



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 02:07 PM UTC

PDB ID : 1GGM / pdb_00001ggm
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

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

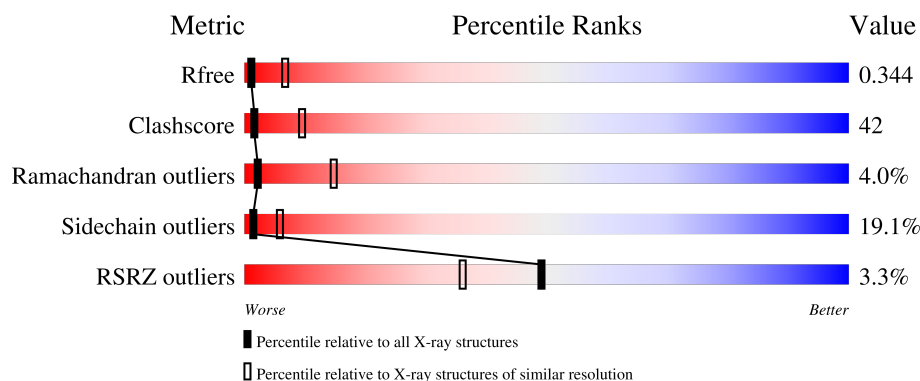
1 Overall quality at a glance

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}	180053	1001 (3.44-3.36)
Clashscore	190562	1022 (3.44-3.36)
Ramachandran outliers	187476	1012 (3.44-3.36)
Sidechain outliers	187428	1012 (3.44-3.36)
RSRZ outliers	180081	1001 (3.44-3.36)

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 of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. 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	3% 31% 48% 19% .
1	B	442	3% 35% 48% 16% .

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 Glycine-tRNA ligase.

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 44 discrepancies between the modelled and reference sequences:

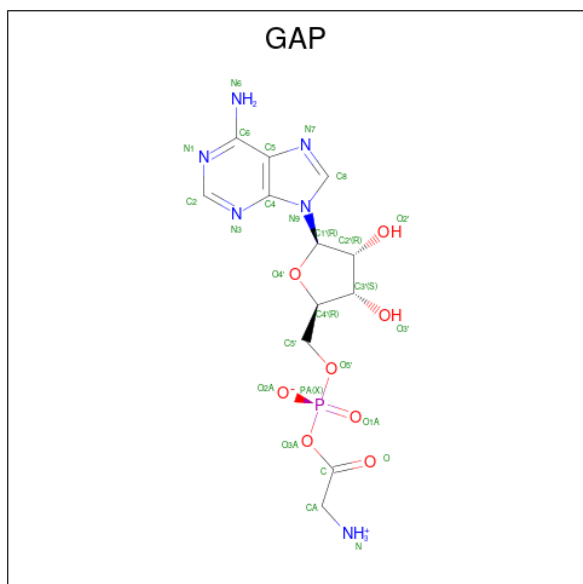
Chain	Residue	Modelled	Actual	Comment	Reference
A	1	ALA	PRO	conflict	UNP P56206
A	91	ALA	ARG	conflict	UNP P56206
A	92	LYS	ILE	conflict	UNP P56206
A	93	ALA	THR	conflict	UNP P56206
A	94	ARG	LYS	conflict	UNP P56206
A	95	TYR	LYS	conflict	UNP P56206
A	170	GLN	LYS	conflict	UNP P56206
A	171	ASP	THR	conflict	UNP P56206
A	172	LEU	TYR	conflict	UNP P56206
A	173	ARG	VAL	conflict	UNP P56206
A	176	ARG	VAL	conflict	UNP P56206
A	177	GLY	GLU	conflict	UNP P56206
A	178	GLY	ASP	conflict	UNP P56206
A	179	ARG	GLU	conflict	UNP P56206
A	180	GLY	ALA	conflict	UNP P56206
A	181	LEU	SER	conflict	UNP P56206
A	209	GLY	PRO	conflict	UNP P56206
A	283	SER	GLU	conflict	UNP P56206
A	284	SER	LEU	conflict	UNP P56206
A	302	SER	LEU	conflict	UNP P56206
A	303	LEU	GLU	conflict	UNP P56206
A	310	GLN	ASN	conflict	UNP P56206
B	1	ALA	PRO	conflict	UNP P56206
B	91	ALA	ARG	conflict	UNP P56206
B	92	LYS	ILE	conflict	UNP P56206

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Chain	Residue	Modelled	Actual	Comment	Reference
B	93	ALA	THR	conflict	UNP P56206
B	94	ARG	LYS	conflict	UNP P56206
B	95	TYR	LYS	conflict	UNP P56206
B	170	GLN	LYS	conflict	UNP P56206
B	171	ASP	THR	conflict	UNP P56206
B	172	LEU	TYR	conflict	UNP P56206
B	173	ARG	VAL	conflict	UNP P56206
B	176	ARG	VAL	conflict	UNP P56206
B	177	GLY	GLU	conflict	UNP P56206
B	178	GLY	ASP	conflict	UNP P56206
B	179	ARG	GLU	conflict	UNP P56206
B	180	GLY	ALA	conflict	UNP P56206
B	181	LEU	SER	conflict	UNP P56206
B	209	GLY	PRO	conflict	UNP P56206
B	283	SER	GLU	conflict	UNP P56206
B	284	SER	LEU	conflict	UNP P56206
B	302	SER	LEU	conflict	UNP P56206
B	303	LEU	GLU	conflict	UNP P56206
B	310	GLN	ASN	conflict	UNP P56206

- Molecule 2 is GLYCYL-ADENOSINE-5'-PHOSPHATE (CCD ID: GAP) (formula: $C_{12}H_{17}N_6O_8P$).



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

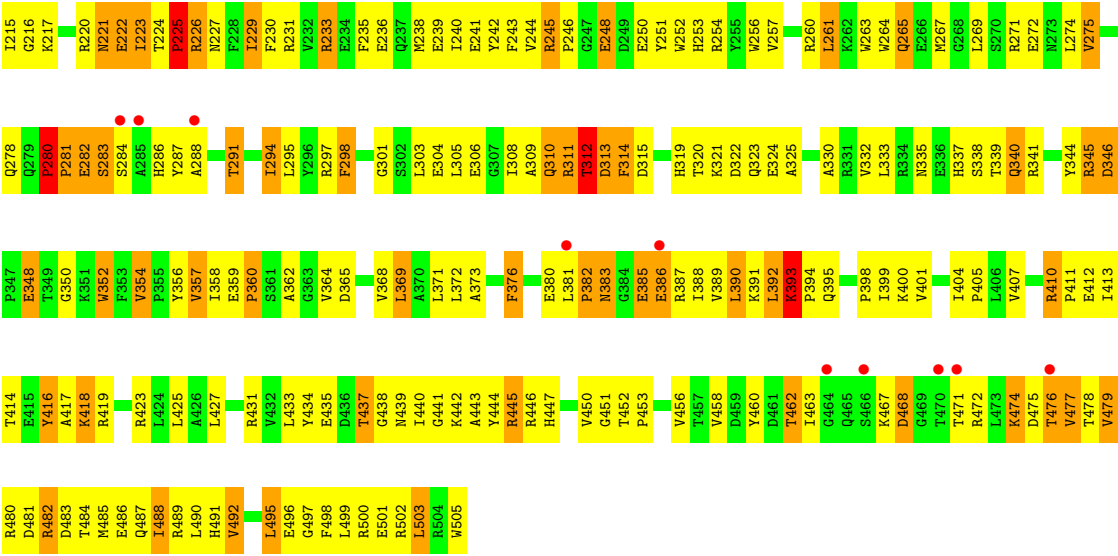
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Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	B	1	Total	C	H	N	O	P	0	0
			33	12	6	6	8	1		

- Molecule 3 is water.

