



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 07:37 PM GMT

PDB ID : 1GGM
Title : GLYCYL-TRNA SYNTHETASE FROM THERMUS THERMOPHILUS
COMPLEXED WITH GLYCYL-ADENYLATE
Authors : Arnez, J.G.; Moras, D.
Deposited on : 1999-01-27
Resolution : 3.40 Å(reported)

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

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

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

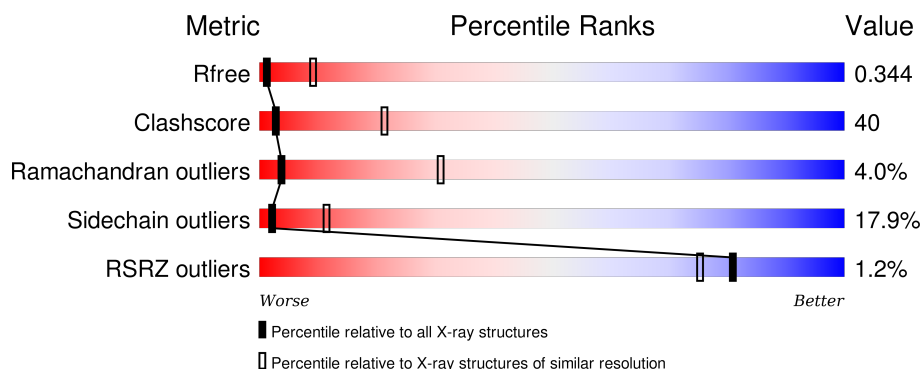
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.40 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	1476 (3.50-3.30)
Clashscore	102246	1611 (3.50-3.30)
Ramachandran outliers	100387	1571 (3.50-3.30)
Sidechain outliers	100360	1571 (3.50-3.30)
RSRZ outliers	91569	1485 (3.50-3.30)

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	442	<div> <div>37%</div> <div>50%</div> <div>13%</div> </div>
1	B	442	<div> <div>2%</div> <div>39%</div> <div>48%</div> <div>13%</div> </div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 8959 atoms, of which 1692 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.

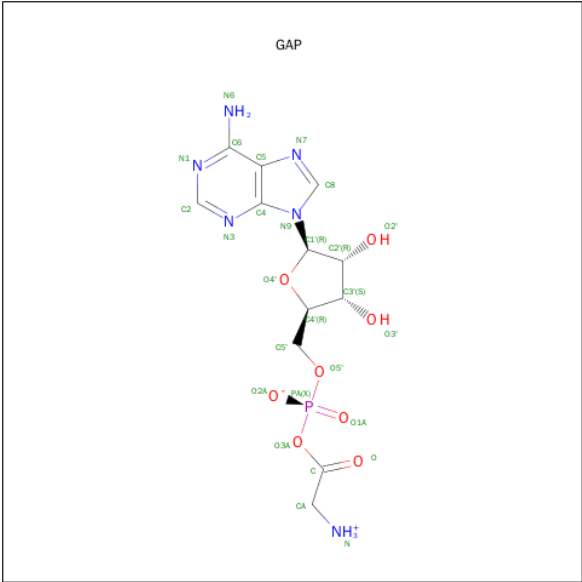
- Molecule 1 is a protein called PROTEIN (GLYCYL-TRNA SYNTHETASE).

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	442	Total	C	H	N	O	S	0	0	0
			4451	2297	841	649	656	8			
1	B	442	Total	C	H	N	O	S	0	0	0
			4440	2288	839	649	656	8			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	?	-	ARG	GAP	UNP P56206
A	?	-	ILE	GAP	UNP P56206
A	91	ALA	THR	conflict	UNP P56206
A	93	ALA	LYS	conflict	UNP P56206
B	?	-	ARG	GAP	UNP P56206
B	?	-	ILE	GAP	UNP P56206
B	91	ALA	THR	conflict	UNP P56206
B	93	ALA	LYS	conflict	UNP P56206

- Molecule 2 is GLYCYL-ADENOSINE-5'-PHOSPHATE (three-letter code: GAP) (formula: C₁₂H₁₇N₆O₈P).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	A	1	Total	C	H	N	O	P	0	0
			33	12	6	6	8	1		
2	B	1	Total	C	H	N	O	P	0	0
			33	12	6	6	8	1		

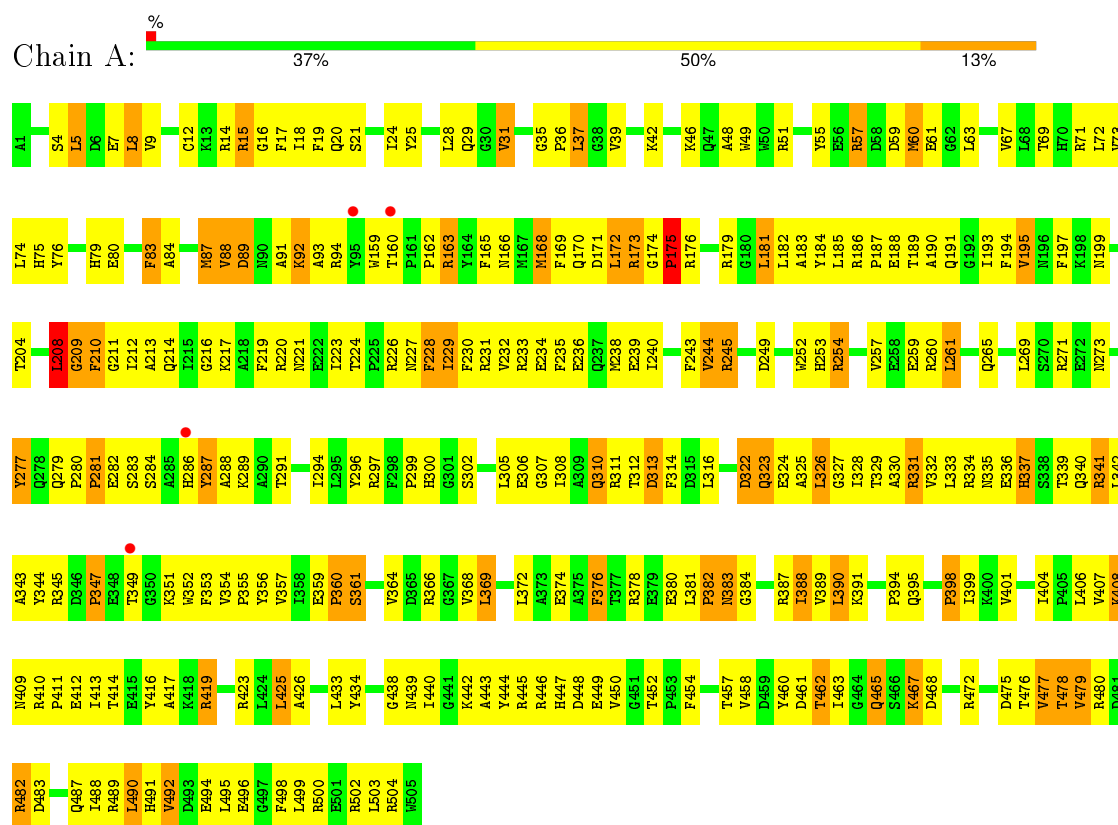
- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total O 1 1	0	0
3	B	1	Total O 1 1	0	0

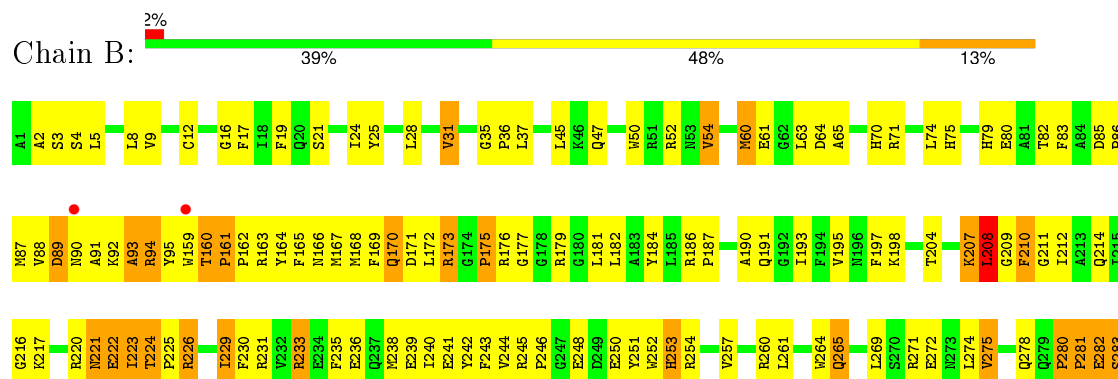
3 Residue-property plots

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: PROTEIN (GLYCYL-TRNA SYNTHETASE)



