Full wwPDB X-ray Structure Validation Report (i)

Dec 17, 2023 – 11:59 am GMT

PDB ID	:	4BWP
Title	:	Structure of Drosophila Melanogaster PAN3 pseudokinase
Authors	:	Christie, M.; Boland, A.; Huntzinger, E.; Weichenrieder, O.; Izaurralde, E.
Deposited on	:	2013-07-03
Resolution	:	3.60 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 (i) 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 (i)) were used in the production of this report:

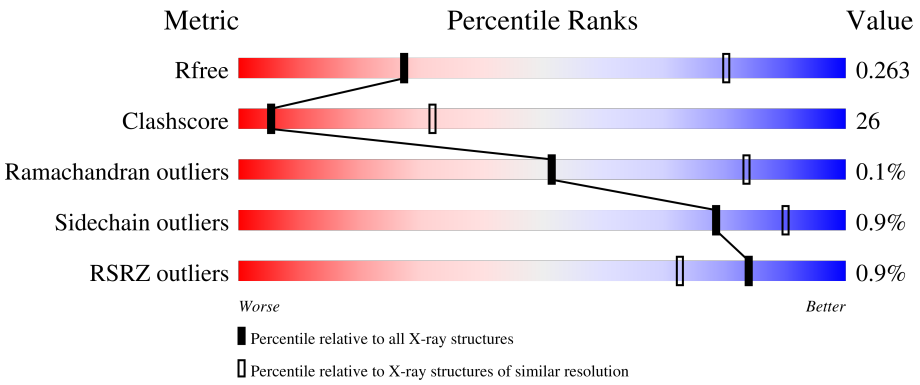
MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 3.60 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}	130704	1257 (3.70-3.50)
Clashscore	141614	1353 (3.70-3.50)
Ramachandran outliers	138981	1307 (3.70-3.50)
Sidechain outliers	138945	1307 (3.70-3.50)
RSRZ outliers	127900	1161 (3.70-3.50)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments 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 <=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	448	% 51% 35% 14%
1	B	448	% 51% 32% 17%

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 6125 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.

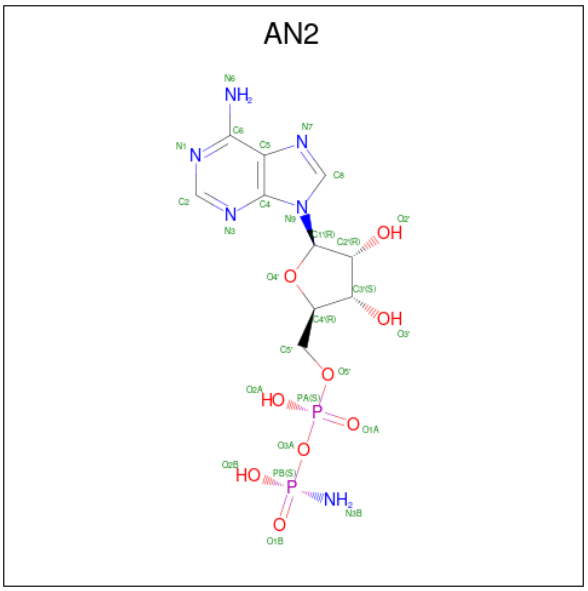
- Molecule 1 is a protein called PAB-DEPENDENT POLY(A)-SPECIFIC RIBONUCLEASE SUBUNIT PAN-3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	386	3093	1957	541	573	22	0	0	0
1	B	372	2978	1886	522	549	21	0	0	0

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	343	GLY	-	expression tag	UNP Q95RR8
A	344	PRO	-	expression tag	UNP Q95RR8
A	345	HIS	-	expression tag	UNP Q95RR8
A	346	MET	-	expression tag	UNP Q95RR8
A	347	LEU	-	expression tag	UNP Q95RR8
A	348	GLU	-	expression tag	UNP Q95RR8
B	343	GLY	-	expression tag	UNP Q95RR8
B	344	PRO	-	expression tag	UNP Q95RR8
B	345	HIS	-	expression tag	UNP Q95RR8
B	346	MET	-	expression tag	UNP Q95RR8
B	347	LEU	-	expression tag	UNP Q95RR8
B	348	GLU	-	expression tag	UNP Q95RR8

- Molecule 2 is AMP PHOSPHORAMIDATE (three-letter code: AN2) (formula: $C_{10}H_{16}N_6O_9P_2$).



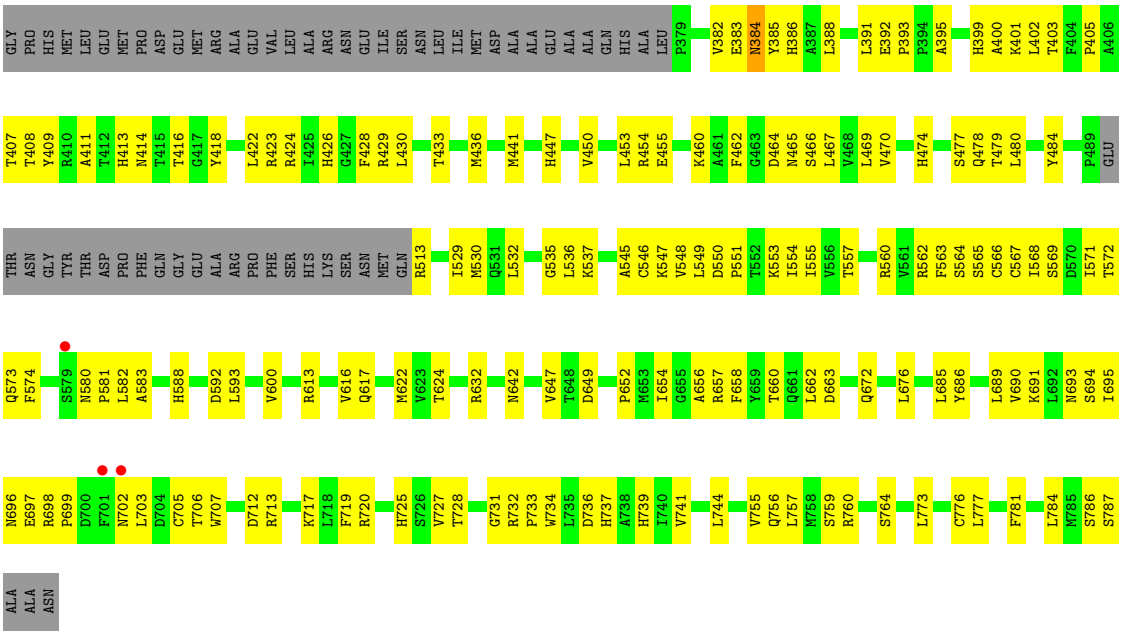
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			27	10	6	9	2		
2	B	1	Total	C	N	O	P	0	0
			27	10	6	9	2		

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.

