



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 14, 2026 – 04:56 PM UTC

PDB ID : 2X19 / pdb_00002x19
Title : Crystal structure of Importin13 - RanGTP complex
Authors : Bono, F.; Cook, A.G.; Gruenwald, M.; Ebert, J.; Conti, E.
Deposited on : 2009-12-23
Resolution : 2.80 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

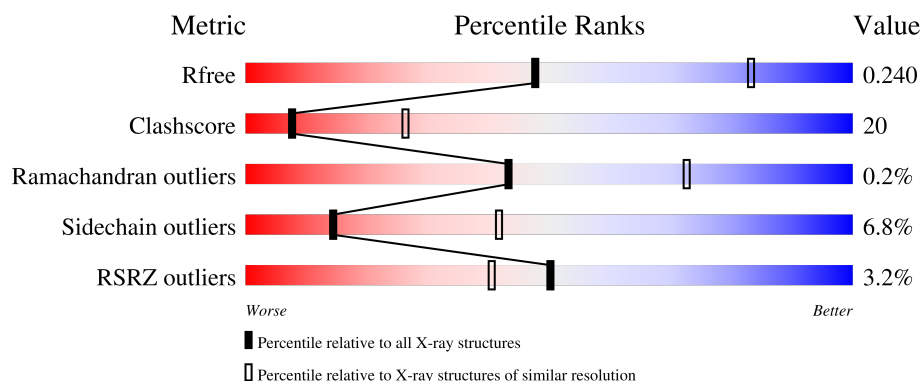
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

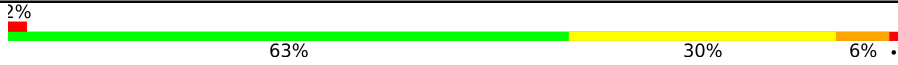
The reported resolution of this entry is 2.80 Å.

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	3866 (2.80-2.80)
Clashscore	190562	4276 (2.80-2.80)
Ramachandran outliers	187476	4196 (2.80-2.80)
Sidechain outliers	187428	4198 (2.80-2.80)
RSRZ outliers	180081	3869 (2.80-2.80)

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	172	
2	B	963	

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 8440 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called GTP-BINDING NUCLEAR PROTEIN GSP1/CNR1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	172	Total	C	N	O	S	0	0	0
			1372	892	231	245	4			

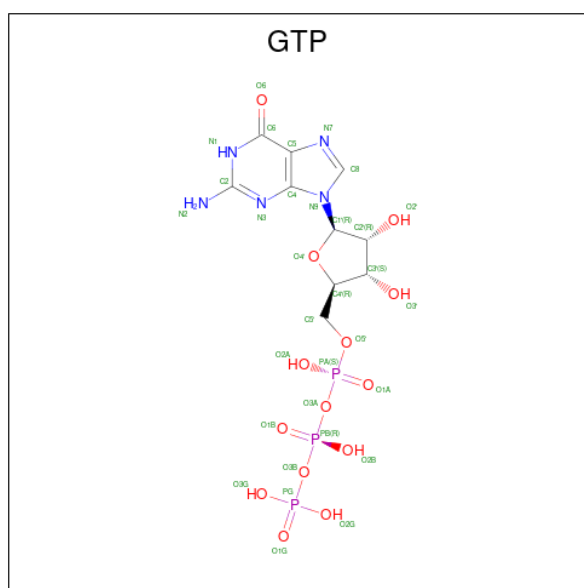
There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	71	LEU	GLN	engineered mutation	UNP P32835

- Molecule 2 is a protein called IMPORTIN-13.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	B	907	Total	C	N	O	S	Se	0	0	1
			6977	4505	1159	1270	21	22			

- Molecule 3 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: C₁₀H₁₆N₅O₁₄P₃).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			32	10	5	14	3		

- Molecule 4 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

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

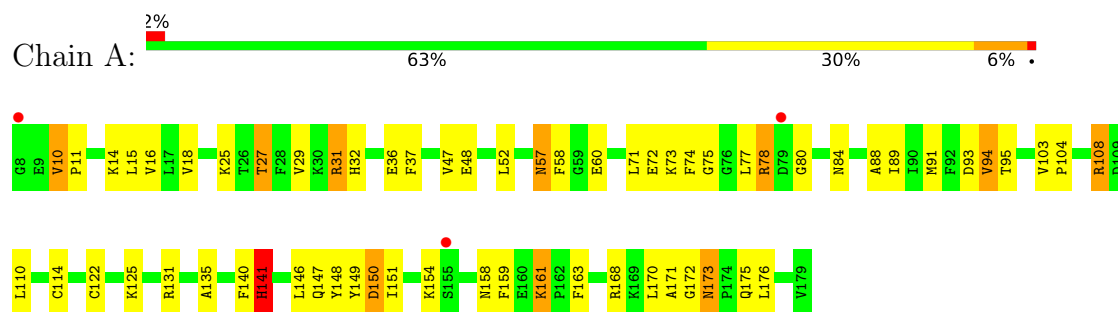
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	16	Total	O	0	0
			16	16		
5	B	42	Total	O	0	0
			42	42		

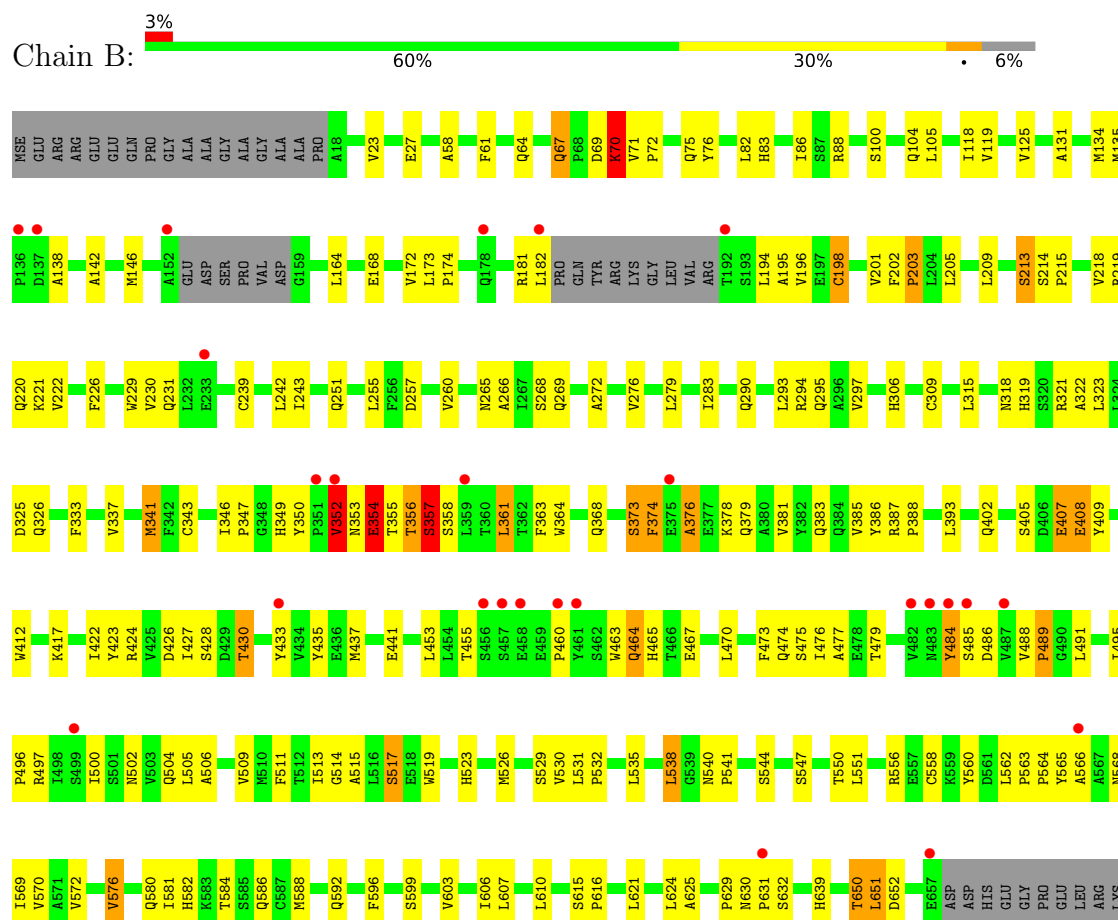
3 Residue-property plots [i](#)