• Molecule 1: PROTEIN (GLYCYL-TRNA SYNTHETASE)





4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	122.50Å 250.10Å 106.00Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	9.00 – 3.40 11.99 – 3.39	Depositor EDS
% Data completeness (in resolution range)	89.0 (9.00-3.40) 90.3 (11.99-3.39)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	7.30	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.53 (at 3.35Å)	Xtriage
Refinement program	X-PLOR	Depositor
R, R_{free}	0.242 , 0.334 0.256 , 0.344	Depositor DCC
R_{free} test set	No test flags present.	DCC
Wilson B-factor (Å ²)	82.4	Xtriage
Anisotropy	0.229	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.24 , 92.2	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.54$, $\langle L^2 \rangle = 0.37$	Xtriage
Outliers	3 of 20314 reflections (0.015%)	Xtriage
F_o, F_c correlation	0.89	EDS
Total number of atoms	8959	wwPDB-VP
Average B, all atoms (Å ²)	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.99% 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

5.1 Standard geometry

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

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	0.72	1/3696 (0.0%)	0.95	5/4999 (0.1%)
1	B	0.67	0/3686	0.91	4/4986 (0.1%)
All	All	0.70	1/7382 (0.0%)	0.93	9/9985 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	B	0	1
All	All	0	2

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	194	PHE	CB-CG	-5.30	1.42	1.51

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	174	GLY	C-N-CD	-10.13	98.30	120.60
1	B	208	LEU	N-CA-C	6.67	129.01	111.00
1	A	208	LEU	N-CA-C	6.24	127.84	111.00
1	A	59	ASP	CB-CG-OD1	5.89	123.60	118.30
1	B	224	THR	C-N-CD	-5.52	108.45	120.60
1	A	57	ARG	NE-CZ-NH1	-5.36	117.62	120.30
1	B	345	ARG	N-CA-C	5.31	125.33	111.00
1	A	390	LEU	CA-CB-CG	5.27	127.42	115.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	305	LEU	CA-CB-CG	5.02	126.85	115.30

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	25	TYR	Sidechain
1	B	416	TYR	Sidechain

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	3610	841	3565	325	0
1	B	3601	839	3547	272	0
2	A	27	6	17	3	0
2	B	27	6	17	1	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
All	All	7267	1692	7146	578	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 40.

All (578) 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:366:ARG:NH1	2:A:1550:GAP:H2'	1.65	1.12
1:A:15:ARG:HH12	1:A:446:ARG:HA	1.23	1.03
1:B:310:GLN:NE2	1:B:312:THR:HG23	1.74	1.03
1:B:381:LEU:HD21	1:B:387:ARG:HD3	1.41	1.02
1:A:313:ASP:HB2	1:A:354:VAL:HG12	1.49	0.94
1:B:94:ARG:HD3	1:B:95:TYR:H	1.33	0.91
1:A:15:ARG:NH1	1:A:446:ARG:HA	1.83	0.91
1:B:287:TYR:HD2	1:B:311:ARG:HG2	1.36	0.89