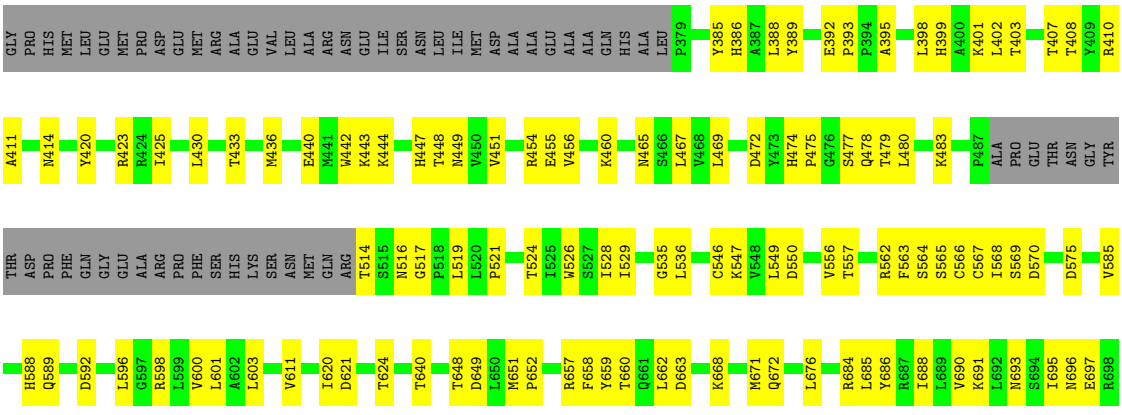
• Molecule 1: PAB-DEPENDENT POLY(A)-SPECIFIC RIBONUCLEASE SUBUNIT PAN-3

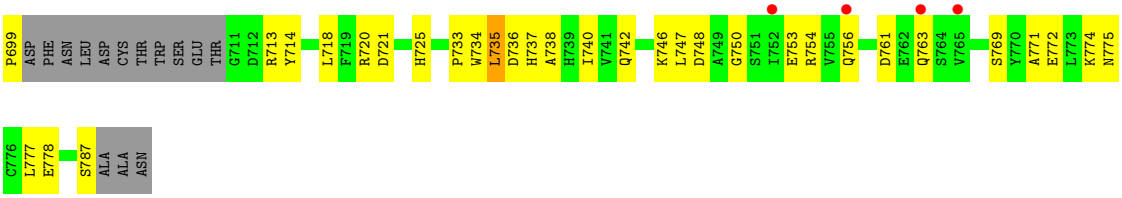
Chain A:



• Molecule 1: PAB-DEPENDENT POLY(A)-SPECIFIC RIBONUCLEASE SUBUNIT PAN-3

Chain B:




P699
ASP
PHE
ASN
LEU
ASP
CYS
THR
TRP
SER
GLU
THR
G711
D712
R713
Y714
L718
F719
R720
D721
H725
P733
W734
L735
D736
H737
A738
H739
I740
V741
Q742
K746
L747
D748
A749
G750
S751
I752
E753
R754
V755
Q756
D761
E762
Q763
S764
V765
S769
Y770
A771
E772
L773
K774
N775
C776
L777
E778
S787
ALA
ALA
ASN

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 43 2 2	Depositor
Cell constants a, b, c, α, β, γ	102.17Å 102.17Å 264.71Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.80 – 3.60 48.80 – 3.60	Depositor EDS
% Data completeness (in resolution range)	99.7 (48.80-3.60) 99.8 (48.80-3.60)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.05 (at 3.57Å)	Xtriage
Refinement program	REFMAC 5.6.0117	Depositor
R, R_{free}	0.220 , 0.269 0.212 , 0.263	Depositor DCC
R_{free} test set	862 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å^2)	122.1	Xtriage
Anisotropy	0.125	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.31 , 86.3	EDS
L-test for twinning[2]	$< \|L\| > = 0.45$, $< L^2 > = 0.28$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	6125	wwPDB-VP
Average B, all atoms (Å^2)	135.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.36% of the height of the origin peak. No significant pseudotranslation is detected.*

[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: AN2

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	0.62	0/3157	0.76	0/4282
1	B	0.57	2/3037 (0.1%)	0.71	0/4115
All	All	0.59	2/6194 (0.0%)	0.74	0/8397

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

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	734	TRP	CD2-CE2	5.46	1.47	1.41
1	B	526	TRP	CD2-CE2	5.05	1.47	1.41

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	384	ASN	Peptide

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	3093	0	3093	201	1
1	B	2978	0	2993	134	1
2	A	27	0	14	5	0
2	B	27	0	14	5	0
All	All	6125	0	6114	322	1

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 26.

All (322) 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:698:ARG:CZ	1:A:784:LEU:HD11	1.59	1.30
1:A:697:GLU:OE2	1:A:717:LYS:HE2	1.30	1.27
1:A:698:ARG:CZ	1:A:784:LEU:CD1	2.27	1.11
1:B:423:ARG:NH1	2:B:1788:AN2:O1A	1.81	1.11
1:A:698:ARG:NE	1:A:784:LEU:HD11	1.67	1.08
1:A:547:LYS:HG2	1:A:569:SER:HB2	1.37	1.06
1:A:699:PRO:HB3	1:A:713:ARG:HE	1.15	1.05
1:A:698:ARG:HH21	1:B:733:PRO:HB3	1.21	1.03
1:A:698:ARG:NH1	1:A:702:ASN:CG	2.13	1.02
1:A:386:HIS:ND1	1:A:414:ASN:OD1	1.92	1.01
1:B:479:THR:HG23	2:B:1788:AN2:H3'	1.41	1.00
1:A:424:ARG:NH1	1:A:466:SER:OG	1.93	0.99
1:A:698:ARG:HH12	1:A:702:ASN:CG	1.64	0.99
1:A:736:ASP:OD2	1:A:739:HIS:HB2	1.64	0.97
1:B:460:LYS:HG2	1:B:465:ASN:CB	1.94	0.97
1:A:382:VAL:HG12	1:A:383:GLU:H	1.28	0.97
1:B:386:HIS:CE1	1:B:414:ASN:HA	2.00	0.96
1:A:547:LYS:CG	1:A:569:SER:HB2	1.97	0.94
1:A:694:SER:O	1:A:698:ARG:HB2	1.67	0.93
1:A:697:GLU:OE2	1:A:717:LYS:CE	2.16	0.92
1:A:696:ASN:C	1:A:697:GLU:OE1	2.09	0.91
1:A:698:ARG:NH1	1:A:784:LEU:CD1	2.34	0.90
1:A:388:LEU:CD2	1:A:411:ALA:HB2	2.02	0.90
1:B:563:PHE:HB3	1:B:566:CYS:SG	2.13	0.88
1:A:547:LYS:HG2	1:A:569:SER:CB	2.04	0.87
1:B:386:HIS:HE1	1:B:414:ASN:HA	1.37	0.87
1:B:398:LEU:HD21	1:B:425:ILE:HG12	1.55	0.87