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



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 9.00 – 3.40	Depositor EDS
% Data completeness (in resolution range)	89.0 (9.00-3.40) 85.9 (9.00-3.40)	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	807 reflections (3.97%)	wwPDB-VP
Wilson B-factor (Å ²)	82.4	Xtriage
Anisotropy	0.229	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.17 , 68.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.54$, $\langle L^2 \rangle = 0.37$	Xtriage
Estimated twinning fraction	No twinning to report.	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, 0.333 respectively for untwinned datasets, and 0.375, 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	0.90	2/3696 (0.1%)	1.37	72/4999 (1.4%)
1	B	0.81	1/3686 (0.0%)	1.33	52/4986 (1.0%)
All	All	0.86	3/7382 (0.0%)	1.35	124/9985 (1.2%)

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 (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	312	THR	CA-C	-5.89	1.46	1.53
1	A	401	VAL	CA-CB	-5.65	1.47	1.54
1	A	399	ILE	CA-CB	-5.16	1.48	1.54

All (124) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	161	PRO	CA-C-N	10.56	133.04	119.84
1	B	161	PRO	C-N-CA	10.56	133.04	119.84
1	B	345	ARG	N-CA-C	9.86	125.33	112.72
1	A	93	ALA	N-CA-C	9.25	123.01	109.69
1	A	345	ARG	N-CA-C	8.86	124.22	113.23
1	B	208	LEU	N-CA-C	8.55	129.01	110.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	3	SER	N-CA-C	8.46	121.27	111.11
1	A	463	ILE	N-CA-C	8.15	118.20	110.53
1	B	227	ASN	N-CA-C	8.03	120.31	110.91
1	A	208	LEU	N-CA-C	8.00	127.84	110.80
1	A	81	ALA	N-CA-C	7.97	120.05	111.36
1	A	381	LEU	CA-C-N	7.96	129.79	119.84
1	A	381	LEU	C-N-CA	7.96	129.79	119.84
1	A	311	ARG	N-CA-C	-7.90	100.10	110.53
1	B	346	ASP	N-CA-C	7.90	124.10	107.91
1	A	437	THR	N-CA-C	7.75	121.10	109.25
1	B	280	PRO	CA-C-N	7.48	129.19	119.84
1	B	280	PRO	C-N-CA	7.48	129.19	119.84
1	A	453	PRO	N-CA-C	7.38	123.79	113.53
1	A	5	LEU	N-CA-C	-7.31	103.31	111.28
1	B	215	ILE	N-CA-C	-7.29	97.81	108.89
1	A	406	LEU	N-CA-C	7.27	119.28	111.36
1	B	453	PRO	N-CA-C	7.26	124.56	113.75
1	A	161	PRO	CA-C-N	-7.25	113.25	120.21
1	A	161	PRO	C-N-CA	-7.25	113.25	120.21
1	A	174	GLY	CA-C-N	7.18	128.81	119.84
1	A	174	GLY	C-N-CA	7.18	128.81	119.84
1	A	232	VAL	N-CA-C	6.88	118.85	108.80
1	A	358	ILE	N-CA-C	-6.70	98.79	108.17
1	B	311	ARG	N-CA-C	-6.61	101.77	110.43
1	B	173	ARG	N-CA-C	6.61	120.02	108.52
1	B	358	ILE	N-CA-C	-6.58	98.96	108.17
1	B	393	LYS	CA-C-N	6.58	128.06	119.84
1	B	393	LYS	C-N-CA	6.58	128.06	119.84
1	B	165	PHE	N-CA-C	6.55	119.81	109.39
1	A	247	GLY	N-CA-C	6.51	121.11	112.77
1	A	174	GLY	C-N-CD	-6.51	98.30	125.00
1	B	248	GLU	N-CA-C	6.50	120.81	113.01
1	A	348	GLU	N-CA-C	-6.47	104.65	112.54
1	A	354	VAL	CA-C-N	6.45	126.47	119.89
1	A	354	VAL	C-N-CA	6.45	126.47	119.89
1	A	503	LEU	N-CA-C	6.41	120.82	113.19
1	B	207	LYS	N-CA-C	-6.41	101.04	110.52
1	A	388	ILE	N-CA-C	-6.33	99.25	108.87
1	B	404	ILE	N-CA-C	6.32	117.69	107.71
1	A	289	LYS	N-CA-C	-6.30	104.51	111.82
1	B	441	GLY	N-CA-C	-6.26	105.21	112.73
1	B	337	HIS	N-CA-C	6.22	124.06	110.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	447	HIS	N-CA-C	6.22	118.14	111.36
1	A	53	ASN	N-CA-C	6.21	120.71	113.20
1	A	10	ALA	N-CA-C	6.20	118.12	111.36
1	A	185	LEU	N-CA-C	-6.18	99.21	109.46
1	A	230	PHE	N-CA-C	6.17	123.94	110.80
1	A	280	PRO	CA-C-N	6.16	127.54	119.84
1	A	280	PRO	C-N-CA	6.16	127.54	119.84
1	A	245	ARG	CA-C-N	6.13	127.51	119.84
1	A	245	ARG	C-N-CA	6.13	127.51	119.84
1	A	85	ASP	N-CA-C	6.12	119.19	109.40
1	A	383	ASN	N-CA-C	-6.10	104.95	113.37
1	A	320	THR	N-CA-C	6.00	119.50	109.95
1	A	451	GLY	N-CA-C	6.00	122.24	113.48
1	B	164	TYR	N-CA-C	-5.99	99.05	108.63
1	A	447	HIS	N-CA-C	5.97	117.86	111.36
1	B	298	PHE	CA-C-N	-5.94	113.63	120.04
1	B	298	PHE	C-N-CA	-5.94	113.63	120.04
1	B	503	LEU	N-CA-C	5.92	119.97	112.87
1	A	167	MET	N-CA-C	5.90	120.61	113.17
1	B	160	THR	CA-C-N	5.90	126.45	120.38
1	B	160	THR	C-N-CA	5.90	126.45	120.38
1	A	346	ASP	N-CA-C	5.86	121.13	109.01
1	A	356	TYR	N-CA-C	-5.83	101.38	110.42
1	A	502	ARG	N-CA-C	5.81	118.74	111.24
1	B	185	LEU	N-CA-C	-5.79	99.85	109.46
1	B	53	ASN	N-CA-C	5.75	120.04	113.19
1	A	256	TRP	N-CA-C	5.74	117.53	111.28
1	A	404	ILE	N-CA-C	5.71	116.74	107.71
1	B	340	GLN	N-CA-C	5.71	117.96	108.99
1	A	173	ARG	N-CA-C	5.64	118.33	108.52
1	A	77	SER	N-CA-C	-5.61	106.39	113.18
1	A	224	THR	CA-C-N	5.61	125.79	119.90
1	A	224	THR	C-N-CA	5.61	125.79	119.90
1	B	85	ASP	CA-C-N	-5.59	114.83	120.31
1	B	85	ASP	C-N-CA	-5.59	114.83	120.31
1	B	354	VAL	CA-C-N	5.56	125.48	119.76
1	B	354	VAL	C-N-CA	5.56	125.48	119.76
1	A	23	GLU	N-CA-C	5.53	117.75	111.11
1	A	85	ASP	CA-C-N	5.53	126.75	119.84
1	A	85	ASP	C-N-CA	5.53	126.75	119.84
1	A	286	HIS	N-CA-C	5.50	122.51	110.80
1	B	213	ALA	N-CA-C	5.49	118.41	108.69