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:175:PRO:HA	1:B:165:PHE:HE1	1.36	0.89
1:B:460:TYR:O	1:B:463:ILE:HG12	1.73	0.88
1:A:480:ARG:HG2	1:A:480:ARG:HH11	1.38	0.87
1:A:226:ARG:HB2	1:A:231:ARG:HH11	1.39	0.87
1:A:244:VAL:HG21	1:A:252:TRP:CD1	2.10	0.87
1:B:476:THR:HA	1:B:491:HIS:HA	1.57	0.85
1:A:323:GLN:HE22	1:A:335:ASN:H	1.25	0.84
1:A:388:ILE:HD12	1:A:388:ILE:H	1.43	0.82
1:A:175:PRO:HA	1:B:165:PHE:CE1	2.15	0.82
1:A:366:ARG:HH11	2:A:1550:GAP:H2'	1.45	0.81
1:B:387:ARG:HB2	1:B:445:ARG:NH1	1.95	0.81
1:B:170:GLN:OE1	1:B:182:LEU:HG	1.81	0.81
1:B:287:TYR:HA	1:B:314:PHE:CD2	2.16	0.81
1:A:410:ARG:CZ	1:A:460:TYR:HE1	1.93	0.81
1:B:310:GLN:HE22	1:B:312:THR:HG23	1.42	0.81
1:B:233:ARG:HG3	1:B:233:ARG:HH11	1.45	0.80
1:B:87:MET:HG3	1:B:94:ARG:HH12	1.46	0.80
1:A:273:ASN:HA	1:A:297:ARG:HD2	1.63	0.80
1:B:399:ILE:HG12	1:B:433:LEU:HD12	1.61	0.80
1:A:227:ASN:HB2	1:A:230:PHE:HB3	1.64	0.80
1:B:244:VAL:HG11	1:B:252:TRP:CD1	2.16	0.80
1:A:410:ARG:HH12	1:A:465:GLN:NE2	1.80	0.80
1:B:287:TYR:CD2	1:B:311:ARG:HG2	2.16	0.79
1:A:20:GLN:HE21	1:A:21:SER:N	1.80	0.78
1:A:490:LEU:HD11	1:A:495:LEU:HD13	1.66	0.77
1:A:410:ARG:NH1	1:A:460:TYR:HE1	1.83	0.77
1:A:323:GLN:NE2	1:A:335:ASN:H	1.81	0.77
1:A:460:TYR:O	1:A:463:ILE:HG12	1.85	0.76
1:B:400:LYS:HB3	1:B:503:LEU:HD13	1.67	0.76
1:A:76:TYR:CE1	1:A:335:ASN:HA	2.21	0.76
1:A:4:SER:OG	1:A:7:GLU:HG3	1.85	0.76
1:B:264:TRP:HB3	1:B:269:LEU:HD12	1.68	0.76
1:A:89:ASP:O	1:A:159:TRP:HA	1.86	0.75
1:A:193:ILE:HD11	1:A:214:GLN:HG2	1.69	0.75
1:A:410:ARG:HG3	1:A:460:TYR:CE1	2.21	0.74
1:B:2:ALA:HB2	1:B:376:PHE:HB3	1.67	0.74
1:B:496:GLU:O	1:B:500:ARG:HG3	1.88	0.74
1:A:163:ARG:N	1:A:163:ARG:HD3	2.03	0.74
1:B:173:ARG:HB3	1:B:181:LEU:HB3	1.68	0.74
1:A:229:ILE:HG22	1:A:369:LEU:HG	1.69	0.74
1:A:394:PRO:HG2	1:A:395:GLN:OE1	1.87	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:287:TYR:CD2	1:A:311:ARG:HG2	2.24	0.73
1:A:199:ASN:H	1:A:199:ASN:HD22	1.37	0.72
1:A:223:ILE:HG22	1:A:224:THR:HG23	1.71	0.72
1:B:224:THR:HB	1:B:226:ARG:NH2	2.04	0.72
1:A:88:VAL:HG22	1:A:162:PRO:HB3	1.71	0.72
1:B:410:ARG:HH21	1:B:412:GLU:HG3	1.55	0.72
1:A:28:LEU:O	1:A:31:VAL:HG13	1.90	0.72
1:A:326:LEU:HG	1:A:341:ARG:HH21	1.55	0.72
1:B:186:ARG:HH21	1:B:217:LYS:N	1.88	0.72
1:A:476:THR:HA	1:A:491:HIS:HA	1.71	0.72
1:B:75:HIS:HA	1:B:80:GLU:HG3	1.72	0.72
1:A:186:ARG:HD2	1:A:189:THR:HA	1.72	0.71
1:B:502:ARG:N	1:B:502:ARG:HD2	2.05	0.71
1:A:254:ARG:HB3	1:A:254:ARG:HH11	1.56	0.71
1:A:74:LEU:HB3	1:A:168:MET:HE1	1.73	0.71
1:B:479:VAL:HG21	1:B:498:PHE:HE2	1.55	0.71
1:A:176:ARG:HD2	1:B:163:ARG:NH2	2.06	0.70
1:A:339:THR:HG23	1:B:24:ILE:O	1.91	0.70
1:A:289:LYS:HD2	1:A:312:THR:HG21	1.72	0.70
1:A:171:ASP:OD2	1:B:169:PHE:HB3	1.91	0.70
1:B:387:ARG:HD2	1:B:445:ARG:NH2	2.06	0.70
1:A:63:LEU:CD1	1:B:35:GLY:HA2	2.22	0.70
1:A:226:ARG:HB2	1:A:231:ARG:NH1	2.04	0.70
1:B:88:VAL:HG12	1:B:159:TRP:HE3	1.57	0.70
1:A:347:PRO:HG2	1:A:349:THR:OG1	1.92	0.69
1:B:414:THR:O	1:B:418:LYS:HG3	1.92	0.69
1:A:381:LEU:HB2	1:A:382:PRO:HD2	1.73	0.69
1:A:399:ILE:HB	1:A:452:THR:HG21	1.75	0.68
1:A:399:ILE:HB	1:A:452:THR:CG2	2.22	0.68
1:B:244:VAL:HG11	1:B:252:TRP:HD1	1.58	0.68
1:B:269:LEU:HB2	1:B:274:LEU:HD11	1.75	0.68
1:A:169:PHE:HE1	1:B:173:ARG:HH21	1.40	0.68
1:A:387:ARG:HB2	1:A:445:ARG:NH1	2.09	0.68
1:A:408:LYS:NZ	1:A:408:LYS:H	1.91	0.68
1:B:310:GLN:HG3	1:B:310:GLN:O	1.94	0.68
1:A:172:LEU:HA	1:A:173:ARG:NH2	2.09	0.67
1:B:240:ILE:HB	1:B:360:PRO:HD2	1.76	0.67
1:A:71:ARG:HE	1:A:182:LEU:HD23	1.59	0.67
1:A:296:TYR:HB2	1:A:305:LEU:HD12	1.76	0.67
1:B:407:VAL:HG22	1:B:413:ILE:HD12	1.77	0.67
1:B:60:MET:HG3	1:B:211:GLY:O	1.94	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:490:LEU:CD1	1:B:495:LEU:HD12	2.25	0.66
1:A:37:LEU:HD23	1:A:398:PRO:HB2	1.77	0.66
1:B:314:PHE:C	1:B:314:PHE:HD1	1.99	0.66
1:B:467:LYS:HG3	1:B:468:ASP:N	2.11	0.66
1:B:278:GLN:O	1:B:280:PRO:HD3	1.96	0.66
1:B:387:ARG:NH1	1:B:445:ARG:HH22	1.92	0.66
1:A:488:ILE:HD12	1:A:488:ILE:H	1.60	0.66
1:A:323:GLN:HE22	1:A:335:ASN:N	1.94	0.66
1:A:199:ASN:H	1:A:199:ASN:ND2	1.92	0.66
1:A:208:LEU:O	1:A:210:PHE:N	2.29	0.66
1:A:457:THR:O	1:A:477:VAL:HG12	1.95	0.66
1:A:410:ARG:HB2	1:A:413:ILE:HD12	1.78	0.65
1:B:86:PRO:HG3	1:B:164:TYR:CE1	2.31	0.65
1:B:427:LEU:HD21	1:B:496:GLU:HG2	1.78	0.65
1:B:233:ARG:HG3	1:B:233:ARG:NH1	2.10	0.65
1:A:376:PHE:HD1	1:A:376:PHE:O	1.81	0.64
1:A:316:LEU:HD12	1:A:355:PRO:HD2	1.79	0.64
1:B:287:TYR:HD2	1:B:311:ARG:CG	2.10	0.64
1:B:5:LEU:O	1:B:9:VAL:HG23	1.97	0.64
1:A:12:CYS:HG	1:A:228:PHE:HE2	1.44	0.64
1:A:89:ASP:HB3	1:A:94:ARG:CD	2.28	0.64
1:B:61:GLU:HG2	1:B:204:THR:HG21	1.79	0.64
1:B:462:THR:HG21	1:B:477:VAL:HG13	1.80	0.64
1:A:287:TYR:HD1	1:A:287:TYR:H	1.46	0.63
1:A:476:THR:OG1	1:A:489:ARG:NH1	2.31	0.63
1:A:37:LEU:HD23	1:A:398:PRO:CB	2.29	0.63
1:B:314:PHE:CD1	1:B:314:PHE:C	2.72	0.63
1:A:410:ARG:NH1	1:A:460:TYR:CE1	2.66	0.63
1:B:502:ARG:HG2	1:B:502:ARG:HH11	1.64	0.63
1:B:265:GLN:NE2	1:B:271:ARG:HD3	2.15	0.62
1:B:387:ARG:HD2	1:B:445:ARG:HH22	1.63	0.62
1:B:191:GLN:O	1:B:195:VAL:HG22	1.99	0.62
1:A:326:LEU:HD22	1:A:354:VAL:CG2	2.30	0.62
1:B:474:LYS:NZ	1:B:474:LYS:HB2	2.15	0.62
1:B:312:THR:HG22	1:B:356:TYR:CD2	2.34	0.62
1:B:170:GLN:HE22	1:B:182:LEU:HD21	1.64	0.62
1:A:63:LEU:HD12	1:B:35:GLY:HA2	1.81	0.62
1:B:224:THR:HB	1:B:226:ARG:CZ	2.30	0.62
1:B:389:VAL:HG12	1:B:391:LYS:HG3	1.80	0.61
1:A:410:ARG:NH1	1:A:465:GLN:NE2	2.47	0.61
1:B:387:ARG:CZ	1:B:389:VAL:HG21	2.30	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:324:GLU:HB3	1:A:334:ARG:NH1	2.14	0.61
1:A:416:TYR:HA	1:A:419:ARG:NH1	2.15	0.61
1:A:16:GLY:HA2	1:A:19:PHE:CZ	2.35	0.61
1:B:497:GLY:HA2	1:B:500:ARG:HD2	1.82	0.61
1:A:195:VAL:HG23	1:B:24:ILE:HG12	1.81	0.61
1:B:229:ILE:HG13	1:B:365:ASP:HB3	1.80	0.61
1:A:176:ARG:O	1:A:181:LEU:HD11	2.00	0.61
1:B:395:GLN:HB3	1:B:505:TRP:CE2	2.36	0.61
1:B:495:LEU:O	1:B:499:LEU:HG	2.01	0.61
1:A:21:SER:HB3	1:A:31:VAL:HG22	1.82	0.61
1:A:326:LEU:HD23	1:A:343:ALA:HB2	1.83	0.60
1:A:75:HIS:HA	1:A:80:GLU:HB3	1.83	0.60
1:A:226:ARG:H	1:A:231:ARG:HB3	1.66	0.60
1:B:173:ARG:HA	1:B:173:ARG:CZ	2.32	0.60
1:A:216:GLY:O	1:A:236:GLU:HA	2.01	0.60
1:B:413:ILE:HG12	1:B:463:ILE:HD13	1.83	0.60
1:A:227:ASN:HB2	1:A:230:PHE:CB	2.30	0.60
1:A:84:ALA:CB	1:A:166:ASN:HA	2.32	0.60
1:A:312:THR:HB	1:A:356:TYR:CE2	2.37	0.60