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:698:ARG:NH1	1:A:702:ASN:ND2	2.24	0.85
1:B:460:LYS:HG2	1:B:465:ASN:HB3	1.55	0.84
1:A:469:LEU:HD13	1:A:568:ILE:HG12	1.56	0.84
1:A:563:PHE:HB3	1:A:566:CYS:SG	2.16	0.84
1:B:565:SER:OG	1:B:568:ILE:HD12	1.78	0.84
1:A:399:HIS:CD2	1:A:403:THR:HG22	2.13	0.83
1:A:382:VAL:HG21	1:A:388:LEU:HD11	1.58	0.83
1:A:698:ARG:NH1	1:A:702:ASN:OD1	2.08	0.83
1:B:460:LYS:HG2	1:B:465:ASN:HB2	1.59	0.83
1:A:699:PRO:HB3	1:A:713:ARG:NE	1.94	0.83
1:B:693:ASN:HA	1:B:696:ASN:ND2	1.93	0.82
1:B:721:ASP:OD1	1:B:725:HIS:CE1	2.32	0.82
1:A:695:ILE:O	1:A:699:PRO:HD3	1.80	0.81
1:B:721:ASP:O	1:B:725:HIS:HB2	1.79	0.81
1:A:703:LEU:HD12	1:A:713:ARG:HH12	1.46	0.81
1:B:699:PRO:HG3	1:B:713:ARG:HD2	1.63	0.81
1:A:725:HIS:NE2	1:A:760:ARG:NH1	2.29	0.81
1:A:382:VAL:HB	1:A:385:TYR:HB2	1.64	0.79
1:A:413:HIS:HB3	1:A:416:THR:OG1	1.83	0.78
1:A:424:ARG:HD3	1:A:462:PHE:CE2	2.17	0.78
1:A:698:ARG:N	1:A:699:PRO:HD2	1.99	0.78
1:B:447:HIS:HD2	1:B:535:GLY:HA2	1.48	0.77
1:A:698:ARG:HH21	1:B:733:PRO:CB	1.95	0.77
1:A:423:ARG:HD2	1:A:568:ILE:HD11	1.66	0.76
1:A:727:VAL:CG1	1:A:731:GLY:HA2	2.16	0.75
1:A:550:ASP:OD1	1:A:553:LYS:HG2	1.86	0.75
1:A:736:ASP:OD2	1:A:739:HIS:CB	2.34	0.75
1:B:714:TYR:CE1	1:B:718:LEU:HD11	2.23	0.73
1:A:698:ARG:HH12	1:A:702:ASN:ND2	1.84	0.73
1:B:401:LYS:HG3	1:B:402:LEU:N	2.03	0.73
1:B:401:LYS:CG	1:B:402:LEU:N	2.52	0.73
1:A:388:LEU:CD2	1:A:411:ALA:CB	2.66	0.73
1:B:454:ARG:O	1:B:455:GLU:HG3	1.88	0.73
1:A:698:ARG:N	1:A:699:PRO:CD	2.52	0.72
1:A:694:SER:O	1:A:698:ARG:CB	2.38	0.71
1:A:697:GLU:CD	1:A:717:LYS:HE2	2.10	0.71
1:B:750:GLY:O	1:B:771:ALA:HB2	1.91	0.70
1:A:424:ARG:CD	1:A:462:PHE:CD2	2.74	0.70
1:A:382:VAL:HG12	1:A:383:GLU:N	2.06	0.69
1:A:624:THR:OG1	1:A:632:ARG:HG3	1.91	0.69
1:A:401:LYS:HD2	1:A:401:LYS:O	1.91	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:699:PRO:CB	1:A:713:ARG:HE	1.99	0.68
1:A:386:HIS:HE1	1:A:414:ASN:HA	1.59	0.67
1:A:460:LYS:HG2	1:A:465:ASN:OD1	1.95	0.67
1:A:547:LYS:CG	1:A:569:SER:CB	2.68	0.67
1:B:401:LYS:CG	1:B:402:LEU:H	2.06	0.67
1:A:685:LEU:HD22	1:A:744:LEU:HB3	1.77	0.67
1:A:719:PHE:CD1	1:A:773:LEU:HD21	2.30	0.66
1:A:727:VAL:HG12	1:A:731:GLY:HA2	1.77	0.66
1:A:654:ILE:O	1:A:657:ARG:HD2	1.95	0.66
1:A:547:LYS:HB3	1:A:569:SER:OG	1.94	0.66
1:A:405:PRO:HB2	1:A:426:HIS:CD2	2.31	0.66
1:A:467:LEU:HD21	1:A:571:ILE:HD12	1.77	0.66
1:A:698:ARG:NH1	1:A:784:LEU:HD12	2.11	0.65
1:A:581:PRO:HB2	1:A:582:LEU:HD12	1.78	0.65
1:A:696:ASN:CB	1:A:697:GLU:OE1	2.43	0.65
1:A:382:VAL:CG2	1:A:388:LEU:HD11	2.27	0.65
1:A:388:LEU:HD22	1:A:411:ALA:HB2	1.77	0.65
1:B:398:LEU:O	1:B:403:THR:HA	1.96	0.65
1:B:747:LEU:O	1:B:774:LYS:HD2	1.97	0.65
1:B:738:ALA:O	1:B:742:GLN:HG3	1.98	0.64
1:B:748:ASP:O	1:B:774:LYS:HE2	1.97	0.64
1:A:530:MET:HG2	1:A:658:PHE:HE1	1.62	0.64
1:B:691:LYS:O	1:B:695:ILE:HG12	1.98	0.64
1:B:423:ARG:HD2	1:B:568:ILE:HD11	1.78	0.64
1:A:560:ARG:HG2	1:A:562:ARG:CZ	2.28	0.64
1:A:565:SER:HB2	1:A:568:ILE:HD12	1.80	0.64
1:B:433:THR:O	1:B:436:MET:HB2	1.98	0.63
1:B:447:HIS:CD2	1:B:535:GLY:HA2	2.32	0.63
1:A:424:ARG:HD2	1:A:462:PHE:CD2	2.34	0.62
1:B:392:GLU:HA	1:B:393:PRO:C	2.19	0.62
1:B:754:ARG:HG2	1:B:769:SER:HA	1.80	0.62
1:B:769:SER:OG	1:B:772:GLU:HB2	1.98	0.62
1:A:545:ALA:CB	1:A:588:HIS:HB3	2.29	0.62