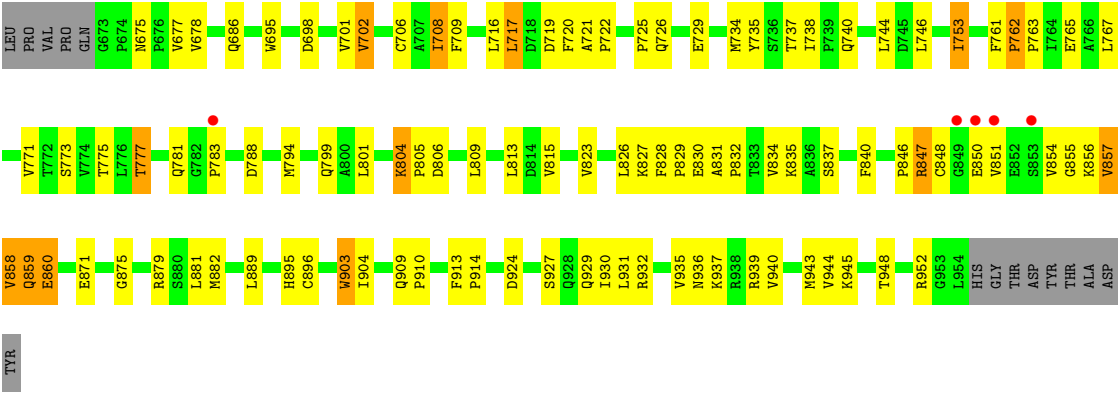
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density.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

• Molecule 1: GTP-BINDING NUCLEAR PROTEIN GSP1/CNR1



• Molecule 2: IMPORTIN-13





4 Data and refinement statistics

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, α , β , γ	99.93Å 99.93Å 276.84Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	50.00 – 2.80 50.00 – 2.80	Depositor EDS
% Data completeness (in resolution range)	99.7 (50.00-2.80) 99.6 (50.00-2.80)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.44 (at 2.81Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.236 , 0.268 0.231 , 0.240	Depositor DCC
R_{free} test set	2022 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å ²)	62.1	Xtriage
Anisotropy	0.078	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 49.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	0.043 for -h,-k,l	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	8440	wwPDB-VP
Average B, all atoms (Å ²)	67.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.38% 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: MG, GTP

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	0.53	0/1407	0.99	5/1906 (0.3%)
2	B	0.52	0/7109	1.01	32/9659 (0.3%)
All	All	0.52	0/8516	1.01	37/11565 (0.3%)

There are no bond length outliers.

All (37) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	860	GLU	N-CA-C	-12.42	98.22	113.50
2	B	753	ILE	N-CA-C	8.10	118.11	110.74
2	B	352	VAL	N-CA-C	7.63	123.11	112.50
2	B	460	PRO	N-CA-CB	7.33	110.94	103.25
2	B	357	SER	N-CA-C	7.20	119.13	111.28
2	B	386	TYR	N-CA-C	6.89	121.85	113.17
2	B	356	THR	N-CA-C	6.66	118.54	111.28
2	B	717	LEU	N-CA-C	6.62	119.83	111.69
2	B	67	GLN	CA-C-N	6.34	126.03	119.56
2	B	67	GLN	C-N-CA	6.34	126.03	119.56
2	B	762	PRO	N-CA-C	6.31	118.40	110.70
2	B	629	PRO	N-CA-CB	6.25	109.81	103.25
2	B	781	GLN	N-CA-C	6.09	117.72	111.14
2	B	651	LEU	N-CA-C	5.99	118.54	107.99
2	B	777	THR	N-CA-C	-5.93	104.74	111.14
2	B	361	LEU	N-CA-C	5.85	117.66	111.28
2	B	560	TYR	N-CA-C	5.85	120.26	113.18
2	B	624	LEU	N-CA-C	-5.73	106.12	113.23
2	B	213	SER	N-CA-C	5.68	119.83	113.01
1	A	110	LEU	N-CA-C	-5.65	105.03	111.14
2	B	354	GLU	N-CA-C	5.62	120.36	107.48
2	B	904	ILE	N-CA-C	5.59	116.32	110.62

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	173	ASN	CA-C-N	5.55	125.26	119.82
1	A	173	ASN	C-N-CA	5.55	125.26	119.82
2	B	272	ALA	N-CA-C	5.50	118.79	111.75
2	B	463	TRP	N-CA-C	-5.47	105.71	112.38
2	B	373	SER	N-CA-C	5.46	119.78	113.18
2	B	70	LYS	N-CA-C	5.40	118.38	109.85
2	B	376	ALA	N-CA-C	5.32	122.13	110.80
2	B	322	ALA	N-CA-C	-5.29	105.68	111.82
2	B	341	MSE	N-CA-C	-5.25	105.64	111.36
2	B	761	PHE	N-CA-C	5.18	121.26	109.81
1	A	150	ASP	N-CA-C	-5.17	100.74	108.96
1	A	80	GLY	N-CA-C	5.17	120.01	113.24
2	B	804	LYS	CA-C-N	5.13	125.17	119.32
2	B	804	LYS	C-N-CA	5.13	125.17	119.32
2	B	194	LEU	N-CA-C	-5.07	106.25	112.90

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1372	0	1342	62	0
2	B	6977	0	6839	278	0
3	A	32	0	12	5	0
4	A	1	0	0	0	0
5	A	16	0	0	1	0
5	B	42	0	0	9	0
All	All	8440	0	8193	333	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 20.

