Full wwPDB X-ray Structure Validation Report (i)

Jun 12, 2024 – 04:29 AM EDT

PDB ID	:	2HE5
Title	:	Crystal structure of 17alpha-hydroxysteroid dehydrogenase in binary complex with NADP(H) in an open conformation
Authors	:	Faucher, F.; Pereira de Jesus-Tran, K.; Cantin, L.; Luu-the, V.; Labrie, F.; Breton, R.
Deposited on	:	2006-06-21
Resolution	:	2.90 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:

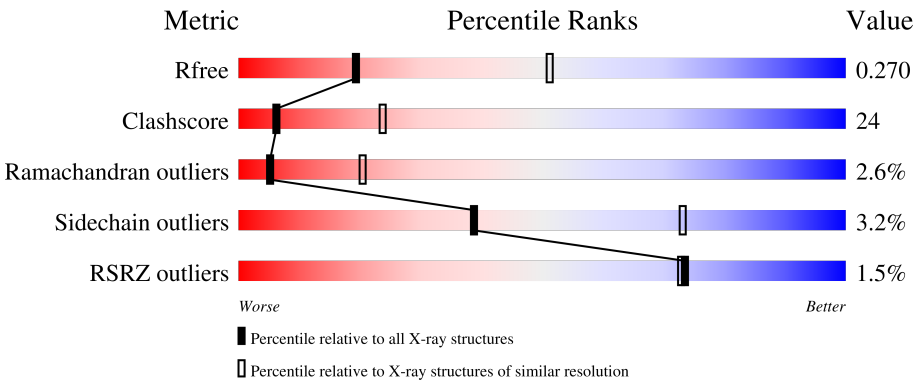
MolProbity	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.20.1
EDS	:	2.36.2
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36.2

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 2.90 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	1957 (2.90-2.90)
Clashscore	141614	2172 (2.90-2.90)
Ramachandran outliers	138981	2115 (2.90-2.90)
Sidechain outliers	138945	2117 (2.90-2.90)
RSRZ outliers	127900	1906 (2.90-2.90)

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	323	2% 59% 35%
1	B	323	2% 46% 48%
1	C	323	52% 43%
1	D	323	% 57% 38%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	ACT	C	324	-	-	X	-
3	ACT	D	324	-	-	X	-

2 Entry composition (i)

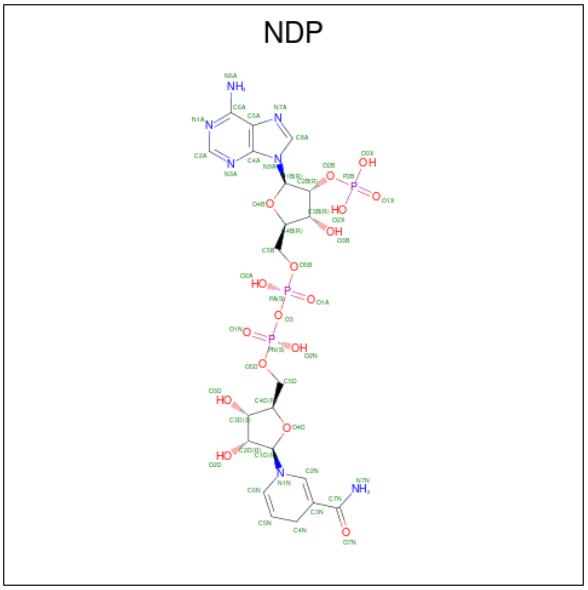
There are 5 unique types of molecules in this entry. The entry contains 10489 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Aldo-keto reductase family 1, member C21.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	318	2555	1639	433	467	16	0	0	0
1	B	318	2555	1639	433	467	16	0	0	0
1	C	314	2519	1617	425	461	16	0	0	0
1	D	314	2519	1617	425	461	16	0	0	0

- Molecule 2 is NADPH DIHYDRO-NICOTINAMIDE-ADENINE-DINUCLEOTIDE PHOSPHATE (three-letter code: NDP) (formula: $C_{21}H_{30}N_7O_{17}P_3$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
2	A	1	48	21	7	17	3	0	0
2	B	1	48	21	7	17	3	0	0

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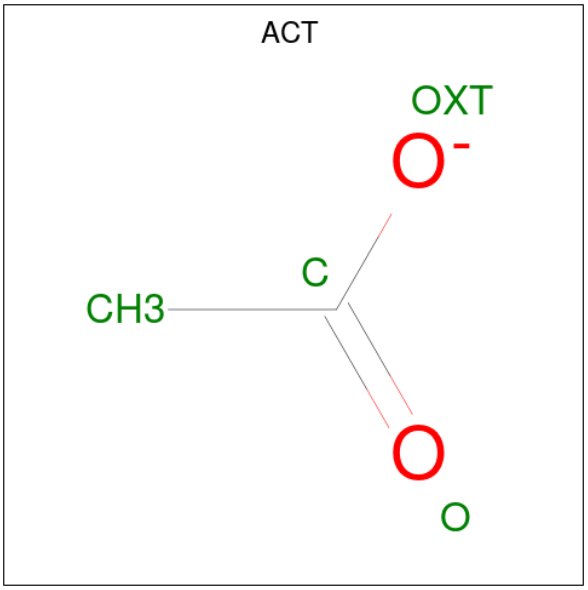
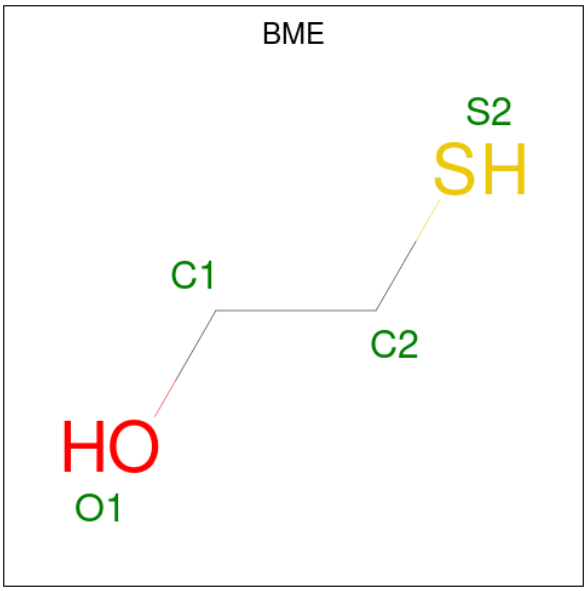
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
2	C	1	48	21	7	17	3	0	0
2	D	1	48	21	7	17	3	0	0