2:B:1788:AN2:O5'	2:B:1788:AN2:H8	2.00	0.62
1:B:389:TYR:HB3	1:B:410:ARG:HB3	1.82	0.61
1:A:657:ARG:O	1:A:660:THR:HB	2.00	0.61
1:A:401:LYS:HD2	1:A:401:LYS:C	2.19	0.61
1:A:388:LEU:HD23	1:A:411:ALA:CB	2.29	0.61
1:A:416:THR:HB	1:A:418:TYR:HD2	1.66	0.61
2:A:1788:AN2:O2A	2:A:1788:AN2:N3B	2.33	0.61
1:A:424:ARG:HD3	1:A:462:PHE:CD2	2.35	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:530:MET:HG2	1:A:658:PHE:CE1	2.36	0.61
1:A:732:ARG:HD2	1:B:787:SER:C	2.21	0.61
1:A:553:LYS:O	1:A:564:SER:OG	2.16	0.60
1:A:759:SER:HB2	1:A:764:SER:HB2	1.84	0.60
1:A:429:ARG:HE	1:A:465:ASN:ND2	1.99	0.60
1:A:696:ASN:ND2	1:A:720:ARG:HD3	2.17	0.60
1:A:693:ASN:HD21	1:B:693:ASN:HD21	1.50	0.60
1:B:398:LEU:CD2	1:B:425:ILE:HG12	2.31	0.60
1:B:547:LYS:HG3	1:B:570:ASP:CB	2.32	0.60
1:A:698:ARG:CZ	1:A:784:LEU:HD12	2.28	0.59
1:B:456:VAL:HG22	1:B:469:LEU:HG	1.84	0.59
1:A:413:HIS:CG	1:A:416:THR:HG1	2.20	0.59
1:B:401:LYS:HG2	1:B:402:LEU:H	1.65	0.59
1:B:430:LEU:HD12	1:B:430:LEU:O	2.03	0.59
1:A:424:ARG:HG3	1:A:466:SER:HB3	1.84	0.58
1:B:756:GLN:HG3	1:B:756:GLN:O	2.02	0.58
1:B:696:ASN:OD1	1:B:697:GLU:N	2.36	0.58
1:A:424:ARG:HH11	1:A:466:SER:CB	2.16	0.58
1:A:699:PRO:CB	1:A:713:ARG:NE	2.64	0.58
1:A:429:ARG:NE	1:A:465:ASN:ND2	2.51	0.58
1:A:454:ARG:O	1:A:455:GLU:HG3	2.04	0.58
1:A:547:LYS:HG3	1:A:569:SER:HB2	1.83	0.58
1:B:395:ALA:HB3	1:B:407:THR:HA	1.86	0.58
1:B:477:SER:HB3	1:B:557:THR:OG1	2.02	0.58
1:A:424:ARG:NH1	1:A:464:ASP:OD1	2.37	0.57
1:A:479:THR:HG23	2:A:1788:AN2:H3'	1.86	0.57
1:B:386:HIS:CE1	1:B:414:ASN:CA	2.83	0.57
1:B:585:VAL:O	1:B:589:GLN:HG3	2.04	0.57
1:A:580:ASN:HB3	1:A:583:ALA:HB2	1.86	0.56
1:A:728:THR:O	1:A:731:GLY:N	2.29	0.56
1:A:422:LEU:HD12	1:A:422:LEU:O	2.06	0.56
1:A:478:GLN:HA	2:A:1788:AN2:O2'	2.06	0.56
1:A:529:ILE:HD11	1:A:600:VAL:HG21	1.88	0.56
1:A:474:HIS:O	2:A:1788:AN2:H2	2.06	0.56
1:B:460:LYS:HA	1:B:465:ASN:HA	1.88	0.56
1:B:477:SER:O	2:B:1788:AN2:O2'	2.23	0.55
1:A:386:HIS:CE1	1:A:414:ASN:OD1	2.60	0.55
1:A:642:ASN:OD1	1:A:642:ASN:N	2.40	0.55
1:A:686:TYR:O	1:A:690:VAL:HG23	2.06	0.54
1:A:513:ARG:HD3	1:A:622:MET:SD	2.47	0.54
1:B:733:PRO:HB2	1:B:735:LEU:HD13	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:728:THR:N	1:A:732:ARG:O	2.34	0.54
1:A:413:HIS:ND1	1:A:416:THR:OG1	2.38	0.54
1:A:698:ARG:NH2	1:B:733:PRO:HB3	2.06	0.54
1:B:436:MET:O	1:B:440:GLU:HG2	2.08	0.54
1:A:469:LEU:CD1	1:A:568:ILE:HG12	2.33	0.53
1:B:547:LYS:HG3	1:B:570:ASP:CA	2.38	0.53
1:A:695:ILE:O	1:A:699:PRO:CD	2.54	0.53
1:A:395:ALA:HB2	1:A:408:THR:HG23	1.90	0.53
1:B:601:LEU:HD11	1:B:620:ILE:HG12	1.89	0.52
1:A:737:HIS:O	1:A:741:VAL:HG23	2.09	0.52
1:B:386:HIS:HE1	1:B:414:ASN:CA	2.16	0.52
1:A:405:PRO:HB2	1:A:426:HIS:HD2	1.75	0.52
1:A:736:ASP:HB3	1:A:739:HIS:HB3	1.92	0.51
1:B:648:THR:O	1:B:651:MET:HB2	2.11	0.51
1:A:424:ARG:HD3	1:A:462:PHE:CZ	2.45	0.51
1:B:693:ASN:HA	1:B:696:ASN:HD21	1.71	0.51
1:A:460:LYS:HE2	1:A:465:ASN:OD1	2.11	0.51
1:B:754:ARG:HG2	1:B:769:SER:CA	2.41	0.51
1:A:685:LEU:HD22	1:A:744:LEU:CB	2.39	0.51
1:A:546:CYS:N	1:A:592:ASP:OD2	2.40	0.50
1:A:728:THR:OG1	1:A:734:TRP:HB2	2.10	0.50
1:B:721:ASP:OD1	1:B:725:HIS:ND1	2.44	0.50
1:A:654:ILE:HG21	1:A:658:PHE:CE1	2.47	0.50
1:A:658:PHE:O	1:A:662:LEU:HB2	2.12	0.50
1:A:698:ARG:CD	1:A:784:LEU:HD11	2.38	0.50