All (333) 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:78:ARG:NH2	2:B:88:ARG:HD3	1.66	1.10
2:B:815:VAL:HG21	2:B:854:VAL:HG11	1.35	1.03
1:A:78:ARG:HH22	2:B:88:ARG:HD3	1.17	1.00
2:B:290:GLN:HE21	2:B:294:ARG:HE	1.05	0.95
1:A:78:ARG:HH12	2:B:88:ARG:NH1	1.64	0.94
2:B:368:GLN:HG2	2:B:433:TYR:CE2	2.04	0.93
2:B:513:ILE:HD13	2:B:530:VAL:HG13	1.54	0.90
2:B:464:GLN:H	2:B:464:GLN:HE21	1.16	0.89
2:B:485:SER:O	2:B:489:PRO:HD2	1.74	0.87
1:A:10:VAL:HG12	1:A:11:PRO:HD2	1.55	0.86
1:A:78:ARG:HH22	2:B:88:ARG:CD	1.88	0.86
2:B:354:GLU:CD	2:B:357:SER:HB3	2.00	0.86
2:B:854:VAL:O	2:B:857:VAL:HG12	1.76	0.86
2:B:290:GLN:NE2	2:B:294:ARG:HE	1.76	0.82
2:B:794:MSE:CE	2:B:837:SER:HA	2.10	0.82
1:A:78:ARG:H	1:A:78:ARG:HD3	1.44	0.81
2:B:716:LEU:O	2:B:716:LEU:HD12	1.81	0.80
2:B:488:VAL:HB	2:B:489:PRO:HD3	1.61	0.80
2:B:815:VAL:HG21	2:B:854:VAL:CG1	2.14	0.78
1:A:75:GLY:HA3	1:A:78:ARG:HH11	1.48	0.77
2:B:474:GLN:NE2	2:B:511:PHE:HB3	1.99	0.76
2:B:131:ALA:O	2:B:135:MSE:HB2	1.86	0.75
2:B:290:GLN:HE21	2:B:294:ARG:NE	1.82	0.74
2:B:716:LEU:CD1	2:B:720:PHE:HB2	2.18	0.74
2:B:773:SER:O	2:B:777:THR:HG23	1.87	0.73
2:B:361:LEU:HD22	2:B:430:THR:HG21	1.69	0.72
2:B:257:ASP:O	2:B:260:VAL:HG12	1.89	0.72
2:B:488:VAL:HG11	2:B:519:TRP:CD2	2.24	0.72
2:B:737:THR:HG22	2:B:738:ILE:HG13	1.72	0.71
2:B:783:PRO:O	2:B:828:PHE:CZ	2.44	0.71
1:A:75:GLY:HA3	1:A:78:ARG:NH1	2.05	0.71
2:B:488:VAL:HG11	2:B:519:TRP:CE2	2.26	0.71
1:A:27:THR:OG1	3:A:1181:GTP:H5''	1.91	0.71
2:B:201:VAL:HG21	2:B:229:TRP:CZ2	2.26	0.71
2:B:519:TRP:O	2:B:523:HIS:HD2	1.74	0.71
2:B:455:THR:CB	2:B:497:ARG:HH12	2.04	0.71
2:B:407:GLU:HG2	5:B:2020:HOH:O	1.90	0.70
2:B:913:PHE:HB3	2:B:914:PRO:HD3	1.73	0.70
2:B:592:GLN:O	2:B:650:THR:HG21	1.91	0.69
2:B:464:GLN:H	2:B:464:GLN:NE2	1.88	0.69
2:B:502:ASN:HD21	2:B:504:GLN:HB2	1.56	0.69
2:B:815:VAL:HG11	2:B:854:VAL:HG12	1.74	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:603:VAL:O	2:B:607:LEU:HG	1.93	0.69
2:B:829:PRO:HG2	5:B:2033:HOH:O	1.93	0.69
2:B:142:ALA:O	2:B:146:MSE:HG3	1.92	0.69
2:B:794:MSE:HE3	2:B:837:SER:HA	1.74	0.69
2:B:502:ASN:ND2	2:B:504:GLN:HB2	2.09	0.68
2:B:562:LEU:N	2:B:563:PRO:CD	2.55	0.68
2:B:721:ALA:HB3	2:B:722:PRO:HD3	1.76	0.68
2:B:794:MSE:HE2	2:B:837:SER:HA	1.74	0.68
2:B:940:VAL:O	2:B:944:VAL:HG23	1.93	0.68
1:A:47:VAL:HG22	1:A:48:GLU:N	2.08	0.68
2:B:599:SER:HB2	2:B:652:ASP:O	1.93	0.68
2:B:455:THR:CB	2:B:497:ARG:HH22	2.07	0.67
1:A:75:GLY:CA	1:A:78:ARG:HH11	2.07	0.67
2:B:134:MSE:HB2	2:B:138:ALA:HB3	1.77	0.67
2:B:726:GLN:HG3	5:B:2032:HOH:O	1.92	0.67
2:B:376:ALA:HA	2:B:379:GLN:HB3	1.75	0.67
2:B:804:LYS:HE2	2:B:806:ASP:OD1	1.95	0.66
2:B:368:GLN:NE2	2:B:437:MSE:HB2	2.11	0.66
2:B:474:GLN:HE21	2:B:511:PHE:HB3	1.61	0.65
2:B:735:TYR:OH	2:B:775:THR:HG22	1.97	0.65
1:A:31:ARG:HB3	1:A:159:PHE:HZ	1.61	0.65
2:B:426:ASP:O	2:B:430:THR:HG22	1.96	0.65
1:A:78:ARG:NH1	2:B:88:ARG:NH1	2.42	0.64
1:A:57:ASN:HD22	1:A:57:ASN:N	1.94	0.64
2:B:215:PRO:O	2:B:219:ARG:HG3	1.98	0.64
2:B:675:ASN:HD22	2:B:678:VAL:H	1.45	0.64
2:B:239:CYS:O	2:B:243:ILE:HG12	1.98	0.63
2:B:464:GLN:HE21	2:B:464:GLN:N	1.93	0.63
2:B:484:TYR:CD2	2:B:484:TYR:N	2.67	0.62
2:B:716:LEU:HD12	2:B:720:PHE:HB2	1.81	0.62
1:A:131:ARG:HH22	1:A:150:ASP:CG	2.08	0.62
2:B:453:LEU:HD22	2:B:465:HIS:HD2	1.65	0.61
2:B:58:ALA:HA	2:B:61:PHE:CE2	2.35	0.61
2:B:855:GLY:CA	5:B:2040:HOH:O	2.47	0.61
2:B:930:ILE:HB	2:B:943:MSE:HE1	1.82	0.61
2:B:584:THR:O	2:B:588:MSE:HG2	2.00	0.61
2:B:479:THR:HG22	2:B:479:THR:O	1.99	0.61
2:B:354:GLU:O	2:B:354:GLU:HG2	1.99	0.61
2:B:283:ILE:HD11	2:B:323:LEU:HD22	1.81	0.60
2:B:325:ASP:OD1	2:B:378:LYS:NZ	2.35	0.60
2:B:387:ARG:N	2:B:388:PRO:HD2	2.15	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:794:MSE:HE3	2:B:840:PHE:HB3	1.81	0.60
