A	110	MET
1	A	118	ARG
1	A	138	MET
1	A	168	ARG
1	A	189	SER
1	A	252	SER
1	A	261	ASP
1	A	279	GLU
1	A	306	GLU
1	A	329	GLN
1	A	339	LYS
1	A	341	ARG
1	A	350	PRO
1	A	367	LYS
1	A	379	SER
1	A	391	VAL
1	A	417	LYS
1	A	426	LEU
1	A	448	ILE
1	A	461	SER
1	A	463	SER
1	A	467	ARG
1	B	32	SER
1	B	44	GLN
1	B	50	ILE
1	B	54	VAL
1	B	72	GLU
1	B	75	ILE
1	B	95	VAL
1	B	110	MET
1	B	111	LEU
1	B	114	ILE
1	B	118	ARG

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Mol	Chain	Res	Type
1	B	131	THR
1	B	168	ARG
1	B	171	ILE
1	B	181	PHE
1	B	186	PRO
1	B	225	LEU
1	B	247	ILE
1	B	270	HIS
1	B	280	ARG
1	B	326	ARG
1	B	348	HIS
1	B	355	VAL
1	B	368	ARG
1	B	426	LEU
1	B	448	ILE
1	B	453	LEU
1	B	469	LEU
1	B	475	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (22) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	19	GLN
1	A	20	GLN
1	A	44	GLN
1	A	61	GLN
1	A	99	GLN
1	A	106	GLN
1	A	254	GLN
1	A	268	GLN
1	A	278	ASN
1	A	446	GLN
1	A	449	GLN
1	B	19	GLN
1	B	20	GLN
1	B	61	GLN
1	B	74	HIS
1	B	99	GLN
1	B	264	GLN
1	B	268	GLN
1	B	295	ASN
1	B	337	ASN

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Mol	Chain	Res	Type
1	B	449	GLN
1	B	475	ASN

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](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates ⓘ

EDS was not executed - this section is therefore empty.

6.4 Ligands ⓘ

EDS was not executed - this section is therefore empty.

6.5 Other polymers ⓘ

EDS was not executed - this section is therefore empty.