1:A:725:HIS:CE1	1:A:760:ARG:HH12	2.27	0.50
1:B:547:LYS:NZ	1:B:588:HIS:CE1	2.79	0.50
1:A:698:ARG:HH11	1:A:702:ASN:ND2	2.09	0.50
1:B:388:LEU:HG	1:B:411:ALA:HB2	1.93	0.50
1:A:676:LEU:HD13	1:B:676:LEU:HD12	1.92	0.50
1:A:697:GLU:N	1:A:699:PRO:HD2	2.27	0.50
1:A:400:ALA:HA	1:A:573:GLN:HE22	1.76	0.50
1:A:407:THR:HG1	1:A:409:TYR:HE2	1.51	0.50
1:B:693:ASN:O	1:B:696:ASN:OD1	2.29	0.49
1:A:424:ARG:CD	1:A:462:PHE:CE2	2.90	0.49
1:A:697:GLU:C	1:A:699:PRO:HD2	2.33	0.49
1:B:479:THR:CG2	2:B:1788:AN2:H3'	2.29	0.49
1:B:529:ILE:HD11	1:B:600:VAL:HG21	1.94	0.49
1:A:477:SER:HB3	1:A:557:THR:HG23	1.95	0.49
1:A:413:HIS:CB	1:A:416:THR:OG1	2.57	0.49
1:A:546:CYS:O	1:A:547:LYS:HB3	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:480:LEU:HD21	1:B:603:LEU:HD21	1.94	0.49
1:A:433:THR:O	1:A:436:MET:HB3	2.12	0.49
1:A:549:LEU:O	1:A:550:ASP:HB3	2.13	0.49
1:B:451:VAL:HG21	1:B:564:SER:HA	1.95	0.49
1:B:686:TYR:O	1:B:690:VAL:HG23	2.13	0.49
1:A:400:ALA:HA	1:A:573:GLN:NE2	2.28	0.48
1:A:759:SER:CB	1:A:764:SER:HB2	2.44	0.48
1:B:389:TYR:N	1:B:410:ARG:O	2.36	0.48
1:A:413:HIS:CE1	1:A:416:THR:HG23	2.48	0.48
2:A:1788:AN2:O5'	2:A:1788:AN2:H8	2.12	0.48
1:B:440:GLU:HA	1:B:443:LYS:HD3	1.95	0.48
1:B:657:ARG:O	1:B:660:THR:N	2.46	0.48
1:B:696:ASN:HD22	1:B:720:ARG:HD2	1.78	0.48
1:B:388:LEU:HA	1:B:410:ARG:O	2.13	0.48
1:A:736:ASP:CG	1:A:739:HIS:HB3	2.34	0.48
1:B:460:LYS:CG	1:B:465:ASN:HB2	2.37	0.48
1:B:451:VAL:CG2	1:B:564:SER:HA	2.44	0.47
1:B:442:TRP:CD1	1:B:567:CYS:SG	2.97	0.47
1:B:659:TYR:O	1:B:663:ASP:HB2	2.15	0.47
1:B:733:PRO:HB2	1:B:735:LEU:CD1	2.44	0.47
1:A:384:ASN:C	1:A:385:TYR:CD1	2.88	0.47
1:A:656:ALA:HA	1:B:651:MET:SD	2.55	0.47
1:A:698:ARG:NH2	1:B:733:PRO:HG3	2.30	0.47
1:A:698:ARG:NH2	1:B:733:PRO:CG	2.78	0.47
1:A:727:VAL:CG1	1:A:731:GLY:CA	2.90	0.47
1:A:736:ASP:CG	1:A:739:HIS:CB	2.83	0.47
1:A:550:ASP:HB2	1:A:551:PRO:CD	2.45	0.47
1:A:550:ASP:HB2	1:A:551:PRO:HD2	1.97	0.47
1:A:422:LEU:HA	1:A:469:LEU:O	2.15	0.46
1:A:413:HIS:CG	1:A:416:THR:OG1	2.68	0.46
1:A:441:MET:CE	1:A:582:LEU:HD21	2.46	0.46
1:B:696:ASN:ND2	1:B:720:ARG:HD2	2.31	0.46
1:A:399:HIS:CD2	1:A:403:THR:CG2	2.92	0.46
1:A:447:HIS:HD2	1:A:535:GLY:HA2	1.80	0.46
1:B:649:ASP:O	1:B:652:PRO:HD2	2.16	0.46
1:A:663:ASP:OD1	1:B:448:THR:HG23	2.15	0.46
1:B:621:ASP:O	1:B:624:THR:HG22	2.15	0.46
1:A:447:HIS:HB3	1:A:450:VAL:HG12	1.96	0.46
1:A:574:PHE:HE1	1:A:581:PRO:HB3	1.79	0.46
1:A:725:HIS:CD2	1:A:760:ARG:HH12	2.32	0.46
1:A:409:TYR:HB2	1:A:422:LEU:CD1	2.46	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:547:LYS:CB	1:A:569:SER:OG	2.64	0.45
1:A:593:LEU:HD21	1:A:647:VAL:HG22	1.98	0.45
1:B:521:PRO:HG2	1:B:524:THR:OG1	2.16	0.45
1:A:460:LYS:CG	1:A:465:ASN:OD1	2.64	0.45
1:B:536:LEU:HD23	1:B:536:LEU:HA	1.80	0.45
1:B:658:PHE:O	1:B:662:LEU:HB2	2.16	0.45
1:B:753:GLU:HG2	1:B:754:ARG:N	2.32	0.45
1:A:571:ILE:HG13	1:A:572:THR:N	2.32	0.45
1:A:676:LEU:HD13	1:B:676:LEU:CD1	2.46	0.45
1:B:714:TYR:CE1	1:B:718:LEU:CD1	2.97	0.45
1:B:454:ARG:NH2	1:B:472:ASP:OD2	2.50	0.45
1:A:672:GLN:OE1	1:B:672:GLN:NE2	2.44	0.45
1:A:546:CYS:SG	1:A:548:VAL:O	2.74	0.45
1:B:601:LEU:O	1:B:601:LEU:HD23	2.17	0.45
1:A:416:THR:HB	1:A:418:TYR:CD2	2.50	0.45
1:A:755:VAL:HG13	1:A:757:LEU:CD1	2.47	0.45
1:B:449:ASN:O	1:B:562:ARG:HA	2.17	0.45
1:B:546:CYS:O	1:B:547:LYS:HB2	2.17	0.45