1:B:90:ASN:HA	1:B:159:TRP:HA	1.84	0.60
1:A:170:GLN:HG2	1:A:184:TYR:CE1	2.37	0.60
1:A:89:ASP:HA	1:A:93:ALA:O	2.02	0.59
1:B:60:MET:HE1	1:B:242:TYR:HD1	1.67	0.59
1:B:173:ARG:HA	1:B:173:ARG:NE	2.18	0.59
1:B:313:ASP:HB3	1:B:356:TYR:HD1	1.67	0.59
1:B:264:TRP:CE2	1:B:305:LEU:HD11	2.36	0.59
1:A:490:LEU:CD1	1:A:495:LEU:HD13	2.33	0.59
1:A:460:TYR:HB3	1:A:465:GLN:O	2.03	0.59
1:A:18:ILE:HD13	1:A:229:ILE:HG12	1.85	0.59
1:A:35:GLY:O	1:A:39:VAL:HG23	2.03	0.59
1:B:244:VAL:HG12	1:B:245:ARG:N	2.18	0.58
1:B:281:PRO:HB2	1:B:282:GLU:OE1	2.03	0.58
1:A:190:ALA:HB2	1:A:239:GLU:OE1	2.03	0.58
1:A:445:ARG:HA	1:A:445:ARG:NE	2.19	0.58
1:A:71:ARG:NE	1:A:182:LEU:HD23	2.19	0.58
1:B:399:ILE:HB	1:B:452:THR:HG21	1.84	0.58
1:A:89:ASP:HB3	1:A:94:ARG:HD2	1.85	0.58
1:A:387:ARG:HB2	1:A:445:ARG:CZ	2.34	0.58
1:A:391:LYS:HA	1:A:482:ARG:CZ	2.33	0.58
1:A:72:LEU:HB3	1:B:25:TYR:CD2	2.39	0.58
1:B:393:LYS:HD3	1:B:505:TRP:CH2	2.39	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:253:HIS:CE1	1:A:310:GLN:HB3	2.39	0.57
1:A:240:ILE:HB	1:A:360:PRO:HD2	1.87	0.57
1:A:287:TYR:O	1:A:311:ARG:HA	2.03	0.57
1:A:326:LEU:CD2	1:A:341:ARG:HE	2.16	0.57
1:A:173:ARG:NH1	1:A:173:ARG:HB2	2.19	0.57
1:B:311:ARG:HD3	1:B:315:ASP:OD2	2.05	0.57
1:A:217:LYS:HD2	1:A:236:GLU:HG2	1.85	0.57
1:A:24:ILE:HA	1:B:339:THR:OG1	2.05	0.57
1:A:87:MET:HE2	1:A:223:ILE:HD11	1.86	0.57
1:A:84:ALA:HB2	1:A:166:ASN:HA	1.85	0.57
1:A:197:PHE:CE2	1:A:316:LEU:HD11	2.40	0.56
1:B:324:GLU:HG2	1:B:325:ALA:N	2.20	0.56
1:B:172:LEU:HD13	1:B:177:GLY:HA2	1.87	0.56
1:A:88:VAL:O	1:A:94:ARG:HA	2.05	0.56
1:B:312:THR:HG22	1:B:356:TYR:CG	2.40	0.56
1:A:227:ASN:OD1	1:A:300:HIS:ND1	2.39	0.56
1:A:87:MET:HE2	1:A:165:PHE:CG	2.40	0.56
1:A:387:ARG:HD2	1:A:445:ARG:HH22	1.69	0.56
1:B:28:LEU:HD23	1:B:31:VAL:HG11	1.87	0.56
1:B:208:LEU:O	1:B:210:PHE:N	2.38	0.56
1:A:324:GLU:HB3	1:A:334:ARG:HH12	1.70	0.56
1:A:480:ARG:NH1	1:A:480:ARG:HG2	2.12	0.56
1:B:172:LEU:CD2	1:B:182:LEU:HD12	2.36	0.56
1:A:410:ARG:HG3	1:A:460:TYR:CZ	2.41	0.56
1:A:208:LEU:HG	1:A:344:TYR:CD2	2.41	0.56
1:A:340:GLN:HG3	1:B:24:ILE:HG22	1.88	0.56
1:B:445:ARG:HA	1:B:445:ARG:NE	2.19	0.56
1:A:479:VAL:HG11	1:A:490:LEU:HD11	1.88	0.56
1:A:331:ARG:HH21	1:A:332:VAL:HA	1.70	0.56
1:B:439:ASN:O	1:B:442:LYS:HB3	2.06	0.56
1:B:208:LEU:HD23	1:B:344:TYR:CE1	2.41	0.56
1:B:166:ASN:OD1	1:B:168:MET:HG2	2.06	0.56
1:A:480:ARG:HB2	1:A:487:GLN:HG2	1.89	0.55
1:B:60:MET:HA	1:B:211:GLY:O	2.05	0.55
1:B:172:LEU:HD21	1:B:182:LEU:HD12	1.88	0.55
1:A:279:GLN:HG2	1:A:283:SER:HB3	1.88	0.55
1:B:313:ASP:OD2	1:B:356:TYR:HE1	1.89	0.55
1:B:450:VAL:HG23	1:B:452:THR:HG23	1.87	0.55
1:B:490:LEU:HD11	1:B:495:LEU:HD12	1.89	0.55
1:A:94:ARG:HH11	1:A:163:ARG:NH2	2.04	0.55
1:A:227:ASN:O	1:A:228:PHE:O	2.24	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:382:PRO:C	1:A:384:GLY:H	2.10	0.55
1:B:400:LYS:HD2	1:B:503:LEU:HD22	1.88	0.55
1:A:74:LEU:HD13	1:A:168:MET:CE	2.37	0.55
1:A:423:ARG:HH12	1:A:496:GLU:HG3	1.72	0.55
1:A:308:ILE:N	1:A:308:ILE:HD12	2.21	0.55
1:A:269:LEU:HD22	1:A:296:TYR:CE1	2.42	0.54
1:A:37:LEU:HD22	1:A:450:VAL:HB	1.88	0.54
1:B:392:LEU:HD12	1:B:451:GLY:HA3	1.90	0.54
1:B:490:LEU:HD12	1:B:495:LEU:HD12	1.88	0.54
1:B:197:PHE:HE1	1:B:243:PHE:CD2	2.26	0.54
1:B:265:GLN:HE22	1:B:271:ARG:HD3	1.73	0.54
1:A:74:LEU:HD13	1:A:168:MET:HE2	1.89	0.54
1:A:434:TYR:CD2	1:A:434:TYR:O	2.61	0.54
1:A:281:PRO:HG2	1:A:282:GLU:OE1	2.07	0.54
1:B:387:ARG:HH11	1:B:445:ARG:HH22	1.56	0.53
1:A:499:LEU:HB3	1:A:503:LEU:HD23	1.89	0.53
1:A:376:PHE:CD1	1:A:376:PHE:C	2.82	0.53
1:B:437:THR:HB	1:B:442:LYS:HE2	1.90	0.53
1:B:380:GLU:O	1:B:382:PRO:HD3	2.08	0.53
1:A:287:TYR:HE2	1:A:311:ARG:NH1	2.05	0.53
1:B:86:PRO:C	1:B:87:MET:SD	2.87	0.53
1:A:444:TYR:CE1	1:A:480:ARG:HD3	2.43	0.53
1:A:408:LYS:HZ2	1:A:408:LYS:H	1.56	0.53
1:B:480:ARG:NH1	1:B:480:ARG:HG2	2.24	0.53
1:B:313:ASP:HB3	1:B:356:TYR:CD1	2.43	0.53
1:A:326:LEU:CD2	1:A:343:ALA:HB2	2.39	0.53
1:A:325:ALA:HB3	1:A:341:ARG:NH2	2.24	0.53
1:A:503:LEU:H	1:A:503:LEU:HD22	1.73	0.53
1:A:9:VAL:HG22	1:A:228:PHE:CG	2.43	0.53
1:A:48:ALA:HB1	1:A:51:ARG:HH21	1.72	0.53
1:A:287:TYR:CE2	1:A:311:ARG:CZ	2.92	0.53
1:B:387:ARG:CZ	1:B:485:MET:SD	2.98	0.53
1:B:230:PHE:HZ	1:B:303:LEU:HB3	1.74	0.53
1:A:172:LEU:HA	1:A:173:ARG:HH21	1.71	0.52
1:A:254:ARG:HH11	1:A:254:ARG:CB	2.21	0.52
1:B:241:GLU:OE1	1:B:359:GLU:HB2	2.10	0.52
1:B:391:LYS:HA	1:B:482:ARG:CZ	2.39	0.52
1:A:326:LEU:HG	1:A:341:ARG:HE	1.74	0.52
1:A:171:ASP:C	1:A:172:LEU:HG	2.29	0.52
1:A:173:ARG:HH22	1:A:182:LEU:C	2.12	0.52
1:A:404:ILE:HG21	1:A:440:ILE:HD13	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:335:ASN:HD21	1:B:338:SER:HB2	1.73	0.52
1:B:45:LEU:HD13	1:B:371:LEU:HD11	1.90	0.52
1:B:387:ARG:HH11	1:B:445:ARG:NH2	2.07	0.52
1:B:314:PHE:O	1:B:314:PHE:HD1	1.93	0.52
1:A:60:MET:HA	1:A:211:GLY:O	2.10	0.52
1:A:89:ASP:HB3	1:A:94:ARG:HD3	1.91	0.52
1:B:474:LYS:HB2	1:B:474:LYS:HZ2	1.74	0.52
1:B:173:ARG:NH1	1:B:173:ARG:HB2	2.24	0.51
1:B:90:ASN:ND2	1:B:159:TRP:CD1	2.77	0.51
1:B:390:LEU:HD13	1:B:392:LEU:HD11	1.93	0.51
1:B:392:LEU:N	1:B:482:ARG:HH12	2.08	0.51
1:B:364:VAL:O	1:B:368:VAL:HG23	2.10	0.51
1:B:440:ILE:HG12	1:B:444:TYR:CE2	2.44	0.51
1:A:265:GLN:NE2	1:A:271:ARG:HD3	2.25	0.51
1:A:313:ASP:HB2	1:A:354:VAL:CG1	2.33	0.51
1:A:326:LEU:HD22	1:A:354:VAL:HG23	1.92	0.51
1:A:410:ARG:O	1:A:413:ILE:HB	2.09	0.51
1:B:167:MET:O	1:B:221:ASN:HB2	2.11	0.51
1:A:376:PHE:CD1	1:A:376:PHE:O	2.62	0.51
1:B:63:LEU:HG	1:B:64:ASP:H	1.76	0.51
1:A:94:ARG:HH11	1:A:163:ARG:HH21	1.57	0.51
1:A:314:PHE:HE1	1:A:331:ARG:NH2	2.09	0.51
1:A:280:PRO:O	1:A:283:SER:N	2.43	0.51
1:B:224:THR:HG22	1:B:226:ARG:HG3	1.93	0.51
1:A:166:ASN:OD1	1:A:168:MET:HG3	2.11	0.51
1:B:387:ARG:NH1	1:B:445:ARG:NH2	2.58	0.51
1:A:173:ARG:CZ	1:A:173:ARG:HB2	2.41	0.51
1:B:313:ASP:HB2	1:B:354:VAL:HG12	1.93	0.51
1:A:173:ARG:HH22	1:A:182:LEU:CA	2.24	0.51
1:B:193:ILE:HG23	1:B:212:ILE:HG21	1.93	0.51
1:A:243:PHE:HD1	1:A:357:VAL:HG12	1.76	0.51
1:A:287:TYR:HD2	1:A:311:ARG:HG2	1.74	0.50
1:B:387:ARG:NH2	1:B:389:VAL:HG21	2.27	0.50
1:A:21:SER:CB	1:A:31:VAL:HG22	2.41	0.50
1:B:324:GLU:HG2	1:B:325:ALA:H	1.77	0.50
1:B:275:VAL:HG23	1:B:295:LEU:HB2	1.93	0.50
1:B:410:ARG:HG3	1:B:460:TYR:CE2	2.45	0.50
1:B:310:GLN:CG	1:B:310:GLN:O	2.57	0.50
1:A:401:VAL:HG22	1:A:454:PHE:HB2	1.93	0.50