2:B:218:VAL:O	2:B:222:VAL:HG23	2.02	0.60
2:B:855:GLY:HA3	5:B:2040:HOH:O	2.01	0.60
2:B:435:TYR:HE1	2:B:479:THR:O	1.85	0.60
2:B:799:GLN:HA	2:B:799:GLN:NE2	2.17	0.59
1:A:31:ARG:HB3	1:A:159:PHE:CZ	2.36	0.59
3:A:1181:GTP:O2B	5:A:2016:HOH:O	2.16	0.59
2:B:514:GLY:O	2:B:517:SER:HB2	2.03	0.59
2:B:349:HIS:HE1	2:B:402:GLN:O	1.85	0.59
1:A:72:GLU:OE2	2:B:88:ARG:HD2	2.04	0.58
2:B:827:LYS:HZ1	2:B:871:GLU:HB2	1.68	0.58
2:B:847:ARG:HD3	2:B:850:GLU:HG2	1.85	0.58
2:B:71:VAL:O	2:B:75:GLN:HG3	2.04	0.58
2:B:859:GLN:N	2:B:859:GLN:OE1	2.37	0.58
2:B:514:GLY:CA	2:B:550:THR:HG23	2.33	0.57
2:B:801:LEU:O	2:B:805:PRO:HG3	2.04	0.57
2:B:556:ARG:HB2	2:B:596:PHE:CE1	2.39	0.57
2:B:226:PHE:O	2:B:230:VAL:HG23	2.05	0.57
1:A:57:ASN:H	1:A:57:ASN:ND2	2.01	0.57
2:B:939:ARG:O	2:B:943:MSE:HG2	2.03	0.57
2:B:195:ALA:O	2:B:198:CYS:HB3	2.04	0.57
2:B:783:PRO:O	2:B:828:PHE:HZ	1.86	0.57
1:A:10:VAL:HG11	1:A:60:GLU:O	2.04	0.56
1:A:158:ASN:OD1	1:A:161:LYS:HE3	2.04	0.56
2:B:215:PRO:HD2	2:B:218:VAL:CG2	2.36	0.56
2:B:268:SER:HA	2:B:318:ASN:ND2	2.20	0.56
2:B:599:SER:HB3	2:B:651:LEU:HD12	1.86	0.56
2:B:882:MSE:HE2	2:B:882:MSE:HA	1.85	0.56
2:B:354:GLU:OE1	2:B:357:SER:HB3	2.04	0.56
2:B:606:ILE:O	2:B:610:LEU:HB2	2.05	0.56
2:B:368:GLN:NE2	2:B:433:TYR:O	2.38	0.56
2:B:827:LYS:NZ	2:B:871:GLU:HB2	2.20	0.56
2:B:424:ARG:NH2	2:B:467:GLU:OE1	2.31	0.56
2:B:855:GLY:O	2:B:858:VAL:HG23	2.06	0.56
1:A:57:ASN:ND2	1:A:58:PHE:HD2	2.04	0.55
2:B:675:ASN:HD21	2:B:677:VAL:HB	1.71	0.55
2:B:473:PHE:CD2	2:B:491:LEU:HD22	2.41	0.55
1:A:57:ASN:N	1:A:57:ASN:ND2	2.53	0.55
2:B:23:VAL:CG2	2:B:64:GLN:OE1	2.55	0.55
2:B:675:ASN:HD22	2:B:678:VAL:HG23	1.71	0.55
2:B:675:ASN:ND2	2:B:677:VAL:HB	2.22	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:61:PHE:CD1	2:B:61:PHE:C	2.86	0.54
1:A:93:ASP:CG	1:A:125:LYS:HD2	2.32	0.54
2:B:83:HIS:CD2	2:B:125:VAL:HG12	2.43	0.54
2:B:100:SER:O	2:B:104:GLN:HG3	2.07	0.54
2:B:500:ILE:HG22	2:B:500:ILE:O	2.08	0.54
2:B:500:ILE:HG23	2:B:506:ALA:HB2	1.89	0.54
2:B:427:ILE:HA	2:B:430:THR:HG23	1.89	0.54
2:B:805:PRO:HG2	2:B:847:ARG:HD2	1.88	0.54
1:A:75:GLY:C	1:A:78:ARG:HH11	2.16	0.54
2:B:513:ILE:HG23	2:B:530:VAL:HG11	1.89	0.54
2:B:381:VAL:O	2:B:385:VAL:HG23	2.08	0.54
2:B:909:GLN:N	2:B:910:PRO:HD2	2.22	0.54
2:B:23:VAL:HG23	2:B:64:GLN:OE1	2.08	0.54
2:B:350:TYR:HB2	2:B:423:TYR:CZ	2.43	0.54
2:B:767:LEU:O	2:B:771:VAL:HG23	2.07	0.54
1:A:57:ASN:HD21	1:A:176:LEU:HA	1.72	0.53
2:B:675:ASN:HB3	2:B:678:VAL:HG23	1.91	0.53
2:B:856:LYS:HD3	2:B:859:GLN:HB2	1.90	0.53
2:B:368:GLN:HG2	2:B:433:TYR:CD2	2.44	0.53
2:B:164:LEU:HD22	2:B:221:LYS:HD2	1.90	0.53
2:B:855:GLY:HA2	5:B:2040:HOH:O	2.09	0.53
2:B:538:LEU:HD12	2:B:547:SER:OG	2.09	0.53
2:B:846:PRO:HA	2:B:895:HIS:ND1	2.23	0.53
2:B:562:LEU:N	2:B:563:PRO:HD3	2.24	0.53
1:A:131:ARG:HH12	1:A:135:ALA:HB2	1.74	0.53
2:B:27:GLU:OE2	2:B:70:LYS:HD2	2.09	0.52
2:B:231:GLN:HA	2:B:269:GLN:HE22	1.73	0.52
2:B:306:HIS:CD2	2:B:355:THR:HG22	2.45	0.52
2:B:346:ILE:HD12	2:B:356:THR:HB	1.90	0.52
1:A:10:VAL:CG1	1:A:11:PRO:HD2	2.33	0.52
2:B:485:SER:O	2:B:489:PRO:CD	2.53	0.52
2:B:201:VAL:HG21	2:B:229:TRP:CE2	2.45	0.52
2:B:455:THR:CA	2:B:497:ARG:HH22	2.23	0.51
1:A:47:VAL:CG2	1:A:48:GLU:N	2.73	0.51
2:B:686:GLN:H	2:B:686:GLN:CD	2.17	0.51
1:A:125:LYS:HG2	3:A:1181:GTP:C6	2.45	0.51
1:A:173:ASN:OD1	1:A:175:GLN:HB2	2.10	0.51
2:B:82:LEU:O	2:B:86:ILE:HG13	2.10	0.51
2:B:596:PHE:CD2	2:B:650:THR:HG22	2.45	0.51
2:B:198:CYS:HB2	2:B:229:TRP:CE3	2.45	0.51
2:B:708:ILE:HG22	2:B:709:PHE:N	2.25	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:78:ARG:HH12	2:B:88:ARG:HH12	1.54	0.51
2:B:630:ASN:HB2	2:B:631:PRO:HD2	1.92	0.51
2:B:762:PRO:HB2	2:B:763:PRO:HD3	1.92	0.51