1:B:611:VAL:HG12	1:B:611:VAL:O	2.15	0.45
1:B:777:LEU:O	1:B:777:LEU:HD12	2.17	0.45
1:B:736:ASP:O	1:B:740:ILE:HG13	2.16	0.44
1:B:721:ASP:CG	1:B:725:HIS:ND1	2.71	0.44
1:A:547:LYS:HZ1	1:A:573:GLN:HB2	1.83	0.44
1:B:514:THR:HA	1:B:519:LEU:HD13	1.99	0.44
1:A:649:ASP:O	1:A:652:PRO:HD2	2.18	0.44
1:B:592:ASP:O	1:B:596:LEU:N	2.46	0.44
1:A:676:LEU:HD12	1:A:676:LEU:HA	1.86	0.44
1:A:696:ASN:O	1:A:697:GLU:OE1	2.33	0.44
1:A:755:VAL:HG22	1:A:756:GLN:N	2.32	0.44
1:B:556:VAL:O	1:B:556:VAL:HG13	2.17	0.43
1:A:545:ALA:CB	1:A:588:HIS:CB	2.95	0.43
1:B:516:ASN:OD1	1:B:517:GLY:N	2.49	0.43
1:A:392:GLU:HA	1:A:393:PRO:C	2.39	0.43
1:A:563:PHE:CB	1:A:566:CYS:SG	2.97	0.43
1:B:442:TRP:CG	1:B:567:CYS:SG	3.10	0.43
1:A:385:TYR:CE2	1:A:470:VAL:HG21	2.54	0.43
1:B:454:ARG:NE	1:B:472:ASP:OD1	2.50	0.43
1:A:402:LEU:HD23	1:A:403:THR:N	2.34	0.43
1:A:413:HIS:CB	1:A:416:THR:HG1	2.32	0.43
1:A:480:LEU:HD11	1:A:484:TYR:CD2	2.54	0.43
1:A:696:ASN:CA	1:A:697:GLU:OE1	2.67	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:761:ASP:OD2	1:B:763:GLN:OE1	2.36	0.42
1:B:778:GLU:OE1	1:B:778:GLU:HA	2.19	0.42
1:A:786:SER:O	1:A:787:SER:HB2	2.20	0.42
1:B:668:LYS:O	1:B:671:MET:HB2	2.19	0.42
1:B:772:GLU:O	1:B:775:ASN:HB2	2.18	0.42
1:A:689:LEU:HD12	1:A:689:LEU:HA	1.77	0.42
1:B:474:HIS:HA	1:B:475:PRO:HD3	1.45	0.42
1:B:742:GLN:O	1:B:746:LYS:HG3	2.18	0.42
1:A:563:PHE:HB3	1:A:566:CYS:HG	1.80	0.42
1:A:691:LYS:HG2	1:A:781:PHE:CD1	2.54	0.42
1:B:469:LEU:HD22	1:B:568:ILE:HG12	2.02	0.42
1:B:736:ASP:OD1	1:B:738:ALA:N	2.49	0.42
1:A:423:ARG:HD2	1:A:568:ILE:CD1	2.43	0.42
1:A:513:ARG:HG2	1:A:622:MET:HE3	2.01	0.42
1:B:547:LYS:HZ2	1:B:588:HIS:CE1	2.36	0.42
1:A:532:LEU:HD21	1:A:554:ILE:HD13	2.02	0.42
1:A:712:ASP:OD1	1:A:776:CYS:SG	2.71	0.42
1:A:727:VAL:HG13	1:A:731:GLY:C	2.40	0.42
1:A:696:ASN:HB3	1:A:697:GLU:OE1	2.18	0.42
1:B:456:VAL:CG1	1:B:467:LEU:HD11	2.50	0.41
1:B:684:ARG:HD2	1:B:748:ASP:OD2	2.20	0.41
1:A:698:ARG:HH21	1:B:733:PRO:CG	2.32	0.41
1:B:423:ARG:HD2	1:B:568:ILE:CD1	2.48	0.41
1:A:695:ILE:HD12	1:A:777:LEU:CD1	2.50	0.41
1:B:524:THR:O	1:B:528:ILE:HG13	2.21	0.41
1:A:430:LEU:O	1:A:430:LEU:HD12	2.20	0.41
1:A:613:ARG:O	1:A:616:VAL:HG12	2.20	0.41
1:B:444:LYS:HD2	1:B:444:LYS:HA	1.69	0.41
1:A:616:VAL:HG13	1:A:617:GLN:N	2.36	0.41
1:A:698:ARG:NH2	1:B:733:PRO:CB	2.75	0.41
1:A:703:LEU:O	1:A:706:THR:HG22	2.20	0.41
1:A:733:PRO:HD2	1:B:787:SER:O	2.21	0.41
1:B:385:TYR:HE2	1:B:420:TYR:CD2	2.39	0.41
1:A:696:ASN:HB2	1:A:697:GLU:OE1	2.20	0.41
1:A:727:VAL:HG12	1:A:731:GLY:CA	2.49	0.41
1:B:408:THR:HG21	1:B:423:ARG:HH11	1.85	0.41
1:B:478:GLN:OE1	1:B:483:LYS:HD3	2.21	0.41
1:B:549:LEU:O	1:B:550:ASP:HB3	2.21	0.41
1:A:453:LEU:HD22	1:A:567:CYS:SG	2.61	0.41
1:A:705:CYS:O	1:A:707:TRP:HD1	2.03	0.41
1:A:672:GLN:OE1	1:B:672:GLN:HB2	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:696:ASN:HB2	1:A:720:ARG:NH1	2.37	0.40
1:B:389:TYR:O	1:B:410:ARG:N	2.50	0.40
1:A:536:LEU:CD1	1:A:563:PHE:CZ	3.05	0.40
1:B:598:ARG:CZ	1:B:611:VAL:HG11	2.51	0.40
1:A:555:ILE:HG23	1:A:564:SER:HB3	2.02	0.40
1:B:685:LEU:HA	1:B:688:ILE:HG22	2.03	0.40
1:B:736:ASP:OD1	1:B:737:HIS:N	2.54	0.40
1:B:668:LYS:HE3	1:B:672:GLN:OE1	2.22	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:403:THR:OG1	1:B:575:ASP:OD1[4_565]	2.06	0.14