1:B:5:LEU:HD12	1:B:8:LEU:HB2	1.92	0.50
1:A:227:ASN:OD1	1:A:300:HIS:CE1	2.65	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:87:MET:CE	1:A:223:ILE:HD11	2.42	0.50
1:A:277:TYR:HE1	1:A:279:GLN:HG3	1.76	0.50
1:B:480:ARG:HB2	1:B:487:GLN:HE21	1.76	0.50
1:A:88:VAL:HB	1:A:159:TRP:CZ3	2.47	0.50
1:A:42:LYS:HG2	1:A:46:LYS:HE3	1.94	0.50
1:B:94:ARG:HD3	1:B:95:TYR:N	2.15	0.50
1:A:490:LEU:HD21	1:A:498:PHE:CD2	2.47	0.50
1:A:387:ARG:HB2	1:A:445:ARG:HH12	1.76	0.50
1:B:471:THR:O	1:B:474:LYS:HG2	2.11	0.50
1:B:502:ARG:HG2	1:B:502:ARG:NH1	2.27	0.50
1:B:75:HIS:CA	1:B:80:GLU:HG3	2.41	0.50
1:B:475:ASP:O	1:B:492:VAL:HG23	2.11	0.50
1:A:238:MET:HG3	1:A:364:VAL:HG22	1.93	0.49
1:A:490:LEU:HD21	1:A:498:PHE:CE2	2.47	0.49
1:A:88:VAL:HA	1:A:163:ARG:NH1	2.28	0.49
1:B:291:THR:HA	1:B:309:ALA:HA	1.92	0.49
1:B:83:PHE:CG	1:B:166:ASN:HA	2.47	0.49
1:A:495:LEU:O	1:A:499:LEU:HG	2.13	0.49
1:B:394:PRO:O	1:B:400:LYS:HE3	2.13	0.49
1:A:191:GLN:O	1:A:195:VAL:HG12	2.12	0.49
1:B:242:TYR:O	1:B:357:VAL:HA	2.13	0.49
1:B:65:ALA:H	1:B:214:GLN:HE22	1.60	0.49
1:B:12:CYS:HA	1:B:17:PHE:HB2	1.94	0.49
1:A:404:ILE:CD1	1:A:443:ALA:HB1	2.43	0.49
1:B:442:LYS:NZ	1:B:443:ALA:HA	2.28	0.49
1:B:387:ARG:HB2	1:B:445:ARG:CZ	2.42	0.49
1:B:391:LYS:HG2	1:B:483:ASP:OD1	2.13	0.49
1:A:273:ASN:HB3	1:A:297:ARG:HB2	1.95	0.49
1:B:207:LYS:H	1:B:207:LYS:HE2	1.78	0.49
1:A:323:GLN:NE2	1:A:334:ARG:HA	2.28	0.48
1:A:287:TYR:CD2	1:A:311:ARG:CZ	2.96	0.48
1:A:287:TYR:CD1	1:A:287:TYR:N	2.81	0.48
1:A:287:TYR:HD2	1:A:311:ARG:NE	2.10	0.48
1:A:326:LEU:CG	1:A:341:ARG:HE	2.26	0.48
1:B:280:PRO:HB3	1:B:281:PRO:HD2	1.94	0.48
1:A:391:LYS:HG2	1:A:483:ASP:OD1	2.12	0.48
1:A:310:GLN:HG3	1:A:310:GLN:O	2.13	0.48
1:B:410:ARG:NH2	1:B:412:GLU:HG3	2.26	0.48
1:A:199:ASN:ND2	1:A:199:ASN:N	2.61	0.48
1:A:340:GLN:HB2	1:B:24:ILE:CG2	2.43	0.48
1:B:344:TYR:O	1:B:352:TRP:HD1	1.97	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:401:VAL:HA	1:A:454:PHE:O	2.14	0.48
1:B:160:THR:HG23	1:B:161:PRO:HD2	1.95	0.48
1:B:87:MET:HG2	1:B:163:ARG:O	2.14	0.48
1:B:399:ILE:HB	1:B:452:THR:CG2	2.44	0.48
1:A:381:LEU:O	1:A:383:ASN:N	2.47	0.48
1:A:387:ARG:NE	1:A:389:VAL:HG21	2.28	0.48
1:A:208:LEU:O	1:A:209:GLY:C	2.52	0.48
1:A:331:ARG:C	1:A:331:ARG:HE	2.17	0.48
1:A:238:MET:HG3	1:A:364:VAL:CG2	2.44	0.48
1:B:224:THR:HB	1:B:226:ARG:HH21	1.77	0.48
1:B:295:LEU:HD23	1:B:304:GLU:HA	1.95	0.48
1:A:91:ALA:H	1:A:92:LYS:HD3	1.77	0.48
1:A:280:PRO:HD2	1:A:283:SER:HB2	1.96	0.47
1:B:445:ARG:HA	1:B:445:ARG:HE	1.79	0.47
1:A:254:ARG:HH11	1:A:254:ARG:CG	2.27	0.47
1:B:63:LEU:HD23	1:B:214:GLN:NE2	2.29	0.47
1:A:273:ASN:ND2	1:A:374:GLU:OE1	2.48	0.47
1:B:88:VAL:HG12	1:B:159:TRP:CE3	2.44	0.47
1:B:480:ARG:HG2	1:B:480:ARG:HH11	1.79	0.47
1:A:57:ARG:HD3	1:A:60:MET:HG3	1.97	0.47
1:A:381:LEU:CB	1:A:382:PRO:HD2	2.37	0.47
1:A:447:HIS:HA	1:A:450:VAL:HG22	1.95	0.47
1:B:92:LYS:O	1:B:93:ALA:HB2	2.15	0.47
1:B:186:ARG:HH21	1:B:217:LYS:H	1.59	0.47
1:B:401:VAL:HG21	1:B:499:LEU:HD13	1.96	0.47
1:B:322:ASP:HA	1:B:324:GLU:OE2	2.15	0.47
1:A:239:GLU:HG2	1:A:361:SER:OG	2.15	0.47
1:A:69:THR:CG2	1:A:73:VAL:HB	2.44	0.47
1:A:388:ILE:HD13	1:A:449:GLU:OE2	2.15	0.47
1:A:387:ARG:HG3	1:A:389:VAL:CG2	2.45	0.47
1:A:458:VAL:HG22	1:A:477:VAL:HG11	1.97	0.47
1:B:168:MET:HG3	1:B:184:TYR:CD2	2.50	0.47
1:A:378:ARG:O	1:A:378:ARG:HG2	2.15	0.47
1:B:260:ARG:HD3	1:B:306:GLU:OE2	2.15	0.47
1:A:173:ARG:O	1:A:181:LEU:HD13	2.14	0.47
1:A:245:ARG:HG2	1:A:353:PHE:CZ	2.50	0.47
1:A:197:PHE:CD2	1:A:316:LEU:HD11	2.50	0.46
1:A:480:ARG:NH1	1:A:480:ARG:CG	2.78	0.46
1:A:479:VAL:O	1:A:479:VAL:HG22	2.14	0.46
2:B:2550:GAP:H8	2:B:2550:GAP:O2A	2.14	0.46
1:A:496:GLU:O	1:A:500:ARG:HG3	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:472:ARG:O	1:B:472:ARG:NH1	2.47	0.46
1:A:306:GLU:HG3	1:A:307:GLY:N	2.30	0.46
1:B:87:MET:N	1:B:87:MET:SD	2.88	0.46
1:B:496:GLU:HB3	1:B:500:ARG:NH2	2.30	0.46
1:A:475:ASP:O	1:A:492:VAL:HG23	2.16	0.46
1:A:55:TYR:N	1:A:55:TYR:CD1	2.83	0.46
1:A:173:ARG:N	1:A:173:ARG:CZ	2.79	0.46
1:B:173:ARG:CZ	1:B:173:ARG:CA	2.93	0.46
1:B:444:TYR:CE1	1:B:480:ARG:HD3	2.51	0.46
1:B:372:LEU:HA	1:B:372:LEU:HD23	1.79	0.46
1:A:89:ASP:O	1:A:159:TRP:CE3	2.68	0.46
1:B:229:ILE:CG2	1:B:369:LEU:HG	2.46	0.46
1:B:320:THR:OG1	1:B:341:ARG:HA	2.15	0.46
1:A:36:PRO:HB3	1:B:61:GLU:HG3	1.97	0.46
1:A:28:LEU:HD13	1:B:70:HIS:HD2	1.80	0.46
1:A:169:PHE:CE1	1:B:173:ARG:NH2	2.82	0.46
1:A:312:THR:HG22	1:A:356:TYR:CD2	2.51	0.46
1:A:265:GLN:HE22	1:A:271:ARG:HD3	1.79	0.46
1:B:323:GLN:H	1:B:323:GLN:NE2	2.14	0.46
1:A:323:GLN:HE22	1:A:334:ARG:HA	1.81	0.46
1:B:385:GLU:H	1:B:385:GLU:CD	2.19	0.46
1:A:79:HIS:CD2	1:A:83:PHE:CD2	3.04	0.45
1:A:410:ARG:HA	1:A:411:PRO:HD2	1.79	0.45
1:A:72:LEU:CB	1:B:25:TYR:CD2	3.00	0.45
1:B:462:THR:CG2	1:B:477:VAL:HG13	2.46	0.45
1:B:238:MET:HG3	1:B:364:VAL:CG2	2.47	0.45
1:B:437:THR:O	1:B:442:LYS:HE2	2.17	0.45
1:B:16:GLY:HA2	1:B:19:PHE:CZ	2.51	0.45
1:A:12:CYS:SG	1:A:228:PHE:HE2	2.39	0.45
1:A:401:VAL:HG21	1:A:499:LEU:HD13	1.99	0.45
1:B:79:HIS:HB3	1:B:168:MET:HE3	1.99	0.45
1:A:288:ALA:HB1	1:A:291:THR:CG2	2.47	0.45
1:B:253:HIS:CD2	1:B:310:GLN:HB2	2.51	0.45
1:B:387:ARG:NE	1:B:389:VAL:HG21	2.32	0.45
1:A:300:HIS:CD2	1:A:300:HIS:H	2.34	0.45
1:B:244:VAL:CG1	1:B:245:ARG:N	2.79	0.45
1:A:389:VAL:HG13	1:A:448:ASP:HB3	1.98	0.45
1:A:467:LYS:HE2	1:A:467:LYS:N	2.32	0.45
1:B:410:ARG:HA	1:B:411:PRO:HD2	1.82	0.45
1:A:12:CYS:SG	1:A:228:PHE:CE2	3.09	0.45
1:A:423:ARG:O	1:A:426:ALA:HB3	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:311:ARG:NH1	1:A:359:GLU:OE1	2.50	0.45
1:A:503:LEU:HD22	1:A:503:LEU:N	2.32	0.45
1:A:287:TYR:CE2	1:A:311:ARG:NH1	2.84	0.45
1:A:326:LEU:HG	1:A:341:ARG:NH2	2.27	0.45
1:A:312:THR:HB	1:A:356:TYR:CZ	2.52	0.45
1:B:229:ILE:HG22	1:B:369:LEU:HG	1.99	0.45
1:B:261:LEU:HD11	1:B:274:LEU:HB3	1.98	0.44
1:B:8:LEU:HD11	1:B:373:ALA:HA	1.99	0.44
1:A:173:ARG:HH22	1:A:183:ALA:N	2.15	0.44
1:A:296:TYR:OH	1:A:374:GLU:HB2	2.18	0.44
1:B:222:GLU:HA	1:B:222:GLU:OE2	2.17	0.44
1:A:383:ASN:N	1:A:383:ASN:OD1	2.51	0.44
1:B:484:THR:O	1:B:486:GLU:N	2.50	0.44
1:A:444:TYR:CZ	1:A:480:ARG:HD3	2.53	0.44
1:A:188:GLU:OE2	1:A:190:ALA:HB3	2.17	0.44
1:A:410:ARG:CZ	1:A:460:TYR:CE1	2.85	0.44
1:B:481:ASP:O	1:B:485:MET:N	2.49	0.44
1:B:244:VAL:CG1	1:B:252:TRP:CD1	2.97	0.44
1:B:376:PHE:CE2	1:B:388:ILE:CG2	3.01	0.44