2:B:76:TYR:HA	2:B:119:VAL:HG22	1.93	0.51
1:A:131:ARG:NH1	1:A:135:ALA:H	2.09	0.51
1:A:141:HIS:ND1	1:A:141:HIS:N	2.52	0.50
1:A:15:LEU:HD21	1:A:89:ILE:HG13	1.94	0.50
2:B:805:PRO:CG	2:B:847:ARG:HD2	2.41	0.50
2:B:939:ARG:NH1	2:B:943:MSE:HB3	2.26	0.50
2:B:363:PHE:C	2:B:363:PHE:CD2	2.87	0.50
2:B:675:ASN:HB3	2:B:678:VAL:CG2	2.42	0.50
2:B:584:THR:HG22	2:B:639:HIS:CE1	2.47	0.50
2:B:831:ALA:N	2:B:832:PRO:HD2	2.26	0.50
2:B:848:CYS:HB3	2:B:856:LYS:HE3	1.93	0.50
1:A:140:PHE:CZ	1:A:146:LEU:HD22	2.47	0.49
2:B:615:SER:N	2:B:616:PRO:HD2	2.27	0.49
2:B:850:GLU:O	2:B:850:GLU:HG3	2.11	0.49
2:B:717:LEU:O	2:B:753:ILE:HG21	2.11	0.49
2:B:788:ASP:HB3	5:B:2034:HOH:O	2.12	0.49
2:B:349:HIS:H	2:B:353:ASN:HD22	1.61	0.49
2:B:513:ILE:HD13	2:B:530:VAL:CG1	2.34	0.49
2:B:698:ASP:CG	2:B:701:VAL:HG23	2.37	0.49
2:B:584:THR:HG22	2:B:639:HIS:ND1	2.27	0.49
2:B:294:ARG:HG2	2:B:294:ARG:HH11	1.77	0.49
2:B:834:VAL:HG11	2:B:881:LEU:HD13	1.95	0.49
1:A:158:ASN:CG	1:A:161:LYS:HE3	2.38	0.49
2:B:306:HIS:CD2	2:B:355:THR:CG2	2.96	0.49
2:B:531:LEU:N	2:B:532:PRO:HD2	2.27	0.49
2:B:355:THR:HG22	2:B:355:THR:O	2.12	0.49
2:B:562:LEU:H	2:B:563:PRO:HD3	1.78	0.49
2:B:857:VAL:CG1	2:B:858:VAL:N	2.76	0.48
1:A:168:ARG:HA	1:A:176:LEU:HD12	1.94	0.48
2:B:168:GLU:OE1	2:B:168:GLU:HA	2.13	0.48
2:B:294:ARG:HG2	2:B:294:ARG:NH1	2.28	0.48
2:B:319:HIS:O	2:B:323:LEU:HG	2.14	0.48
2:B:544:SER:OG	2:B:586:GLN:HG2	2.12	0.48
2:B:930:ILE:CA	2:B:943:MSE:HE1	2.42	0.48
1:A:103:VAL:HB	1:A:104:PRO:HD3	1.96	0.48
2:B:470:LEU:HD21	2:B:509:VAL:HA	1.95	0.48
2:B:544:SER:HB2	2:B:582:HIS:HD2	1.79	0.48
2:B:321:ARG:HH22	2:B:373:SER:CB	2.26	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:333:PHE:O	2:B:337:VAL:HG23	2.14	0.48
2:B:354:GLU:O	2:B:354:GLU:CG	2.61	0.48
2:B:276:VAL:HA	2:B:279:LEU:HD12	1.95	0.48
1:A:93:ASP:OD1	1:A:95:THR:OG1	2.29	0.47
2:B:484:TYR:H	2:B:484:TYR:HD2	1.61	0.47
2:B:226:PHE:CD1	2:B:242:LEU:HD13	2.49	0.47
2:B:799:GLN:HA	2:B:799:GLN:HE21	1.78	0.47
2:B:858:VAL:C	2:B:860:GLU:H	2.22	0.47
2:B:716:LEU:HD13	2:B:719:ASP:C	2.40	0.47
2:B:835:LYS:HG3	2:B:881:LEU:CD2	2.44	0.47
2:B:930:ILE:CB	2:B:943:MSE:HE1	2.45	0.47
2:B:181:ARG:O	2:B:182:LEU:CB	2.62	0.47
1:A:77:LEU:O	1:A:78:ARG:C	2.56	0.47
1:A:73:LYS:HE3	1:A:74:PHE:CE2	2.50	0.47
2:B:346:ILE:HG23	2:B:347:PRO:HD2	1.97	0.47
2:B:474:GLN:NE2	2:B:511:PHE:CB	2.74	0.47
2:B:889:LEU:HD22	2:B:930:ILE:HD11	1.96	0.47
2:B:464:GLN:NE2	2:B:464:GLN:N	2.60	0.46
2:B:848:CYS:SG	2:B:859:GLN:NE2	2.89	0.46
2:B:576:VAL:HG11	2:B:582:HIS:CE1	2.50	0.46
2:B:735:TYR:OH	2:B:775:THR:CG2	2.63	0.46
2:B:581:ILE:HG22	2:B:582:HIS:CD2	2.50	0.46
2:B:321:ARG:NH2	2:B:373:SER:OG	2.48	0.46
2:B:220:GLN:HG3	2:B:255:LEU:HD23	1.98	0.46
2:B:565:TYR:O	2:B:569:ILE:HG13	2.15	0.46
1:A:91:MET:HE2	1:A:151:ILE:HD11	1.96	0.46
1:A:93:ASP:OD1	1:A:125:LYS:HD2	2.15	0.46
2:B:675:ASN:ND2	2:B:678:VAL:HG23	2.31	0.46
1:A:47:VAL:HG22	1:A:48:GLU:H	1.79	0.46
2:B:505:LEU:O	2:B:509:VAL:HG23	2.16	0.46
2:B:513:ILE:CG2	2:B:530:VAL:HG11	2.46	0.46
1:A:14:LYS:HD3	1:A:84:ASN:O	2.15	0.46
2:B:568:ASN:O	2:B:572:VAL:HG23	2.15	0.46
2:B:744:LEU:HD23	2:B:771:VAL:HG11	1.97	0.46
2:B:815:VAL:HG11	2:B:854:VAL:CG1	2.45	0.46
2:B:309:CYS:HB2	2:B:356:THR:HG23	1.98	0.45
2:B:695:TRP:CE3	2:B:701:VAL:HG21	2.50	0.45
2:B:341:MSE:HE1	2:B:393:LEU:HB2	1.99	0.45
1:A:16:VAL:HG22	1:A:88:ALA:HB2	1.97	0.45
1:A:94:VAL:HG21	1:A:131:ARG:HE	1.81	0.45
2:B:231:GLN:HA	2:B:269:GLN:NE2	2.31	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:854:VAL:O	2:B:858:VAL:HG22	2.17	0.45
2:B:350:TYR:CE1	2:B:358:SER:HB2	2.52	0.45
2:B:405:SER:HB2	5:B:2020:HOH:O	2.16	0.45
2:B:71:VAL:HG13	2:B:72:PRO:HD2	1.98	0.45
1:A:108:ARG:HG3	1:A:108:ARG:HH11	1.82	0.45