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	382/448 (85%)	363 (95%)	19 (5%)	0	100	100
1	B	366/448 (82%)	348 (95%)	17 (5%)	1 (0%)	41	75
All	All	748/896 (84%)	711 (95%)	36 (5%)	1 (0%)	51	83

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	640	THR

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	347/396 (88%)	344 (99%)	3 (1%)	78 90
1	B	334/396 (84%)	331 (99%)	3 (1%)	78 90
All	All	681/792 (86%)	675 (99%)	6 (1%)	78 90

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	391	LEU
1	A	428	PHE
1	A	537	LYS
1	B	399	HIS
1	B	569	SER
1	B	735	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	384	ASN
1	A	426	HIS
1	A	541	HIS
1	A	573	GLN
1	A	666	GLN
1	A	693	ASN
1	A	696	ASN
1	A	745	ASN
1	B	426	HIS
1	B	540	HIS

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 monosaccharides 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	AN2	A	1788	-	24,29,29	2.47	6 (25%)	25,45,45	1.61	6 (24%)
2	AN2	B	1788	-	24,29,29	2.45	4 (16%)	25,45,45	1.59	5 (20%)

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	AN2	A	1788	-	-	5/9/32/32	0/3/3/3
2	AN2	B	1788	-	-	3/9/32/32	0/3/3/3

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1788	AN2	PB-O1B	10.30	1.62	1.46
2	A	1788	AN2	PB-O1B	10.02	1.62	1.46
2	A	1788	AN2	PB-O2B	-3.32	1.47	1.56
2	B	1788	AN2	PB-O2B	-3.13	1.48	1.56
2	A	1788	AN2	PB-O3A	2.86	1.62	1.59
2	B	1788	AN2	O4'-C1'	2.68	1.44	1.41

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1788	AN2	C5-C4	2.44	1.47	1.40
2	B	1788	AN2	C5-C4	2.37	1.47	1.40
2	A	1788	AN2	O4'-C1'	2.15	1.44	1.41
2	A	1788	AN2	C2-N3	2.11	1.35	1.32

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	1788	AN2	PB-O3A-PA	-3.93	120.09	132.56
2	B	1788	AN2	PB-O3A-PA	-3.81	120.48	132.56
2	B	1788	AN2	C3'-C2'-C1'	3.56	106.33	100.98
2	B	1788	AN2	N3-C2-N1	-3.17	123.72	128.68
2	B	1788	AN2	C4-C5-N7	-3.07	106.20	109.40
2	A	1788	AN2	N3-C2-N1	-2.99	124.01	128.68
2	A	1788	AN2	C2'-C3'-C4'	2.77	108.02	102.64
2	A	1788	AN2	C3'-C2'-C1'	2.68	105.01	100.98
2	A	1788	AN2	C4-C5-N7	-2.51	106.78	109.40
2	B	1788	AN2	C2'-C3'-C4'	2.19	106.90	102.64
2	A	1788	AN2	O2B-PB-O3A	2.12	111.72	104.64

There are no chirality outliers.

All (8) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1788	AN2	C5'-O5'-PA-O3A
2	B	1788	AN2	O4'-C4'-C5'-O5'
2	B	1788	AN2	C3'-C4'-C5'-O5'
2	B	1788	AN2	PB-O3A-PA-O1A
2	A	1788	AN2	C5'-O5'-PA-O1A
2	A	1788	AN2	C5'-O5'-PA-O2A
2	A	1788	AN2	O4'-C4'-C5'-O5'
2	A	1788	AN2	C3'-C4'-C5'-O5'

There are no ring outliers.

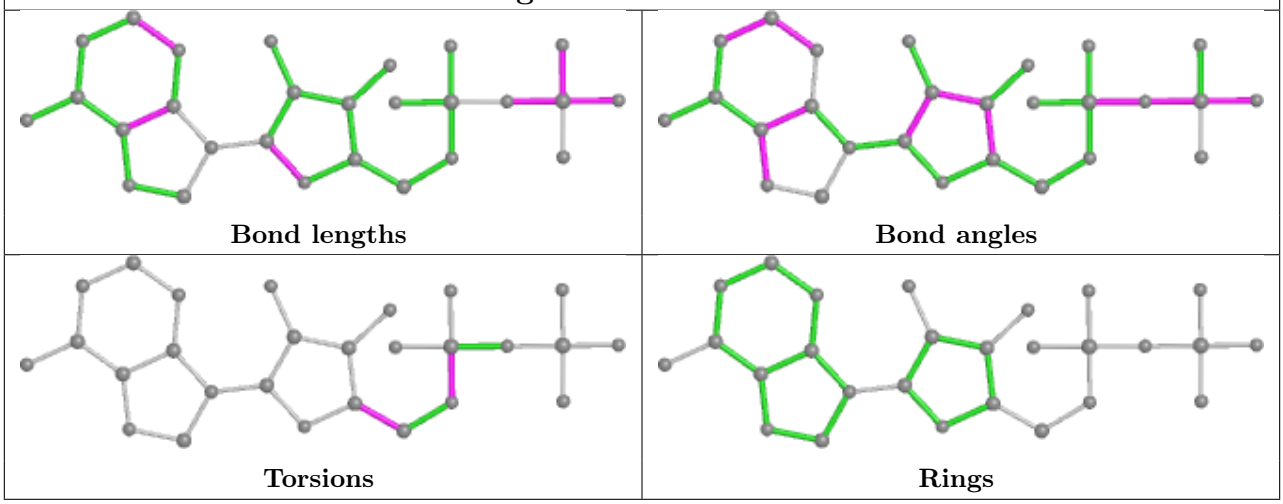
2 monomers are involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1788	AN2	5	0
2	B	1788	AN2	5	0