1:A:169:PHE:CD2	1:A:219:PHE:HB3	2.52	0.44
1:A:387:ARG:HB2	1:A:445:ARG:NH2	2.32	0.44
1:B:60:MET:HE1	1:B:242:TYR:CD1	2.52	0.44
1:B:172:LEU:HD22	1:B:177:GLY:HA2	2.00	0.44
1:B:346:ASP:HB2	1:B:350:GLY:HA2	2.00	0.44
1:A:310:GLN:HE21	1:A:310:GLN:CA	2.30	0.44
1:A:326:LEU:HD13	1:A:328:ILE:CD1	2.48	0.44
1:B:85:ASP:O	1:B:87:MET:SD	2.76	0.44
1:A:229:ILE:HA	1:A:229:ILE:HD12	1.72	0.44
1:B:416:TYR:HD2	1:B:419:ARG:NH2	2.15	0.44
1:A:322:ASP:HB2	1:A:341:ARG:HG2	1.99	0.44
1:B:222:GLU:HG3	1:B:224:THR:O	2.18	0.44
1:B:280:PRO:O	1:B:283:SER:N	2.50	0.44
1:B:416:TYR:HD2	1:B:419:ARG:HH21	1.65	0.44
1:B:321:LYS:HD2	1:B:340:GLN:HA	2.00	0.44
1:B:310:GLN:HE22	1:B:312:THR:CG2	2.22	0.43
1:B:381:LEU:C	1:B:383:ASN:H	2.21	0.43
1:A:387:ARG:CZ	1:A:389:VAL:HG21	2.48	0.43
1:B:235:PHE:CD1	1:B:235:PHE:N	2.85	0.43
1:A:173:ARG:CB	1:A:173:ARG:CZ	2.95	0.43
1:A:406:LEU:HD12	1:A:406:LEU:HA	1.40	0.43
1:A:329:THR:OG1	1:A:330:ALA:N	2.50	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:172:LEU:CA	1:A:173:ARG:HH21	2.31	0.43
1:B:410:ARG:HG3	1:B:460:TYR:CZ	2.53	0.43
1:A:243:PHE:CD1	1:A:357:VAL:HG12	2.53	0.43
1:B:60:MET:CE	1:B:211:GLY:HA3	2.47	0.43
1:B:197:PHE:CE1	1:B:243:PHE:CD2	3.05	0.43
1:A:381:LEU:O	1:A:384:GLY:N	2.51	0.43
1:A:20:GLN:NE2	1:A:21:SER:N	2.59	0.43
1:B:173:ARG:NE	1:B:173:ARG:CA	2.81	0.43
1:B:252:TRP:HA	1:B:252:TRP:CE3	2.53	0.43
1:B:393:LYS:HD3	1:B:505:TRP:CZ3	2.53	0.43
1:A:169:PHE:HB3	1:B:171:ASP:OD2	2.17	0.43
1:B:90:ASN:CG	1:B:91:ALA:N	2.72	0.43
1:A:261:LEU:HG	1:A:294:ILE:HD13	2.01	0.43
1:A:219:PHE:HE2	1:A:234:GLU:OE1	2.01	0.43
1:B:405:PRO:HD2	1:B:435:GLU:O	2.19	0.43
1:B:224:THR:HB	1:B:226:ARG:NE	2.32	0.43
1:B:186:ARG:NH2	1:B:217:LYS:N	2.61	0.43
1:B:502:ARG:N	1:B:502:ARG:CD	2.79	0.43
1:A:439:ASN:HB3	1:A:442:LYS:HB2	2.01	0.43
1:A:359:GLU:OE2	2:A:1550:GAP:HA1	2.19	0.43
1:A:173:ARG:CA	1:A:173:ARG:NE	2.82	0.43
1:A:12:CYS:HA	1:A:17:PHE:HB2	2.00	0.43
1:A:197:PHE:CD1	1:A:197:PHE:C	2.92	0.43
1:A:257:VAL:HG23	1:A:308:ILE:HG21	1.99	0.43
1:A:60:MET:HE1	1:A:213:ALA:CB	2.48	0.43
1:B:294:ILE:HG13	1:B:308:ILE:CD1	2.48	0.43
1:B:190:ALA:HB2	1:B:239:GLU:OE1	2.18	0.43
1:A:382:PRO:C	1:A:384:GLY:N	2.71	0.42
1:A:5:LEU:O	1:A:8:LEU:HB2	2.18	0.42
1:B:253:HIS:O	1:B:257:VAL:HG23	2.19	0.42
1:A:399:ILE:HB	1:A:452:THR:HG22	1.98	0.42
1:B:444:TYR:CD1	1:B:480:ARG:HD3	2.54	0.42
1:A:60:MET:HE2	1:A:60:MET:HB3	1.51	0.42
1:A:61:GLU:HG2	1:A:204:THR:HG21	2.01	0.42
1:A:287:TYR:CD2	1:A:311:ARG:NE	2.88	0.42
1:A:413:ILE:HG12	1:A:463:ILE:HD13	2.01	0.42
1:A:260:ARG:NH1	1:A:306:GLU:OE2	2.52	0.42
1:B:50:TRP:O	1:B:54:VAL:HG23	2.20	0.42
1:B:297:ARG:HD2	1:B:297:ARG:HA	1.88	0.42
1:A:67:VAL:HG21	1:A:219:PHE:HE1	1.84	0.42
1:A:488:ILE:HG22	1:A:489:ARG:N	2.34	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:368:VAL:HG12	1:A:372:LEU:HD12	2.01	0.42
1:A:8:LEU:HD22	1:A:8:LEU:HA	1.72	0.42
1:A:425:LEU:O	1:A:425:LEU:HD12	2.20	0.42
1:B:253:HIS:CD2	1:B:310:GLN:CB	3.02	0.42
1:A:14:ARG:NH1	1:A:449:GLU:OE1	2.53	0.42
1:A:407:VAL:HG21	1:A:460:TYR:CE2	2.54	0.42
1:A:410:ARG:HH12	1:A:465:GLN:CD	2.22	0.42
1:A:49:TRP:HE1	1:A:260:ARG:NH1	2.17	0.42
1:B:37:LEU:CD1	1:B:450:VAL:HG11	2.50	0.42
1:B:74:LEU:HD11	1:B:187:PRO:HD3	2.02	0.42
1:B:216:GLY:O	1:B:236:GLU:HA	2.20	0.42
1:A:220:ARG:O	1:A:233:ARG:HA	2.19	0.42
1:A:72:LEU:HD23	1:A:72:LEU:HA	1.84	0.42
1:B:330:ALA:O	1:B:332:VAL:HG13	2.20	0.42
1:A:328:ILE:CG2	1:A:329:THR:N	2.83	0.42
1:A:162:PRO:C	1:A:163:ARG:HD3	2.39	0.42
1:B:440:ILE:HG12	1:B:444:TYR:CD2	2.55	0.42
1:B:484:THR:C	1:B:486:GLU:H	2.23	0.42
1:A:409:ASN:OD1	1:A:410:ARG:HG2	2.20	0.42
1:B:414:THR:O	1:B:417:ALA:HB3	2.20	0.42
1:A:238:MET:CG	1:A:364:VAL:HG22	2.50	0.42
1:B:484:THR:C	1:B:486:GLU:N	2.73	0.42
1:B:187:PRO:O	1:B:220:ARG:NE	2.52	0.41
1:B:399:ILE:CG1	1:B:433:LEU:HD12	2.42	0.41
1:B:5:LEU:O	1:B:8:LEU:HB2	2.20	0.41
1:A:478:THR:HG23	1:A:489:ARG:HB2	2.02	0.41
1:A:340:GLN:CG	1:B:24:ILE:HG22	2.49	0.41
1:A:413:ILE:CG1	1:A:463:ILE:HD13	2.50	0.41
1:B:458:VAL:HG22	1:B:477:VAL:HG11	2.01	0.41
1:A:197:PHE:CD2	1:A:316:LEU:HD21	2.56	0.41
1:A:94:ARG:NH1	1:A:163:ARG:NH2	2.69	0.41
1:B:225:PRO:C	1:B:226:ARG:HG3	2.41	0.41
1:B:88:VAL:HB	1:B:159:TRP:HZ3	1.85	0.41
1:B:467:LYS:CG	1:B:468:ASP:N	2.82	0.41
1:B:65:ALA:H	1:B:214:GLN:NE2	2.18	0.41
1:B:385:GLU:HB2	1:B:386:GLU:H	1.65	0.41
1:B:433:LEU:HD23	1:B:434:TYR:N	2.35	0.41
1:B:376:PHE:CE2	1:B:388:ILE:HG23	2.55	0.41
1:A:235:PHE:N	1:A:235:PHE:CD1	2.87	0.41
1:A:160:THR:OG1	1:A:163:ARG:NH1	2.53	0.41
1:A:462:THR:HG23	1:A:476:THR:O	2.19	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:74:LEU:HD23	1:A:74:LEU:HA	1.82	0.41
1:B:456:VAL:HG21	1:B:495:LEU:HD21	2.02	0.41
1:A:310:GLN:CG	1:A:310:GLN:O	2.68	0.41
1:A:187:PRO:HA	1:A:219:PHE:O	2.20	0.41
1:B:21:SER:HB3	1:B:31:VAL:O	2.21	0.41
1:A:61:GLU:O	1:A:212:ILE:HA	2.20	0.41
1:A:240:ILE:O	1:A:359:GLU:HG3	2.21	0.41
1:A:388:ILE:HD12	1:A:388:ILE:N	2.21	0.41
1:B:393:LYS:HA	1:B:394:PRO:HD3	1.79	0.41
1:A:445:ARG:HA	1:A:445:ARG:HE	1.83	0.41
1:A:60:MET:HE1	1:A:213:ALA:HB3	2.02	0.41
1:A:364:VAL:O	1:A:368:VAL:HG23	2.21	0.41
1:B:89:ASP:HB2	1:B:160:THR:HB	2.02	0.41
1:A:414:THR:O	1:A:417:ALA:HB3	2.21	0.41
1:B:251:TYR:O	1:B:254:ARG:HB3	2.21	0.41
1:A:311:ARG:HG3	1:A:311:ARG:H	1.58	0.40
1:B:437:THR:C	1:B:442:LYS:HE2	2.42	0.40
1:B:71:ARG:HG3	1:B:184:TYR:HE1	1.86	0.40
1:A:173:ARG:NH2	1:A:183:ALA:N	2.70	0.40
1:A:88:VAL:HA	1:A:163:ARG:CZ	2.51	0.40
1:A:169:PHE:HB2	1:A:185:LEU:HD12	2.03	0.40
1:B:167:MET:CE	1:B:223:ILE:H	2.33	0.40
1:B:445:ARG:O	1:B:446:ARG:C	2.59	0.40
1:A:14:ARG:O	1:A:14:ARG:HG2	2.20	0.40
1:A:223:ILE:HA	1:A:223:ILE:HD13	1.93	0.40
1:B:226:ARG:HD2	1:B:231:ARG:HD3	2.03	0.40
1:A:340:GLN:HB2	1:B:24:ILE:HG22	2.03	0.40
1:A:433:LEU:HD12	1:A:433:LEU:HA	1.87	0.40
1:A:460:TYR:O	1:A:461:ASP:C	2.59	0.40
1:A:337:HIS:ND1	1:A:337:HIS:N	2.70	0.40
1:A:72:LEU:HD11	1:A:337:HIS:CD2	2.56	0.40
1:B:480:ARG:CG	1:B:480:ARG:HH11	2.35	0.40
1:B:220:ARG:O	1:B:233:ARG:HA	2.21	0.40
1:B:399:ILE:H	1:B:452:THR:HG22	1.87	0.40
1:B:298:PHE:HE2	1:B:369:LEU:HB3	1.87	0.40
1:A:404:ILE:HD13	1:A:443:ALA:CB	2.51	0.40
1:B:333:LEU:HD12	1:B:333:LEU:H	1.87	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	438/442 (99%)	359 (82%)	62 (14%)	17 (4%)	4	32
1	B	438/442 (99%)	351 (80%)	69 (16%)	18 (4%)	3	30
All	All	876/884 (99%)	710 (81%)	131 (15%)	35 (4%)	4	31