2:B:702:VAL:HG11	2:B:740:GLN:NE2	2.32	0.45
2:B:488:VAL:CB	2:B:489:PRO:HD3	2.39	0.45
2:B:725:PRO:HG2	5:B:2032:HOH:O	2.17	0.45
1:A:25:LYS:O	1:A:29:VAL:HG23	2.17	0.44
2:B:230:VAL:HG11	2:B:266:ALA:HA	1.98	0.44
2:B:827:LYS:HD3	2:B:827:LYS:HA	1.52	0.44
2:B:293:LEU:O	2:B:297:VAL:HG23	2.18	0.44
2:B:173:LEU:HB3	2:B:174:PRO:CD	2.47	0.44
2:B:363:PHE:HE2	2:B:364:TRP:CZ3	2.36	0.44
2:B:495:ILE:HB	2:B:496:PRO:HD3	1.99	0.44
2:B:488:VAL:HB	2:B:489:PRO:CD	2.39	0.44
2:B:563:PRO:N	2:B:564:PRO:HD2	2.32	0.44
2:B:215:PRO:HD2	2:B:218:VAL:HG21	2.00	0.44
2:B:164:LEU:CD2	2:B:221:LYS:HD2	2.48	0.43
2:B:453:LEU:CD2	2:B:465:HIS:HD2	2.28	0.43
2:B:858:VAL:C	2:B:859:GLN:OE1	2.60	0.43
2:B:903:TRP:HE3	2:B:903:TRP:HA	1.83	0.43
2:B:349:HIS:CE1	2:B:402:GLN:O	2.67	0.43
2:B:903:TRP:HA	2:B:903:TRP:CE3	2.53	0.43
2:B:939:ARG:HH12	2:B:943:MSE:HB3	1.83	0.43
1:A:125:LYS:HE2	3:A:1181:GTP:C4	2.54	0.43
2:B:485:SER:O	2:B:486:ASP:C	2.60	0.43
1:A:122:CYS:HB3	1:A:151:ILE:HG12	2.00	0.43
2:B:387:ARG:N	2:B:388:PRO:CD	2.78	0.43
2:B:435:TYR:HB2	2:B:476:ILE:HD13	2.01	0.43
2:B:927:SER:O	2:B:931:LEU:HG	2.19	0.43
2:B:544:SER:CB	2:B:582:HIS:HD2	2.32	0.43
2:B:566:ALA:O	2:B:570:VAL:HG23	2.19	0.43
2:B:725:PRO:O	2:B:729:GLU:HG3	2.19	0.43
2:B:621:LEU:O	2:B:625:ALA:N	2.51	0.42
2:B:857:VAL:O	2:B:860:GLU:HG2	2.18	0.42
1:A:78:ARG:HH21	2:B:88:ARG:HD3	1.73	0.42
1:A:125:LYS:HG2	3:A:1181:GTP:C5	2.54	0.42
2:B:592:GLN:HA	2:B:650:THR:OG1	2.19	0.42
2:B:580:GLN:OE1	2:B:580:GLN:HA	2.20	0.42
2:B:265:ASN:O	2:B:269:GLN:HG2	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:363:PHE:HE2	2:B:364:TRP:CE3	2.38	0.42
2:B:374:PHE:O	2:B:379:GLN:HB2	2.20	0.42
2:B:409:TYR:CE2	2:B:417:LYS:HE2	2.55	0.42
2:B:343:CYS:HB3	2:B:356:THR:HG22	2.01	0.42
2:B:596:PHE:CG	2:B:650:THR:HG22	2.55	0.42
1:A:71:LEU:HD13	1:A:73:LYS:HE2	2.02	0.42
1:A:148:TYR:CG	1:A:149:TYR:N	2.88	0.42
2:B:540:ASN:HA	2:B:541:PRO:HD2	1.93	0.42
2:B:455:THR:CB	2:B:497:ARG:NH1	2.80	0.41
2:B:945:LYS:O	2:B:948:THR:HG22	2.19	0.41
2:B:500:ILE:CG2	2:B:506:ALA:HB2	2.50	0.41
2:B:794:MSE:HE2	2:B:837:SER:CA	2.44	0.41
2:B:209:LEU:O	2:B:219:ARG:NH2	2.48	0.41
2:B:823:VAL:O	2:B:826:LEU:HB2	2.20	0.41
1:A:131:ARG:NH2	1:A:150:ASP:CG	2.76	0.41
2:B:526:MSE:HE2	2:B:526:MSE:HA	2.03	0.41
1:A:37:PHE:CE2	1:A:154:LYS:HG3	2.55	0.41
2:B:64:GLN:HA	2:B:67:GLN:NE2	2.36	0.41
2:B:544:SER:OG	2:B:582:HIS:CD2	2.73	0.41
2:B:716:LEU:HD11	2:B:720:PHE:HB2	2.01	0.41
2:B:794:MSE:HE3	2:B:840:PHE:CB	2.48	0.41
2:B:913:PHE:CB	2:B:914:PRO:HD3	2.45	0.41
2:B:631:PRO:O	2:B:632:SER:C	2.64	0.41
2:B:706:CYS:SG	2:B:734:MSE:HE1	2.60	0.41
1:A:75:GLY:CA	1:A:78:ARG:NH1	2.75	0.41
2:B:205:LEU:HD22	2:B:222:VAL:HG13	2.02	0.41
2:B:879:ARG:HE	2:B:879:ARG:HB3	1.66	0.41
2:B:352:VAL:O	2:B:352:VAL:HG13	2.20	0.41
1:A:171:ALA:O	1:A:172:GLY:C	2.63	0.41
2:B:387:ARG:NH2	2:B:441:GLU:OE2	2.44	0.41
2:B:408:GLU:OE1	2:B:412:TRP:NE1	2.52	0.41
2:B:477:ALA:HB3	2:B:515:ALA:HB1	2.02	0.41
2:B:929:GLN:HG2	2:B:932:ARG:NH2	2.36	0.41
1:A:93:ASP:OD2	1:A:125:LYS:HD2	2.21	0.40
2:B:383:GLN:NE2	2:B:387:ARG:HH11	2.18	0.40
2:B:875:GLY:HA2	2:B:952:ARG:CZ	2.51	0.40
1:A:147:GLN:HG3	1:A:148:TYR:N	2.36	0.40
2:B:105:LEU:HA	2:B:105:LEU:HD23	1.77	0.40
2:B:202:PHE:HB2	2:B:203:PRO:HD3	2.03	0.40
1:A:32:HIS:CE1	1:A:163:PHE:HE2	2.40	0.40
2:B:830:GLU:H	2:B:830:GLU:CD	2.29	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:936:ASN:O	2:B:937:LYS:C	2.65	0.40
2:B:67:GLN:C	2:B:69:ASP:N	2.79	0.40
2:B:118:ILE:H	2:B:118:ILE:HG13	1.65	0.40
2:B:771:VAL:O	2:B:775:THR:HG23	2.22	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	170/172 (99%)	159 (94%)	10 (6%)	1 (1%)	21	51
2	B	899/963 (93%)	850 (94%)	48 (5%)	1 (0%)	48	77
All	All	1069/1135 (94%)	1009 (94%)	58 (5%)	2 (0%)	43	72