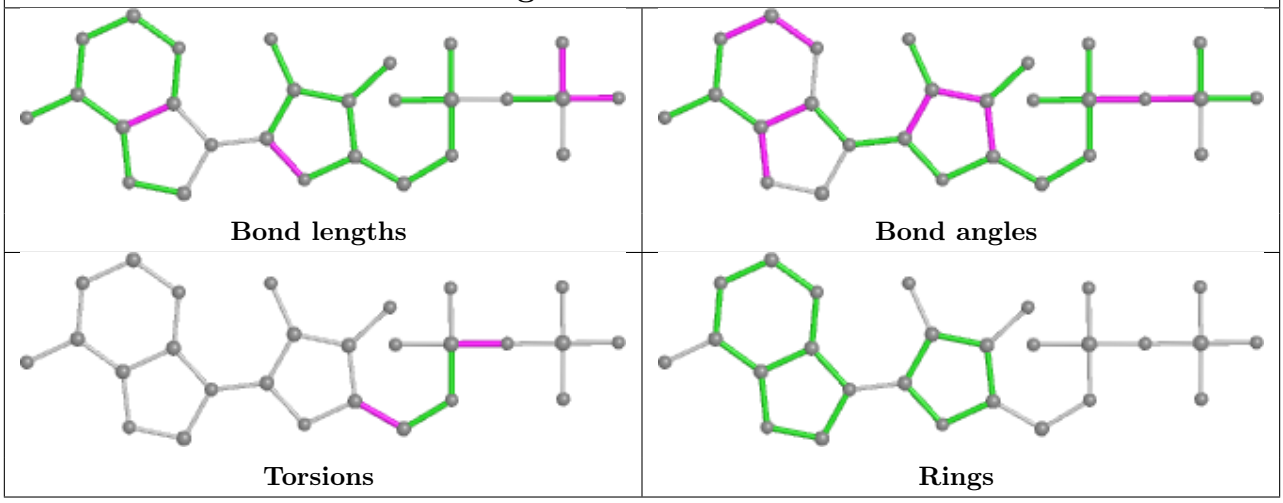
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths,

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 then 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.

Ligand AN2 A 1788



Ligand AN2 B 1788



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	386/448 (86%)	-0.18	3 (0%)	86	75	71, 124, 204, 249	0
1	B	372/448 (83%)	-0.10	4 (1%)	80	68	77, 133, 217, 264	0
All	All	758/896 (84%)	-0.14	7 (0%)	84	73	71, 127, 212, 264	0

All (7) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	702	ASN	3.9
1	B	765	VAL	3.4
1	B	752	ILE	2.9
1	B	763	GLN	2.8
1	A	579	SER	2.7
1	B	756	GLN	2.3
1	A	701	PHE	2.3

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 monosaccharides in this entry.

6.4 Ligands (i)

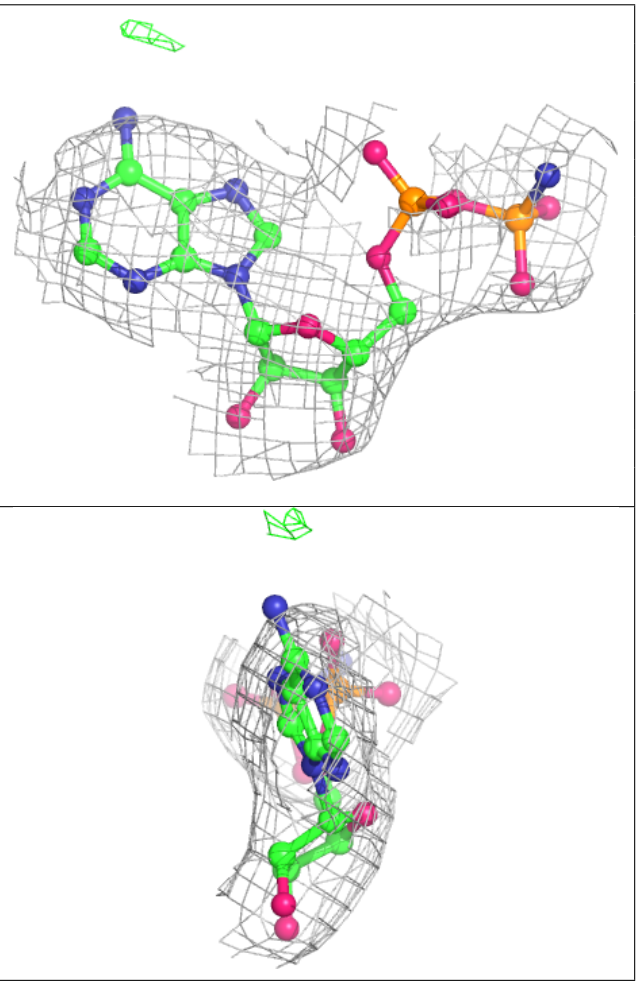
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	AN2	B	1788	27/27	0.92	0.26	102,123,142,148	0
2	AN2	A	1788	27/27	0.94	0.28	87,113,133,151	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.

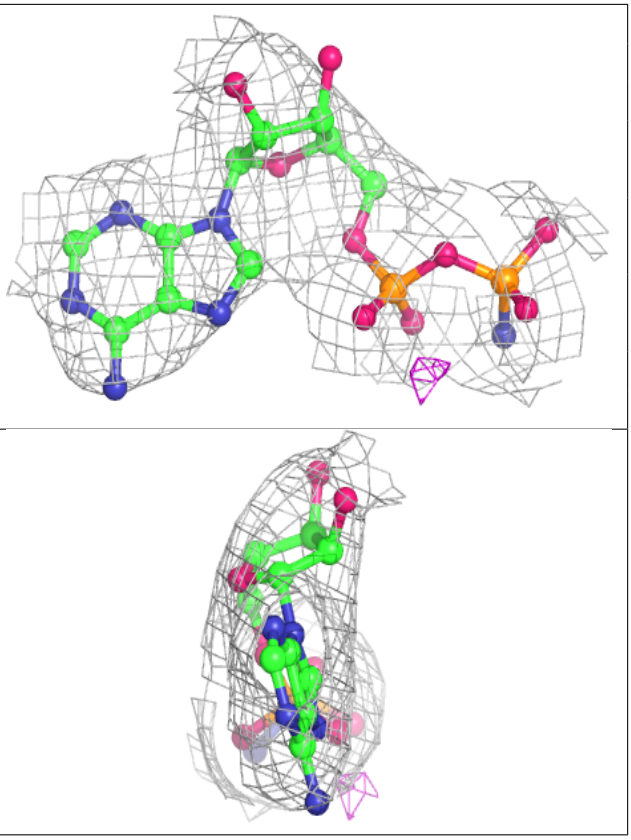
Electron density around AN2 B 1788:

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 AN2 A 1788:

$2mF_o$-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.