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	286	HIS	N-CA-C	5.49	122.48	110.80
1	A	275	VAL	CA-C-N	-5.48	114.33	120.14
1	A	275	VAL	C-N-CA	-5.48	114.33	120.14
1	B	437	THR	N-CA-C	5.47	117.62	109.25
1	A	334	ARG	N-CA-C	-5.46	99.18	110.80
1	A	331	ARG	N-CA-C	5.44	117.91	110.24
1	A	429	LEU	N-CA-C	-5.41	106.68	113.28
1	A	471	THR	N-CA-C	-5.40	105.37	112.72
1	B	488	ILE	CB-CA-C	-5.40	105.65	111.59
1	B	404	ILE	CB-CA-C	-5.39	104.54	110.52
1	A	347	PRO	N-CA-C	-5.35	101.44	112.47
1	A	479	VAL	N-CA-C	5.34	114.43	106.85
1	B	301	GLY	N-CA-C	5.32	118.75	110.88
1	A	90	ASN	N-CA-C	5.26	116.49	108.12
1	A	227	ASN	N-CA-C	5.24	117.99	109.86
1	A	340	GLN	N-CA-C	5.24	118.61	110.17
1	A	294	ILE	N-CA-C	-5.21	99.46	106.85
1	A	338	SER	N-CA-C	5.19	118.09	110.30
1	A	47	GLN	N-CA-C	5.18	117.33	111.11
1	B	66	SER	N-CA-C	5.18	117.21	110.53
1	A	91	ALA	N-CA-C	-5.17	105.02	113.19
1	B	256	TRP	N-CA-C	5.17	116.91	111.28
1	A	215	ILE	N-CA-C	-5.16	101.05	108.89
1	B	225	PRO	N-CA-C	-5.13	101.90	112.47
1	B	161	PRO	N-CA-C	5.12	116.95	110.70
1	B	245	ARG	CA-C-N	5.12	126.24	119.84
1	B	245	ARG	C-N-CA	5.12	126.24	119.84
1	A	249	ASP	N-CA-C	5.10	117.50	111.33
1	B	294	ILE	N-CA-C	-5.10	98.61	106.72
1	B	319	HIS	N-CA-C	5.08	119.43	112.88
1	A	432	VAL	N-CA-C	-5.04	101.09	108.85
1	B	390	LEU	N-CA-C	-5.03	102.19	109.59
1	A	316	LEU	N-CA-C	-5.02	105.81	111.28
1	B	288	ALA	N-CA-C	5.00	116.36	109.15

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	338	0
1	B	3601	839	3547	287	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	605	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 42.