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	141	HIS
2	B	851	VAL

5.3.2 Protein sidechains [i](#)

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

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

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	143/150 (95%)	129 (90%)	14 (10%)	7	25
2	B	738/824 (90%)	692 (94%)	46 (6%)	16	45
All	All	881/974 (90%)	821 (93%)	60 (7%)	14	42

All (60) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	10	VAL
1	A	18	VAL
1	A	27	THR
1	A	31	ARG
1	A	36	GLU
1	A	52	LEU
1	A	57	ASN
1	A	78	ARG
1	A	94	VAL
1	A	108	ARG
1	A	114	CYS
1	A	141	HIS
1	A	161	LYS
1	A	170	LEU
2	B	70	LYS
2	B	172	VAL
2	B	196	VAL
2	B	198	CYS
2	B	203	PRO
2	B	213	SER
2	B	214	SER
2	B	251	GLN
2	B	295	GLN
2	B	315	LEU
2	B	326	GLN
2	B	352	VAL
2	B	354	GLU
2	B	357	SER
2	B	374	PHE
2	B	407	GLU
2	B	408	GLU
2	B	422	ILE

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Mol	Chain	Res	Type
2	B	428	SER
2	B	430	THR
2	B	464	GLN
2	B	475	SER
2	B	484	TYR
2	B	489	PRO
2	B	517	SER
2	B	529	SER
2	B	535	LEU
2	B	538	LEU
2	B	551	LEU
2	B	558	CYS
2	B	576	VAL
2	B	650	THR
2	B	702	VAL
2	B	708	ILE
2	B	746	LEU
2	B	765	GLU
2	B	809	LEU
2	B	813	LEU
2	B	847	ARG
2	B	857	VAL
2	B	858	VAL
2	B	859	GLN
2	B	896	CYS
2	B	903	TRP
2	B	924	ASP
2	B	935	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (33) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	32	HIS
1	A	57	ASN
1	A	102	ASN
1	A	107	HIS
1	A	156	ASN
2	B	67	GLN
2	B	83	HIS
2	B	151	GLN
2	B	211	GLN
2	B	220	GLN

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Mol	Chain	Res	Type
2	B	277	ASN
2	B	290	GLN
2	B	292	GLN
2	B	295	GLN
2	B	299	ASN
2	B	349	HIS
2	B	353	ASN
2	B	368	GLN
2	B	383	GLN
2	B	392	GLN
2	B	464	GLN
2	B	465	HIS
2	B	474	GLN
2	B	502	ASN
2	B	523	HIS
2	B	582	HIS
2	B	586	GLN
2	B	592	GLN
2	B	675	ASN
2	B	689	GLN
2	B	740	GLN
2	B	752	HIS
2	B	799	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 2 ligands modelled in this entry, 1 is monoatomic - leaving 1 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
3	GTP	A	1181	4	33,34,34	0.99	1 (3%)	50,54,54	1.87	19 (38%)

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 Torsions and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	GTP	A	1181	4	-	1/22/38/38	0/3/3/3

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	1181	GTP	PB-O3B	2.05	1.61	1.59

All (19) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1181	GTP	C2-N3-C4	5.25	121.34	112.30
3	A	1181	GTP	C5-C4-N3	-4.75	120.83	128.39
3	A	1181	GTP	N9-C4-N3	3.40	132.75	125.95
3	A	1181	GTP	O2B-PB-O3A	3.22	115.98	107.27
3	A	1181	GTP	O2B-PB-O3B	3.01	115.40	107.27
3	A	1181	GTP	C6-C5-N7	2.79	135.37	130.29
3	A	1181	GTP	C8-N7-C5	2.70	109.08	104.26
3	A	1181	GTP	C5'-C4'-C3'	-2.57	105.94	115.21
3	A	1181	GTP	C2-N1-C6	-2.40	120.76	125.11
3	A	1181	GTP	C2'-C3'-C4'	2.31	107.07	102.61
3	A	1181	GTP	C3'-C2'-C1'	2.24	105.70	101.46
3	A	1181	GTP	C4-C5-N7	-2.18	107.22	110.67
3	A	1181	GTP	C2'-C1'-N9	-2.17	107.22	113.25
3	A	1181	GTP	O4'-C1'-N9	2.14	113.21	108.36
3	A	1181	GTP	O4'-C4'-C3'	2.14	109.39	105.15
3	A	1181	GTP	PA-O5'-C5'	-2.12	109.19	121.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1181	GTP	N9-C8-N7	-2.11	109.49	113.40
3	A	1181	GTP	O6-C6-C5	-2.08	121.04	126.53
3	A	1181	GTP	C5-C6-N1	2.08	118.54	113.25

There are no chirality outliers.