All (35) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	175	PRO
1	A	228	PHE
1	B	89	ASP
1	B	93	ALA
1	B	175	PRO
1	A	209	GLY
1	A	284	SER
1	A	327	GLY
1	A	438	GLY
1	B	209	GLY
1	B	348	GLU
1	B	438	GLY
1	A	83	PHE
1	A	347	PRO
1	A	382	PRO
1	B	221	ASN
1	B	222	GLU
1	B	281	PRO
1	B	284	SER
1	B	482	ARG
1	A	286	HIS
1	B	162	PRO
1	A	221	ASN
1	B	161	PRO
1	B	376	PHE

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Mol	Chain	Res	Type
1	B	492	VAL
1	A	342	LEU
1	A	360	PRO
1	A	376	PHE
1	A	482	ARG
1	A	492	VAL
1	A	281	PRO
1	B	360	PRO
1	B	36	PRO
1	B	229	ILE

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	375/376 (100%)	306 (82%)	69 (18%)	2	10
1	B	374/376 (100%)	309 (83%)	65 (17%)	2	13
All	All	749/752 (100%)	615 (82%)	134 (18%)	2	11

All (134) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	5	LEU
1	A	8	LEU
1	A	15	ARG
1	A	29	GLN
1	A	31	VAL
1	A	37	LEU
1	A	60	MET
1	A	87	MET
1	A	88	VAL
1	A	89	ASP
1	A	92	LYS
1	A	163	ARG
1	A	168	MET