All (605) 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:87:MET:HE2	1:A:223:ILE:HD11	1.45	0.99
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
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:HH11	1:A:480:ARG:HG2	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:60:MET:HE1	1:A:213:ALA:CB	2.15	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:HD3	1:A:163:ARG:N	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
1:B:263:TRP:NE1	1:B:267:MET:HE3	2.04	0.73
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:HD2	1:B:502:ARG:N	2.05	0.71
1:A:254:ARG:HH11	1:A:254:ARG:HB3	1.56	0.71
1:B:314:PHE:C	1:B:314:PHE:HD1	1.99	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:289:LYS:HD2	1:A:312:THR:HG21	1.72	0.70
1:A:339:THR:HG23	1:B:24:ILE:O	1.91	0.70
1:A:171:ASP:OD2	1:B:169:PHE:HB3	1.91	0.70
1:B:60:MET:HE1	1:B:242:TYR:HD1	1.56	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:74:LEU:HB3	1:A:168:MET:HE1	1.74	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:H	1:A:408:LYS:NZ	1.91	0.68
1:B:310:GLN:O	1:B:310:GLN:HG3	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:B:314:PHE:C	1:B:314:PHE:CD1	2.72	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:60:MET:HG3	1:B:211:GLY:O	1.94	0.67
1:B:79:HIS:HB3	1:B:168:MET:HE1	1.76	0.67
1:B:407:VAL:HG22	1:B:413:ILE:HD12	1.77	0.67
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: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:A:488:ILE:HD12	1:A:488:ILE:H	1.60	0.66
1:B:387:ARG:NH1	1:B:445:ARG:HH22	1.92	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:199:ASN:H	1:A:199:ASN:ND2	1.92	0.66
1:A:323:GLN:HE22	1:A:335:ASN:N	1.94	0.66
1:A:60:MET:HE1	1:A:213:ALA:HB3	1.76	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:B:167:MET:HE1	1:B:223:ILE:H	1.61	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:316:LEU:HD12	1:A:355:PRO:HD2	1.79	0.64
1:A:376:PHE:O	1:A:376:PHE:HD1	1.81	0.64
1:B:5:LEU:O	1:B:9:VAL:HG23	1.97	0.64
1:B:287:TYR:HD2	1:B:311:ARG:CG	2.10	0.64
1:A:60:MET:HE1	1:A:213:ALA:HB2	1.79	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: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:191:GLN:O	1:B:195:VAL:HG22	1.99	0.62
1:B:238:MET:HE3	1:B:362:ALA:HB3	1.80	0.62
1:B:387:ARG:HD2	1:B:445:ARG:HH22	1.63	0.62
1:A:326:LEU:HD22	1:A:354:VAL:CG2	2.30	0.62
1:B:474:LYS:HB2	1:B:474:LYS:NZ	2.15	0.62
1:B:312:THR:HG22	1:B:356:TYR:CD2	2.34	0.62
1:A:63:LEU:HD12	1:B:35:GLY:HA2	1.81	0.62
1:B:170:GLN:HE22	1:B:182:LEU:HD21	1.64	0.62
1:B:224:THR:HB	1:B:226:ARG:CZ	2.30	0.62
1:A:410:ARG:NH1	1:A:465:GLN:NE2	2.47	0.61
1:B:389:VAL:HG12	1:B:391:LYS:HG3	1.80	0.61
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:B:387:ARG:CZ	1:B:389:VAL:HG21	2.30	0.61
1:A:16:GLY:HA2	1:A:19:PHE:CZ	2.35	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:497:GLY:HA2	1:B:500:ARG:HD2	1.82	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:A:84:ALA:CB	1:A:166:ASN:HA	2.32	0.60
1:A:227:ASN:HB2	1:A:230:PHE:CB	2.30	0.60
1:B:413:ILE:HG12	1:B:463:ILE:HD13	1.83	0.60
1:A:312:THR:HB	1:A:356:TYR:CE2	2.37	0.60
1:A:170:GLN:HG2	1:A:184:TYR:CE1	2.37	0.60
1:B:90:ASN:HA	1:B:159:TRP:HA	1.84	0.60
1:A:89:ASP:HA	1:A:93:ALA:O	2.02	0.59
1:B:173:ARG:HA	1:B:173:ARG:NE	2.18	0.59
1:B:264:TRP:CE2	1:B:305:LEU:HD11	2.36	0.59
1:B:313:ASP:HB3	1:B:356:TYR:HD1	1.67	0.59
1:A:490:LEU:CD1	1:A:495:LEU:HD13	2.33	0.59
1:A:382:PRO:C	1:A:384:GLY:H	2.10	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:A:190:ALA:HB2	1:A:239:GLU:OE1	2.03	0.58
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:376:PHE:CD1	1:A:376:PHE:C	2.82	0.58
1:A:87:MET:HE2	1:A:223:ILE:CD1	2.27	0.58
1:A:445:ARG:HA	1:A:445:ARG:NE	2.19	0.58
1:A:12:CYS:HG	1:A:228:PHE:HE2	1.50	0.58
1:A:71:ARG:NE	1:A:182:LEU:HD23	2.19	0.58
1:A:72:LEU:HB3	1:B:25:TYR:CD2	2.39	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:B:399:ILE:HB	1:B:452:THR:HG21	1.84	0.58
1:A:253:HIS:CE1	1:A:310:GLN:HB3	2.39	0.57
1:B:393:LYS:HD3	1:B:505:TRP:CH2	2.39	0.57
1:A:240:ILE:HB	1:A:360:PRO:HD2	1.87	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:408:LYS:H	1:A:408:LYS:HZ2	1.52	0.57
1:B:86:PRO:C	1:B:87:MET:SD	2.87	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:HB2	1:A:173:ARG:NH1	2.19	0.57
1:B:90:ASN:HD22	1:B:159:TRP:CD1	2.23	0.57
1:B:311:ARG:HD3	1:B:315:ASP:OD2	2.05	0.57
1:A:24:ILE:HA	1:B:339:THR:OG1	2.05	0.57
1:A:173:ARG:HH22	1:A:182:LEU:C	2.12	0.57
1:A:217:LYS:HD2	1:A:236:GLU:HG2	1.85	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:A:88:VAL:O	1:A:94:ARG:HA	2.05	0.56
1:A:171:ASP:C	1:A:172:LEU:HG	2.29	0.56
1:B:172:LEU:HD13	1:B:177:GLY:HA2	1.87	0.56
1:A:227:ASN:OD1	1:A:300:HIS:ND1	2.39	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:B:312:THR:HG22	1:B:356:TYR:CG	2.40	0.56
1:A:324:GLU:HB3	1:A:334:ARG:HH12	1.70	0.56
1:B:60:MET:HE1	1:B:242:TYR:CD1	2.38	0.56
1:B:87:MET:HE3	1:B:95:TYR:CB	2.35	0.56
1:A:208:LEU:HG	1:A:344:TYR:CD2	2.41	0.56
1:A:410:ARG:HG3	1:A:460:TYR:CZ	2.41	0.56
1:A:480:ARG:HG2	1:A:480:ARG:NH1	2.12	0.56
1:B:172:LEU:CD2	1:B:182:LEU:HD12	2.36	0.56
1:A:340:GLN:HG3	1:B:24:ILE:HG22	1.88	0.56
1:A:331:ARG:HH21	1:A:332:VAL:HA	1.70	0.56
1:A:479:VAL:HG11	1:A:490:LEU:HD11	1.88	0.56
1:B:439:ASN:O	1:B:442:LYS:HB3	2.06	0.56
1:B:445:ARG:NE	1:B:445:ARG:HA	2.19	0.56
1:B:166:ASN:OD1	1:B:168:MET:HG2	2.06	0.56
1:B:208:LEU:HD23	1:B:344:TYR:CE1	2.41	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:A:279:GLN:HG2	1:A:283:SER:HB3	1.88	0.55
1:B:172:LEU:HD21	1:B:182:LEU:HD12	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
1:A:74:LEU:HD13	1:A:168:MET:CE	2.37	0.55
1:A:308:ILE:N	1:A:308:ILE:HD12	2.21	0.55
1:A:423:ARG:HH12	1:A:496:GLU:HG3	1.72	0.55
1:B:400:LYS:HD2	1:B:503:LEU:HD22	1.88	0.55
1:A:37:LEU:HD22	1:A:450:VAL:HB	1.88	0.54
1:A:269:LEU:HD22	1:A:296:TYR:CE1	2.42	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:434:TYR:O	1:A:434:TYR:CD2	2.61	0.54
1:A:281:PRO:HG2	1:A:282:GLU:OE1	2.07	0.54
1:A:499:LEU:HB3	1:A:503:LEU:HD23	1.89	0.53
1:B:387:ARG:HH11	1:B:445:ARG:HH22	1.56	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:A:444:TYR:CE1	1:A:480:ARG:HD3	2.43	0.53
1:B:480:ARG:NH1	1:B:480:ARG:HG2	2.24	0.53
1:A:326:LEU:CD2	1:A:343:ALA:HB2	2.39	0.53
1:B:313:ASP:HB3	1:B:356:TYR:CD1	2.43	0.53
1:A:325:ALA:HB3	1:A:341:ARG:NH2	2.24	0.53
1:A:503:LEU:HD22	1:A:503:LEU:H	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:208:LEU:O	1:A:209:GLY:C	2.52	0.53