All (1) torsion outliers are listed below:

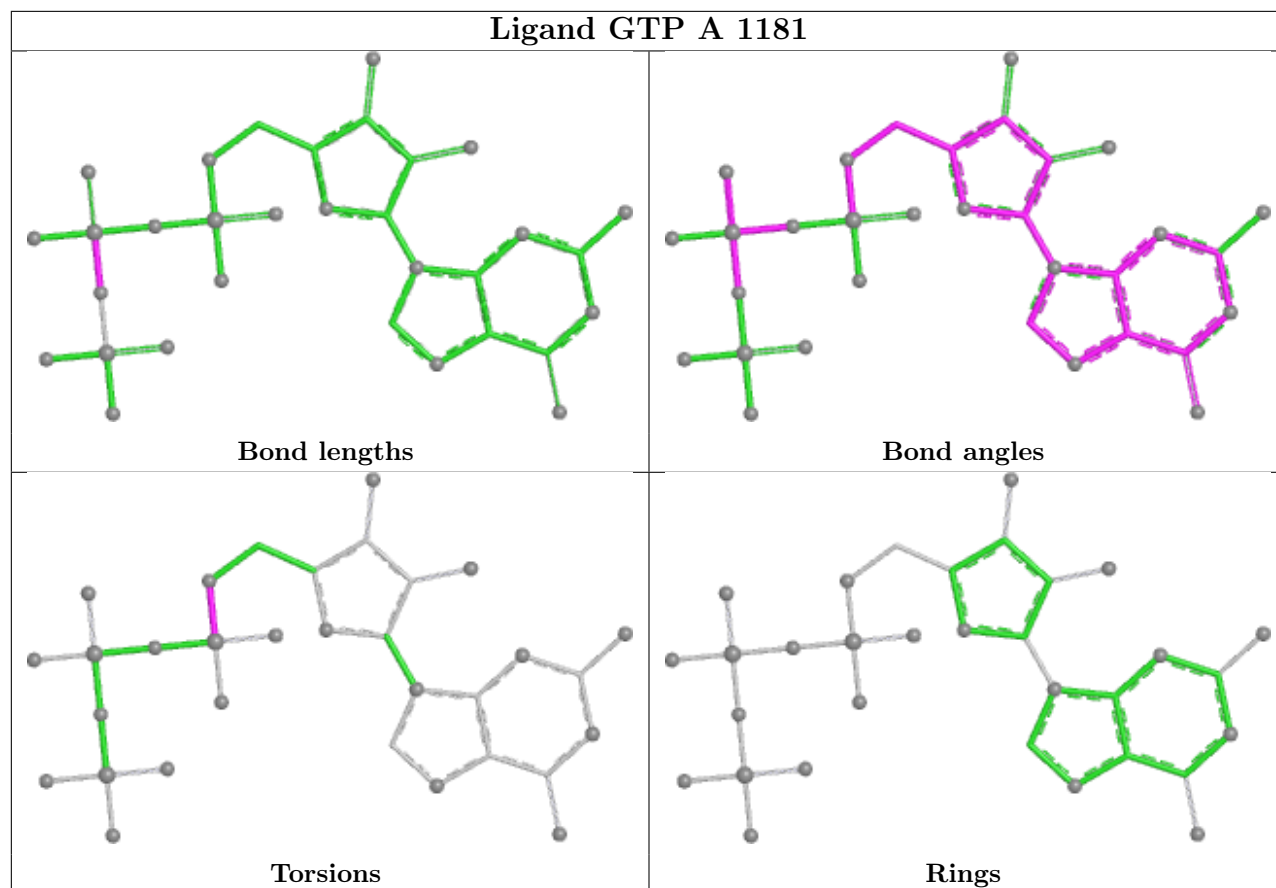
Mol	Chain	Res	Type	Atoms
3	A	1181	GTP	C5'-O5'-PA-O1A

There are no ring outliers.

1 monomer is involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1181	GTP	5	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](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	172/172 (100%)	-0.06	3 (1%) 69 60	39, 53, 80, 88	0
2	B	885/963 (91%)	0.26	31 (3%) 47 38	38, 69, 96, 110	0
All	All	1057/1135 (93%)	0.21	34 (3%) 50 40	38, 67, 95, 110	0

All (34) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	851	VAL	3.7
2	B	850	GLU	3.4
2	B	152	ALA	3.2
2	B	351	PRO	2.9
2	B	458	GLU	2.8
2	B	485	SER	2.7
2	B	178	GLN	2.6
2	B	461	TYR	2.6
2	B	566	ALA	2.6
2	B	352	VAL	2.6
1	A	8	GLY	2.5
2	B	483	ASN	2.5
2	B	375	GLU	2.5
1	A	155	SER	2.4
2	B	657	GLU	2.4
2	B	137	ASP	2.4
2	B	482	VAL	2.4
2	B	182	LEU	2.4
2	B	460	PRO	2.4
2	B	457	SER	2.4
2	B	136	PRO	2.4
2	B	192	THR	2.3
2	B	359	LEU	2.3
2	B	487	VAL	2.3

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Mol	Chain	Res	Type	RSRZ
2	B	631	PRO	2.3
2	B	456	SER	2.2
2	B	853	SER	2.2
2	B	433	TYR	2.1
2	B	484	TYR	2.1
2	B	233	GLU	2.1
2	B	783	PRO	2.1
2	B	849	GLY	2.1
1	A	79	ASP	2.1
2	B	499	SER	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](#)

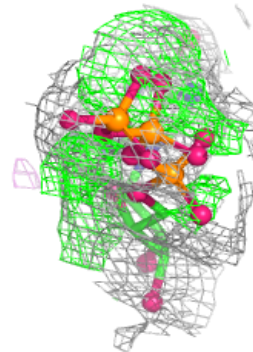
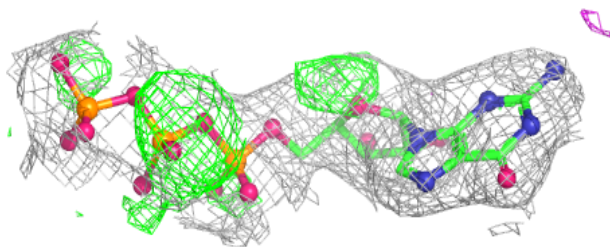
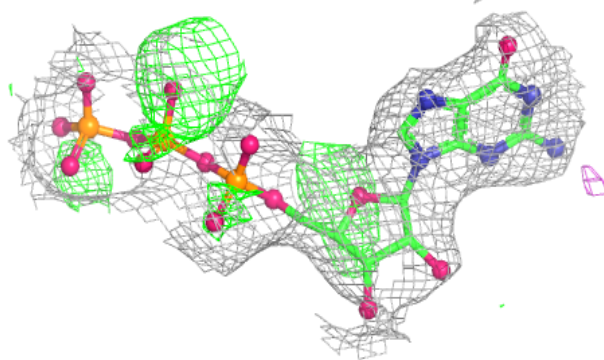
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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
3	GTP	A	1181	32/32	0.92	0.11	48,62,65,69	0
4	MG	A	1182	1/1	0.95	0.12	41,41,41,41	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 GTP A 1181:

$2mF_o-DF_c$ (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.