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Mol	Chain	Res	Type
1	A	172	LEU
1	A	173	ARG
1	A	175	PRO
1	A	179	ARG
1	A	181	LEU
1	A	195	VAL
1	A	208	LEU
1	A	210	PHE
1	A	229	ILE
1	A	232	VAL
1	A	244	VAL
1	A	245	ARG
1	A	249	ASP
1	A	254	ARG
1	A	259	GLU
1	A	261	LEU
1	A	277	TYR
1	A	287	TYR
1	A	299	PRO
1	A	302	SER
1	A	310	GLN
1	A	313	ASP
1	A	322	ASP
1	A	323	GLN
1	A	326	LEU
1	A	331	ARG
1	A	333	LEU
1	A	336	GLU
1	A	337	HIS
1	A	341	ARG
1	A	345	ARG
1	A	351	LYS
1	A	352	TRP
1	A	361	SER
1	A	369	LEU
1	A	380	GLU
1	A	383	ASN
1	A	388	ILE
1	A	390	LEU
1	A	398	PRO
1	A	408	LYS
1	A	412	GLU

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Mol	Chain	Res	Type
1	A	419	ARG
1	A	425	LEU
1	A	462	THR
1	A	465	GLN
1	A	467	LYS
1	A	468	ASP
1	A	472	ARG
1	A	477	VAL
1	A	478	THR
1	A	479	VAL
1	A	490	LEU
1	A	494	GLU
1	A	502	ARG
1	A	504	ARG
1	B	3	SER
1	B	4	SER
1	B	31	VAL
1	B	47	GLN
1	B	52	ARG
1	B	54	VAL
1	B	60	MET
1	B	82	THR
1	B	94	ARG
1	B	160	THR
1	B	170	GLN
1	B	173	ARG
1	B	175	PRO
1	B	176	ARG
1	B	179	ARG
1	B	198	LYS
1	B	207	LYS
1	B	208	LEU
1	B	210	PHE
1	B	223	ILE
1	B	226	ARG
1	B	233	ARG
1	B	246	PRO
1	B	248	GLU
1	B	250	GLU
1	B	253	HIS
1	B	265	GLN
1	B	272	GLU

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Mol	Chain	Res	Type
1	B	275	VAL
1	B	280	PRO
1	B	282	GLU
1	B	283	SER
1	B	291	THR
1	B	310	GLN
1	B	312	THR
1	B	314	PHE
1	B	334	ARG
1	B	345	ARG
1	B	346	ASP
1	B	348	GLU
1	B	352	TRP
1	B	357	VAL
1	B	369	LEU
1	B	382	PRO
1	B	383	ASN
1	B	386	GLU
1	B	392	LEU
1	B	393	LYS
1	B	398	PRO
1	B	410	ARG
1	B	418	LYS
1	B	423	ARG
1	B	425	LEU
1	B	431	ARG
1	B	442	LYS
1	B	445	ARG
1	B	462	THR
1	B	468	ASP
1	B	474	LYS
1	B	477	VAL
1	B	478	THR
1	B	489	ARG
1	B	495	LEU
1	B	501	GLU
1	B	502	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (15) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	20	GLN

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Mol	Chain	Res	Type
1	A	29	GLN
1	A	44	ASN
1	A	199	ASN
1	A	265	GLN
1	A	278	GLN
1	A	310	GLN
1	A	323	GLN
1	A	340	GLN
1	A	465	GLN
1	B	70	HIS
1	B	214	GLN
1	B	265	GLN
1	B	323	GLN
1	B	487	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	GAP	A	1550	-	23,29,29	0.80	0	25,43,43	1.26	2 (8%)
2	GAP	B	2550	-	23,29,29	0.72	0	25,43,43	1.06	3 (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	GAP	A	1550	-	-	0/11/33/33	0/3/3/3
2	GAP	B	2550	-	-	0/11/33/33	0/3/3/3

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	2550	GAP	O-C-CA	-2.02	113.23	117.98
2	A	1550	GAP	O3A-C-O	2.25	126.42	121.67
2	B	2550	GAP	O3A-C-O	2.25	126.43	121.67
2	B	2550	GAP	O2A-PA-O3A	2.47	111.81	104.16
2	A	1550	GAP	C-CA-N	4.33	117.51	111.70

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1550	GAP	3	0
2	B	2550	GAP	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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	442/442 (100%)	-0.44	4 (0%) 85 81	12, 39, 77, 104	0
1	B	442/442 (100%)	-0.38	7 (1%) 74 69	12, 43, 84, 108	0
All	All	884/884 (100%)	-0.41	11 (1%) 81 75	12, 41, 81, 108	0

All (11) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	286	HIS	3.4
1	B	159	TRP	3.4
1	B	90	ASN	2.8
1	A	286	HIS	2.6
1	A	160	THR	2.5
1	B	466	SER	2.5
1	B	284	SER	2.5
1	B	471	THR	2.3
1	A	349	THR	2.2
1	A	95	TYR	2.2
1	B	285	ALA	2.1

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

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

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
2	GAP	B	2550	27/27	0.94	0.20	0.66	0,46,58,61	0
2	GAP	A	1550	27/27	0.94	0.17	-0.09	0,28,42,44	0

6.5 Other polymers [i](#)

There are no such residues in this entry.