1:A:287:TYR:CE2	1:A:311:ARG:CZ	2.92	0.53
1:B:230:PHE:HZ	1:B:303:LEU:HB3	1.74	0.53
1:B:387:ARG:CZ	1:B:485:MET:SD	2.98	0.53
1:A:172:LEU:HA	1:A:173:ARG:HH21	1.71	0.52
1:A:331:ARG:HE	1:A:331:ARG:C	2.17	0.52
1:A:87:MET:HE3	1:A:165:PHE:CG	2.45	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:A:326:LEU:HG	1:A:341:ARG:HE	1.74	0.52
1:B:391:LYS:HA	1:B:482:ARG:CZ	2.39	0.52
1:A:404:ILE:HG21	1:A:440:ILE:HD13	1.92	0.52
1:B:335:ASN:HD21	1:B:338:SER:HB2	1.73	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:A:60:MET:HA	1:A:211:GLY:O	2.10	0.52
1:B:314:PHE:HD1	1:B:314:PHE:O	1.93	0.52
1:A:89:ASP:HB3	1:A:94:ARG:HD3	1.91	0.52
1:B:90:ASN:ND2	1:B:159:TRP:CD1	2.77	0.51
1:B:173:ARG:NH1	1:B:173:ARG:HB2	2.24	0.51
1:B:364:VAL:O	1:B:368:VAL:HG23	2.10	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:A:265:GLN:NE2	1:A:271:ARG:HD3	2.25	0.51
1:B:440:ILE:HG12	1:B:444:TYR:CE2	2.44	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:O	1:A:376:PHE:CD1	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:280:PRO:O	1:A:283:SER:N	2.43	0.51
1:A:314:PHE:HE1	1:A:331:ARG:NH2	2.09	0.51
1:A:166:ASN:OD1	1:A:168:MET:HG3	2.11	0.51
1:B:224:THR:HG22	1:B:226:ARG:HG3	1.93	0.51
1:A:173:ARG:HB2	1:A:173:ARG:CZ	2.41	0.51
1:B:387:ARG:NH1	1:B:445:ARG:NH2	2.58	0.51
1:A:173:ARG:HH22	1:A:182:LEU:CA	2.24	0.51
1:A:243:PHE:HD1	1:A:357:VAL:HG12	1.76	0.51
1:B:193:ILE:HG23	1:B:212:ILE:HG21	1.93	0.51
1:B:313:ASP:HB2	1:B:354:VAL:HG12	1.93	0.51
1:A:21:SER:CB	1:A:31:VAL:HG22	2.41	0.50
1:A:287:TYR:HD2	1:A:311:ARG:HG2	1.74	0.50
1:B:275:VAL:HG23	1:B:295:LEU:HB2	1.93	0.50
1:B:324:GLU:HG2	1:B:325:ALA:H	1.77	0.50
1:B:387:ARG:NH2	1:B:389:VAL:HG21	2.27	0.50
1:B:410:ARG:HG3	1:B:460:TYR:CE2	2.45	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:B:310:GLN:O	1:B:310:GLN:CG	2.57	0.50
1:B:385:GLU:H	1:B:385:GLU:CD	2.19	0.50
1:A:227:ASN:OD1	1:A:300:HIS:CE1	2.65	0.50
1:A:277:TYR:HE1	1:A:279:GLN:HG3	1.76	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:480:ARG:HB2	1:B:487:GLN:HE21	1.76	0.50
1:A:42:LYS:HG2	1:A:46:LYS:HE3	1.94	0.50
1:A:88:VAL:HB	1:A:159:TRP:CZ3	2.47	0.50
1:A:387:ARG:HB2	1:A:445:ARG:HH12	1.76	0.50
1:A:490:LEU:HD21	1:A:498:PHE:CD2	2.47	0.50
1:B:94:ARG:HD3	1:B:95:TYR:N	2.15	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:12:CYS:HA	1:B:17:PHE:HB2	1.94	0.49
1:B:65:ALA:H	1:B:214:GLN:HE22	1.60	0.49
1:B:242:TYR:O	1:B:357:VAL:HA	2.13	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:A:273:ASN:HB3	1:A:297:ARG:HB2	1.95	0.49
1:B:207:LYS:HE2	1:B:207:LYS:H	1.78	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: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:HD2	1:A:311:ARG:NE	2.10	0.48
1:A:287:TYR:CD1	1:A:287:TYR:N	2.81	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:310:GLN:O	1:A:310:GLN:HG3	2.13	0.48
1:A:391:LYS:HG2	1:A:483:ASP:OD1	2.12	0.48
1:B:381:LEU:C	1:B:383:ASN:H	2.21	0.48
1:A:199:ASN:ND2	1:A:199:ASN:N	2.61	0.48
1:B:410:ARG:NH2	1:B:412:GLU:HG3	2.26	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
1:A:401:VAL:HA	1:A:454:PHE:O	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:160:THR:HG23	1:B:161:PRO:HD2	1.95	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: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:238:MET:HG3	1:A:364:VAL:CG2	2.44	0.48
1:B:90:ASN:CG	1:B:91:ALA:N	2.72	0.48
1:A:91:ALA:H	1:A:92:LYS:HD3	1.77	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:280:PRO:HD2	1:A:283:SER:HB2	1.96	0.47
1:A:254:ARG:HH11	1:A:254:ARG:CG	2.27	0.47
1:A:382:PRO:C	1:A:384:GLY:N	2.71	0.47
1:B:63:LEU:HD23	1:B:214:GLN:NE2	2.29	0.47
1:B:445:ARG:HA	1:B:445:ARG:HE	1.79	0.47
1:A:57:ARG:HD3	1:A:60:MET:HG3	1.97	0.47
1:A:197:PHE:CD1	1:A:197:PHE:C	2.92	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: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:A:410:ARG:HH12	1:A:465:GLN:CD	2.22	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:A:162:PRO:C	1:A:163:ARG:HD3	2.39	0.47
1:B:322:ASP:HA	1:B:324:GLU:OE2	2.15	0.47
1:A:69:THR:CG2	1:A:73:VAL:HB	2.44	0.47
1:A:239:GLU:HG2	1:A:361:SER:OG	2.15	0.47
1:A:378:ARG:O	1:A:378:ARG:HG2	2.15	0.47
1:A:387:ARG:HG3	1:A:389:VAL:CG2	2.45	0.47
1:A:388:ILE:HD13	1:A:449:GLU:OE2	2.15	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: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:479:VAL:O	1:A:479:VAL:HG22	2.14	0.46
1:A:480:ARG:NH1	1:A:480:ARG:CG	2.78	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:484:THR:C	1:B:486:GLU:H	2.23	0.46
2:B:2550:GAP:H8	2:B:2550:GAP:O2A	2.14	0.46
1:A:306:GLU:HG3	1:A:307:GLY:N	2.30	0.46
1:A:496:GLU:O	1:A:500:ARG:HG3	2.15	0.46
1:B:472:ARG:O	1:B:472:ARG:NH1	2.47	0.46
1:A:55:TYR:N	1:A:55:TYR:CD1	2.83	0.46
1:A:475:ASP:O	1:A:492:VAL:HG23	2.16	0.46
1:B:87:MET:SD	1:B:87:MET:N	2.88	0.46
1:B:496:GLU:HB3	1:B:500:ARG:NH2	2.30	0.46
1:A:173:ARG:CZ	1:A:173:ARG:N	2.79	0.46
1:B:173:ARG:CZ	1:B:173:ARG:CA	2.93	0.46
1:B:372:LEU:HD23	1:B:372:LEU:HA	1.79	0.46
1:B:444:TYR:CE1	1:B:480:ARG:HD3	2.51	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:B:168:MET:HB3	1:B:168:MET:HE2	1.64	0.46
1:B:225:PRO:C	1:B:226:ARG:HG3	2.41	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:265:GLN:HE22	1:A:271:ARG:HD3	1.79	0.46
1:A:312:THR:HG22	1:A:356:TYR:CD2	2.51	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:A:79:HIS:CD2	1:A:83:PHE:CD2	3.04	0.45
1:A:72:LEU:CB	1:B:25:TYR:CD2	3.00	0.45
1:A:410:ARG:HA	1:A:411:PRO:HD2	1.79	0.45
1:B:238:MET:HG3	1:B:364:VAL:CG2	2.47	0.45
1:B:462:THR:CG2	1:B:477:VAL:HG13	2.46	0.45
1:B:16:GLY:HA2	1:B:19:PHE:CZ	2.51	0.45
1:B:437:THR:C	1:B:442:LYS:HE2	2.42	0.45
1:B:437:THR:O	1:B:442:LYS:HE2	2.17	0.45
1:A:12:CYS:SG	1:A:228:PHE:HE2	2.39	0.45
1:A:288:ALA:HB1	1:A:291:THR:CG2	2.47	0.45
1:A:401:VAL:HG21	1:A:499:LEU:HD13	1.99	0.45
1:A:300:HIS:H	1:A:300:HIS:CD2	2.34	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:244:VAL:CG1	1:B:245:ARG:N	2.79	0.45
1:B:253:HIS:CD2	1:B:310:GLN:HB2	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:387:ARG:NE	1:B:389:VAL:HG21	2.32	0.45
1:B:445:ARG:O	1:B:446:ARG:C	2.59	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
1:A:460:TYR:O	1:A:461:ASP:C	2.59	0.45
1:B:410:ARG:HA	1:B:411:PRO:HD2	1.82	0.45
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:312:THR:HB	1:A:356:TYR:CZ	2.52	0.45
1:A:326:LEU:HG	1:A:341:ARG:NH2	2.27	0.45
1:B:229:ILE:HG22	1:B:369:LEU:HG	1.99	0.45
1:B:8:LEU:HD11	1:B:373:ALA:HA	1.99	0.44
1:B:261:LEU:HD11	1:B:274:LEU:HB3	1.98	0.44
1:B:442:LYS:HZ1	1:B:443:ALA:HA	1.82	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:OE2	1:B:222:GLU:HA	2.17	0.44
1:B:484:THR:C	1:B:486:GLU:N	2.73	0.44
1:B:484:THR:O	1:B:486:GLU:N	2.50	0.44
1:A:188:GLU:OE2	1:A:190:ALA:HB3	2.17	0.44
1:A:444:TYR:CZ	1:A:480:ARG:HD3	2.53	0.44
1:B:220:ARG:C	1:B:222:GLU:H	2.25	0.44
1:A:410:ARG:CZ	1:A:460:TYR:CE1	2.85	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: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:B:474:LYS:HB2	1:B:474:LYS:HZ3	1.79	0.44
1:B:481:ASP:O	1:B:485:MET:N	2.49	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:CA	1:A:310:GLN:HE21	2.30	0.44
1:A:229:ILE:HA	1:A:229:ILE:HD12	1.72	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: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:321:LYS:HD2	1:B:340:GLN:HA	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:416:TYR:HD2	1:B:419:ARG:HH21	1.65	0.44
1:A:383:ASN:N	1:A:383:ASN:OD1	2.51	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:B:310:GLN:HE22	1:B:312:THR:CG2	2.22	0.43
1:A:173:ARG:CZ	1:A:173:ARG:CB	2.95	0.43
1:A:406:LEU:HA	1:A:406:LEU:HD12	1.40	0.43
1:A:74:LEU:CB	1:A:168:MET:HE1	2.47	0.43
1:A:172:LEU:CA	1:A:173:ARG:HH21	2.31	0.43
1:A:243:PHE:CD1	1:A:357:VAL:HG12	2.53	0.43
1:A:329:THR:OG1	1:A:330:ALA:N	2.50	0.43
1:B:410:ARG:HG3	1:B:460:TYR:CZ	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:B:94:ARG:O	1:B:95:TYR:C	2.62	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:A:169:PHE:HB3	1:B:171:ASP:OD2	2.17	0.43
1:A:261:LEU:HG	1:A:294:ILE:HD13	2.01	0.43
1:B:252:TRP:HA	1:B:252:TRP:CE3	2.53	0.43
1:B:253:HIS:C	1:B:253:HIS:HD1	2.27	0.43
1:B:393:LYS:HD3	1:B:505:TRP:CZ3	2.53	0.43
1:A:89:ASP:C	1:A:159:TRP:CE3	2.97	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:A:439:ASN:HB3	1:A:442:LYS:HB2	2.01	0.43
1:B:186:ARG:NH2	1:B:217:LYS:N	2.61	0.43
1:B:224:THR:HB	1:B:226:ARG:NE	2.32	0.43
1:B:502:ARG:N	1:B:502:ARG:CD	2.79	0.43
1:A:12:CYS:HA	1:A:17:PHE:HB2	2.00	0.43
1:A:173:ARG:CA	1:A:173:ARG:NE	2.82	0.43
1:A:257:VAL:HG23	1:A:308:ILE:HG21	1.99	0.43
1:A:359:GLU:OE2	2:A:1550:GAP:HA1	2.19	0.43
1:A:470:THR:C	1:A:472:ARG:H	2.27	0.43
1:B:190:ALA:HB2	1:B:239:GLU:OE1	2.18	0.43
1:B:294:ILE:HG13	1:B:308:ILE:CD1	2.48	0.43
1:A:5:LEU:O	1:A:8:LEU:HB2	2.18	0.42
1:A:74:LEU:HD13	1:A:168:MET:HE1	2.01	0.42
1:A:61:GLU:HG2	1:A:204:THR:HG21	2.01	0.42
1:A:399:ILE:HB	1:A:452:THR:HG22	1.98	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:222:GLU:O	1:B:223:ILE:C	2.61	0.42
1:B:253:HIS:O	1:B:257:VAL:HG23	2.19	0.42
1:B:444:TYR:CD1	1:B:480:ARG:HD3	2.54	0.42
1:A:260:ARG:NH1	1:A:306:GLU:OE2	2.52	0.42
1:A:287:TYR:CD2	1:A:311:ARG:NE	2.88	0.42
1:A:298:PHE:O	1:A:299:PRO:C	2.62	0.42
1:A:413:ILE:HG12	1:A:463:ILE:HD13	2.01	0.42
1:B:50:TRP:O	1:B:54:VAL:HG23	2.20	0.42
1:B:297:ARG:HA	1:B:297:ARG:HD2	1.88	0.42
1:A:8:LEU:HD22	1:A:8:LEU:HA	1.72	0.42
1:A:67:VAL:HG21	1:A:219:PHE:HE1	1.84	0.42
1:A:368:VAL:HG12	1:A:372:LEU:HD12	2.01	0.42
1:A:425:LEU:HD12	1:A:425:LEU:O	2.20	0.42
1:A:488:ILE:HG22	1:A:489:ARG:N	2.34	0.42
1:B:322:ASP:O	1:B:323:GLN:C	2.62	0.42
1:A:14:ARG:NH1	1:A:449:GLU:OE1	2.53	0.42
1:A:49:TRP:HE1	1:A:260:ARG:NH1	2.17	0.42
1:A:407:VAL:HG21	1:A:460:TYR:CE2	2.54	0.42
1:B:253:HIS:CD2	1:B:310:GLN:CB	3.02	0.42
1:A:15:ARG:C	1:B:203:ALA:HB1	2.45	0.42
1:B:37:LEU:CD1	1:B:450:VAL:HG11	2.50	0.42
1:A:220:ARG:O	1:A:233:ARG:HA	2.19	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:B:224:THR:C	1:B:226:ARG:HE	2.27	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:87:MET:HE3	1:A:165:PHE:HB2	2.02	0.42
1:A:328:ILE:CG2	1:A:329:THR:N	2.83	0.42
1:B:440:ILE:HG12	1:B:444:TYR:CD2	2.55	0.42
1:A:238:MET:CG	1:A:364:VAL:HG22	2.50	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:445:ARG:O	1:A:446:ARG:C	2.63	0.41
1:B:5:LEU:O	1:B:8:LEU:HB2	2.20	0.41
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:A:340:GLN:CG	1:B:24:ILE:HG22	2.49	0.41
1:A:478:THR:HG23	1:A:489:ARG:HB2	2.02	0.41
1:A:74:LEU:HD13	1:A:168:MET:HE2	2.02	0.41
1:A:413:ILE:CG1	1:A:463:ILE:HD13	2.50	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:65:ALA:H	1:B:214:GLN:NE2	2.18	0.41
1:B:88:VAL:HB	1:B:159:TRP:HZ3	1.85	0.41
1:B:385:GLU:HB2	1:B:386:GLU:H	1.65	0.41
1:B:467:LYS:CG	1:B:468:ASP:N	2.82	0.41
1:A:60:MET:HB3	1:A:60:MET:HE3	1.43	0.41
1:A:235:PHE:CD1	1:A:235:PHE:N	2.87	0.41
1:B:376:PHE:CE2	1:B:388:ILE:HG23	2.55	0.41
1:B:433:LEU:HD23	1:B:434:TYR:N	2.35	0.41
1:A:74:LEU:HD23	1:A:74:LEU:HA	1.82	0.41
1:A:160:THR:OG1	1:A:163:ARG:NH1	2.53	0.41
1:A:310:GLN:O	1:A:310:GLN:CG	2.68	0.41
1:A:462:THR:HG23	1:A:476:THR:O	2.19	0.41
1:B:456:VAL:HG21	1:B:495:LEU:HD21	2.02	0.41
1:A:61:GLU:O	1:A:212:ILE:HA	2.20	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:240:ILE:O	1:A:359:GLU:HG3	2.21	0.41
1:A:364:VAL:O	1:A:368:VAL:HG23	2.21	0.41
1:A:388:ILE:HD12	1:A:388:ILE:N	2.21	0.41
1:A:414:THR:O	1:A:417:ALA:HB3	2.21	0.41
1:A:445:ARG:HA	1:A:445:ARG:HE	1.83	0.41
1:B:89:ASP:HB2	1:B:160:THR:HB	2.02	0.41
1:B:393:LYS:HA	1:B:394:PRO:HD3	1.79	0.41
1:B:251:TYR:O	1:B:254:ARG:HB3	2.21	0.41
1:A:310:GLN:HE21	1:A:310:GLN:C	2.29	0.40
1:A:311:ARG:H	1:A:311:ARG:HG3	1.58	0.40
1:A:322:ASP:O	1:A:323:GLN:C	2.64	0.40
1:B:71:ARG:HG3	1:B:184:TYR:HE1	1.86	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:A:173:ARG:NH2	1:A:183:ALA:N	2.70	0.40
1:B:282:GLU:H	1:B:282:GLU:CD	2.29	0.40
1:A:14:ARG:O	1:A:14:ARG:HG2	2.20	0.40
1:A:220:ARG:C	1:A:222:GLU:H	2.29	0.40
1:A:223:ILE:HD13	1:A:223:ILE:HA	1.93	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:B:226:ARG:HD2	1:B:231:ARG:HD3	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:481:ASP:OD1	1:B:481:ASP:C	2.64	0.40
1:A:72:LEU:HD11	1:A:337:HIS:CD2	2.56	0.40
1:A:306:GLU:CD	1:A:362:ALA:HB2	2.46	0.40
1:A:337:HIS:ND1	1:A:337:HIS:N	2.70	0.40
1:B:480:ARG:HH11	1:B:480:ARG:CG	2.35	0.40
1:A:404:ILE:HD13	1:A:443:ALA:CB	2.51	0.40
1:B:220:ARG:O	1:B:233:ARG:HA	2.21	0.40
1:B:298:PHE:HE2	1:B:369:LEU:HB3	1.87	0.40
1:B:333:LEU:H	1:B:333:LEU:HD12	1.87	0.40
1:B:399:ILE:H	1:B:452:THR:HG22	1.87	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	438/442 (99%)	359 (82%)	62 (14%)	17 (4%)	2	15
1	B	438/442 (99%)	351 (80%)	69 (16%)	18 (4%)	2	15
All	All	876/884 (99%)	710 (81%)	131 (15%)	35 (4%)	2	15

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

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Mol	Chain	Res	Type
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
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 ⓘ

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%)	300 (80%)	75 (20%)	1	4
1	B	374/376 (100%)	306 (82%)	68 (18%)	2	7
All	All	749/752 (100%)	606 (81%)	143 (19%)	1	6

All (143) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	5	LEU
1	A	8	LEU
1	A	31	VAL
1	A	60	MET
1	A	67	VAL
1	A	87	MET
1	A	88	VAL
1	A	89	ASP
1	A	92	LYS
1	A	163	ARG
1	A	168	MET
1	A	172	LEU
1	A	173	ARG
1	A	175	PRO
1	A	179	ARG
1	A	181	LEU
1	A	189	THR
1	A	195	VAL
1	A	199	ASN
1	A	208	LEU
1	A	210	PHE
1	A	222	GLU
1	A	229	ILE
1	A	232	VAL
1	A	244	VAL
1	A	245	ARG
1	A	254	ARG
1	A	259	GLU
1	A	261	LEU
1	A	265	GLN
1	A	277	TYR
1	A	287	TYR
1	A	295	LEU
1	A	299	PRO
1	A	302	SER
1	A	310	GLN
1	A	313	ASP
1	A	321	LYS
1	A	322	ASP
1	A	323	GLN
1	A	326	LEU
1	A	328	ILE

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Mol	Chain	Res	Type
1	A	331	ARG
1	A	333	LEU
1	A	336	GLU
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	389	VAL
1	A	390	LEU
1	A	398	PRO
1	A	406	LEU
1	A	407	VAL
1	A	408	LYS
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	488	ILE
1	A	490	LEU
1	A	494	GLU
1	A	495	LEU
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	54	VAL
1	B	60	MET
1	B	63	LEU
1	B	82	THR
1	B	88	VAL

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Mol	Chain	Res	Type
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	182	LEU
1	B	198	LYS
1	B	208	LEU
1	B	210	PHE
1	B	223	ILE
1	B	225	PRO
1	B	226	ARG
1	B	233	ARG
1	B	246	PRO
1	B	248	GLU
1	B	250	GLU
1	B	261	LEU
1	B	265	GLN
1	B	272	GLU
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	313	ASP
1	B	314	PHE
1	B	345	ARG
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	385	GLU
1	B	386	GLU
1	B	392	LEU
1	B	393	LYS
1	B	398	PRO

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Mol	Chain	Res	Type
1	B	410	ARG
1	B	418	LYS
1	B	423	ARG
1	B	425	LEU
1	B	431	ARG
1	B	445	ARG
1	B	462	THR
1	B	468	ASP
1	B	474	LYS
1	B	476	THR
1	B	477	VAL
1	B	478	THR
1	B	479	VAL
1	B	488	ILE
1	B	489	ARG
1	B	495	LEU
1	B	501	GLU

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

Mol	Chain	Res	Type
1	A	20	GLN
1	A	29	GLN
1	A	44	ASN
1	A	47	GLN
1	A	199	ASN
1	A	214	GLN
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	44	ASN
1	B	53	ASN
1	B	70	HIS
1	B	90	ASN
1	B	214	GLN
1	B	323	GLN
1	B	487	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

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	B	2550	-	28,29,29	0.51	0	39,43,43	0.75	2 (5%)
2	GAP	A	1550	-	28,29,29	0.61	0	39,43,43	0.67	0

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	B	2550	-	-	2/15/33/33	0/3/3/3
2	GAP	A	1550	-	-	4/15/33/33	0/3/3/3

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	2550	GAP	O-C-CA	-2.29	113.23	118.99
2	B	2550	GAP	O2A-PA-O3A	2.13	111.81	104.94

There are no chirality outliers.

All (6) torsion outliers are listed below:

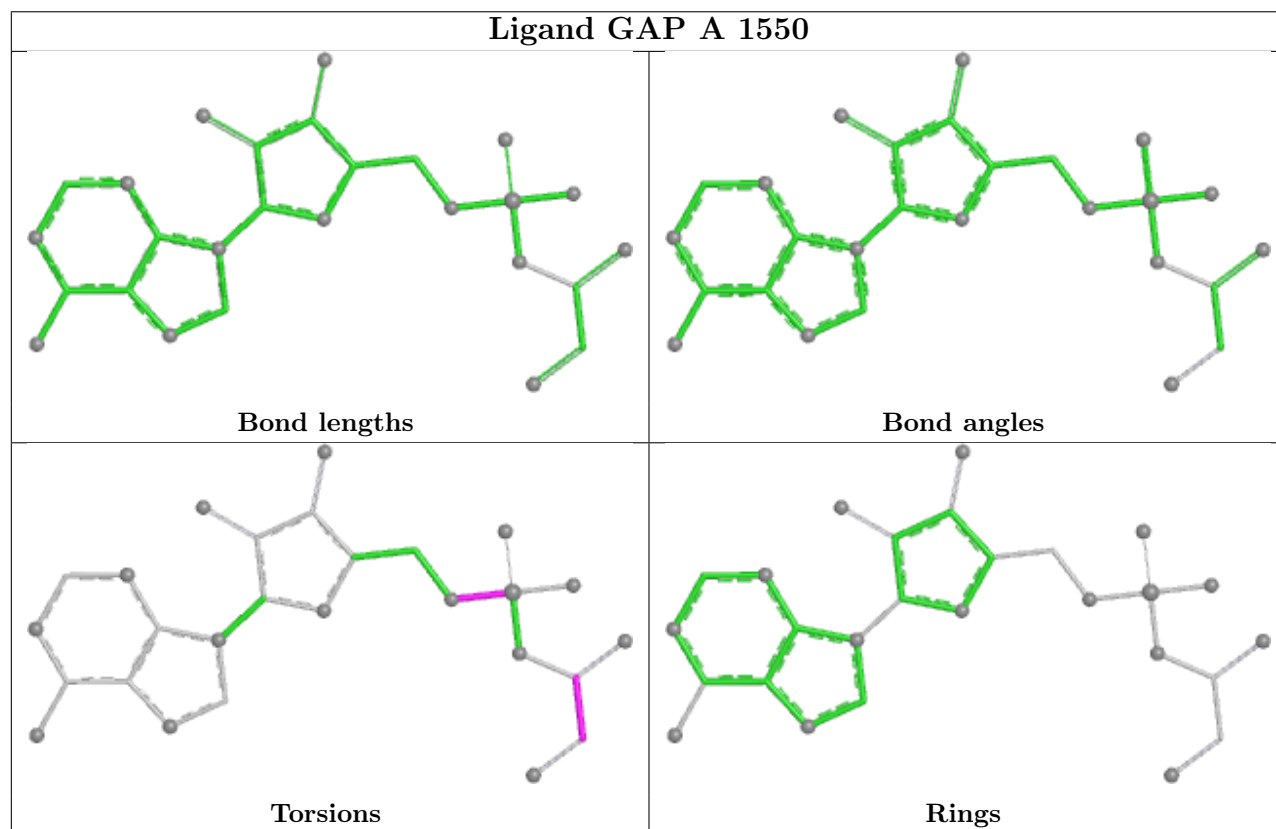
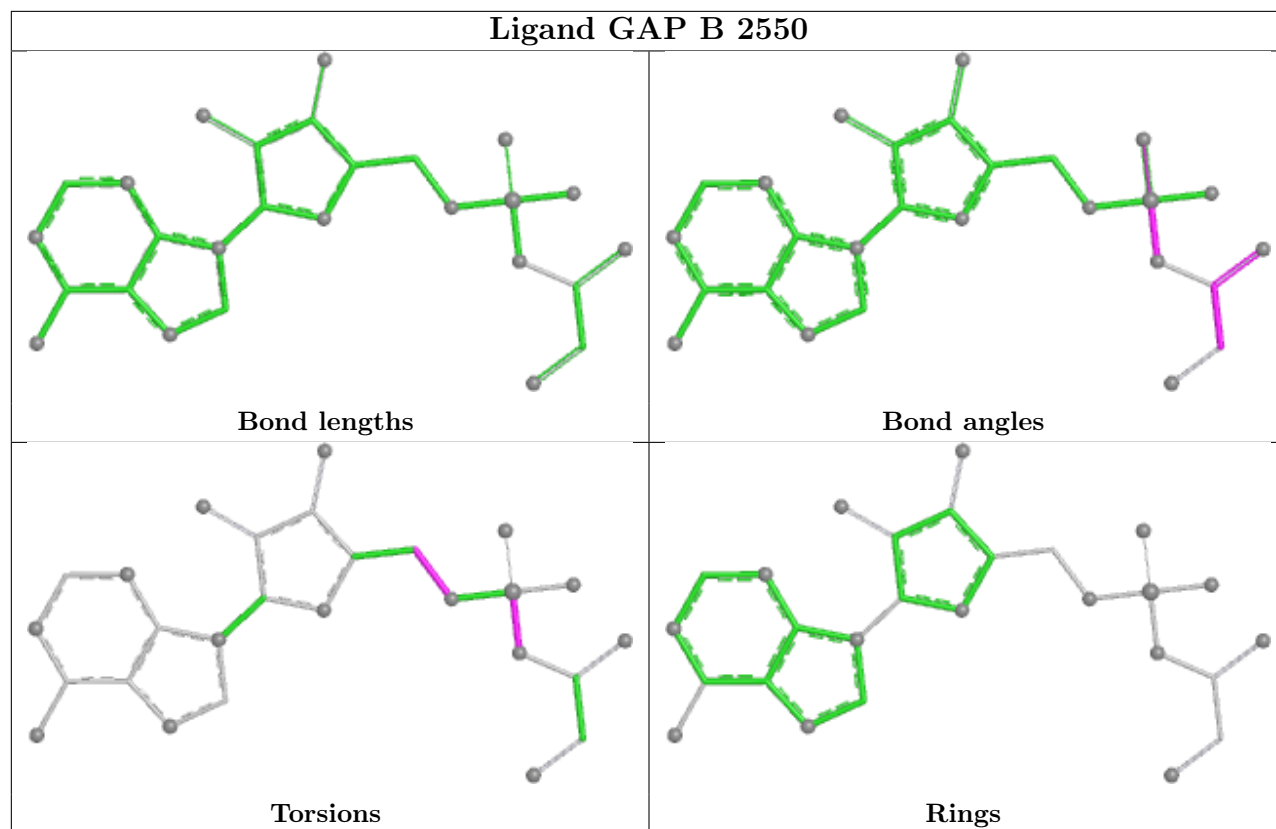
Mol	Chain	Res	Type	Atoms
2	A	1550	GAP	C5'-O5'-PA-O1A
2	A	1550	GAP	C5'-O5'-PA-O3A
2	A	1550	GAP	O3A-C-CA-N
2	A	1550	GAP	O-C-CA-N
2	B	2550	GAP	C4'-C5'-O5'-PA
2	B	2550	GAP	C-O3A-PA-O1A

There are no ring outliers.

2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	2550	GAP	1	0
2	A	1550	GAP	3	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A	1
1	B	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	95:TYR	C	159:TRP	N	11.89
1	B	95:TYR	C	159:TRP	N	10.93

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ > 2		OWAB(Å ²)	Q < 0.9
1	A	442/442 (100%)	0.20	15 (3%)	48 35	11, 33, 60, 92	0
1	B	442/442 (100%)	0.24	14 (3%)	50 37	11, 35, 69, 90	0
All	All	884/884 (100%)	0.22	29 (3%)	49 36	11, 34, 66, 92	0

All (29) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	285	ALA	4.5
1	A	284	SER	3.5
1	B	284	SER	3.5
1	A	301	GLY	3.5
1	B	466	SER	3.3
1	B	285	ALA	3.3
1	A	283	SER	3.1
1	A	445	ARG	3.0
1	A	286	HIS	2.9
1	B	90	ASN	2.8
1	B	470	THR	2.8
1	B	381	LEU	2.8
1	B	174	GLY	2.7
1	A	384	GLY	2.7
1	B	464	GLY	2.7
1	A	347	PRO	2.5
1	B	288	ALA	2.3
1	B	386	GLU	2.2
1	B	167	MET	2.2
1	A	209	GLY	2.2
1	B	209	GLY	2.1
1	A	48	ALA	2.1
1	A	93	ALA	2.1
1	A	409	ASN	2.1

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Mol	Chain	Res	Type	RSRZ
1	B	471	THR	2.1
1	B	476	THR	2.1
1	A	439	ASN	2.0
1	A	287	TYR	2.0
1	A	472	ARG	2.0

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

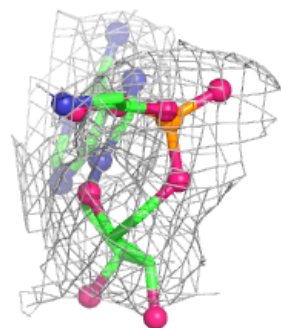
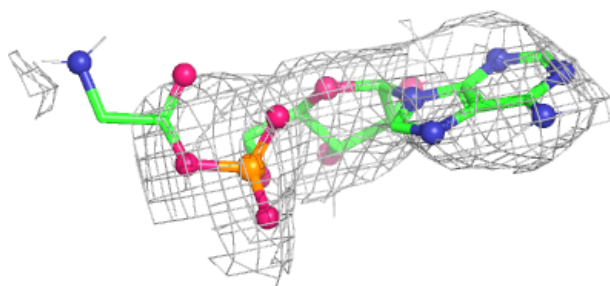
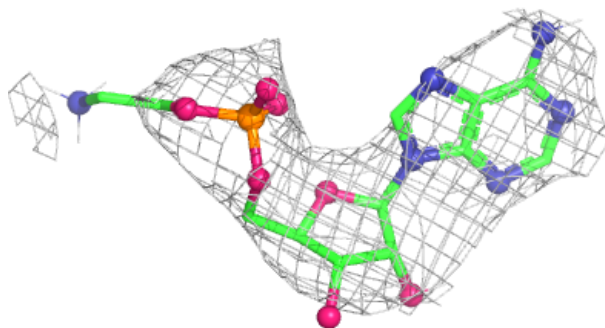
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	GAP	B	2550	27/27	0.91	0.11	0,46,58,61	0
2	GAP	A	1550	27/27	0.92	0.09	0,28,42,44	0

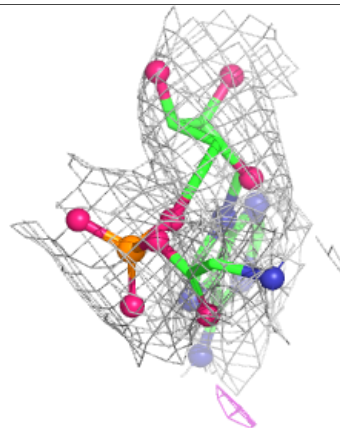
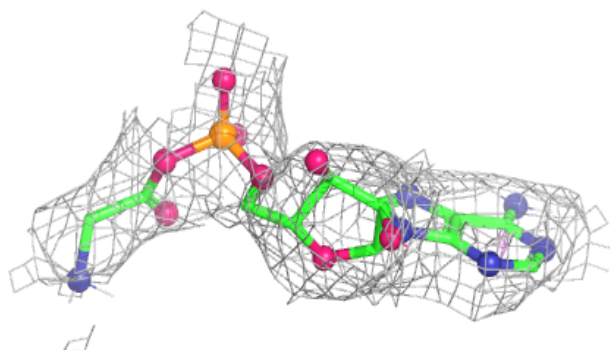
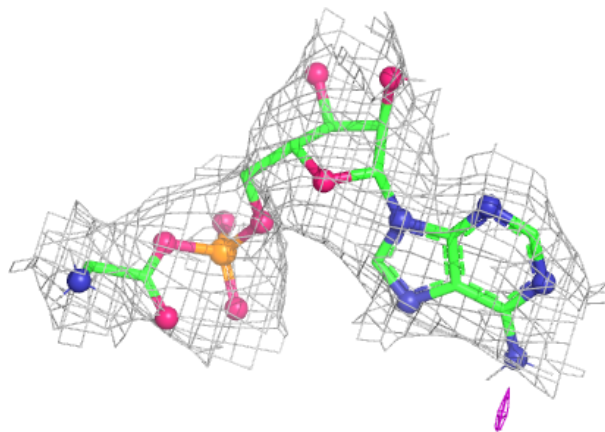
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around GAP B 2550:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

**Electron density around GAP A 1550:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



6.5 Other polymers [i](#)

There are no such residues in this entry.