- Molecule 3 is ACETATE ION (three-letter code: ACT) (formula: $C_2H_3O_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
3	C	1	4	2	2	0	0
3	D	1	4	2	2	0	0

- Molecule 4 is BETA-MERCAPTOETHANOL (three-letter code: BME) (formula: C_2H_6OS).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	O	S		
4	C	1	4	2	1	1	0	0

- Molecule 5 is water.

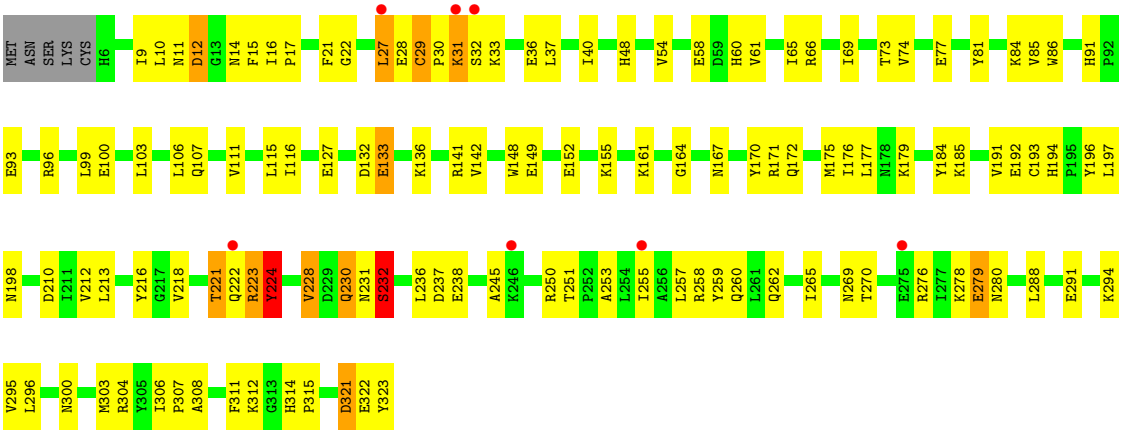
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
5	A	46	46	46	0	0
			Total	O		
5	B	29	29	29	0	0
			Total	O		
5	C	35	35	35	0	0
			Total	O		
5	D	27	27	27	0	0

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.

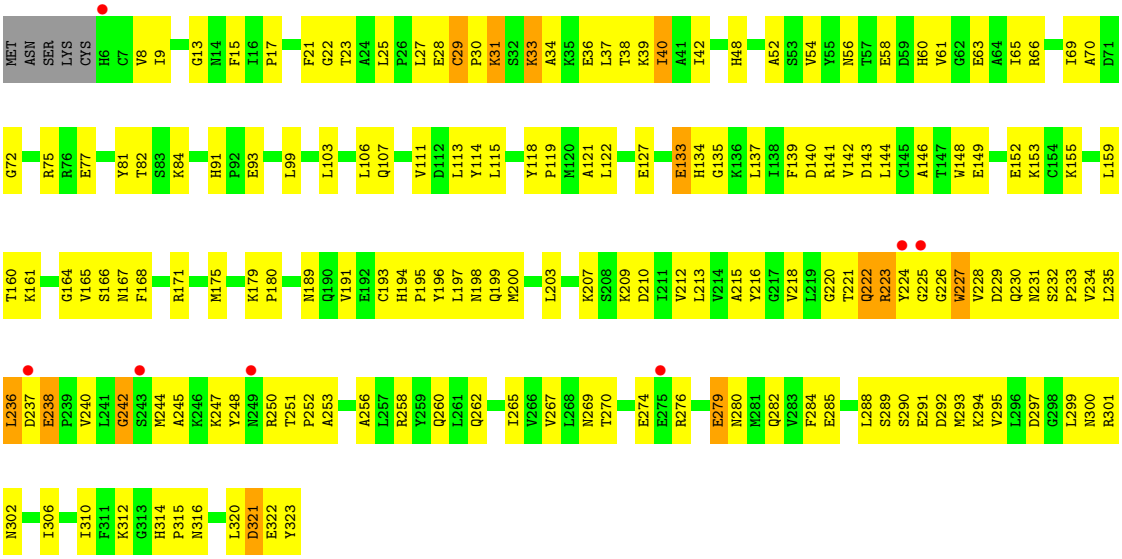
• Molecule 1: Aldo-keto reductase family 1, member C21

Chain A:



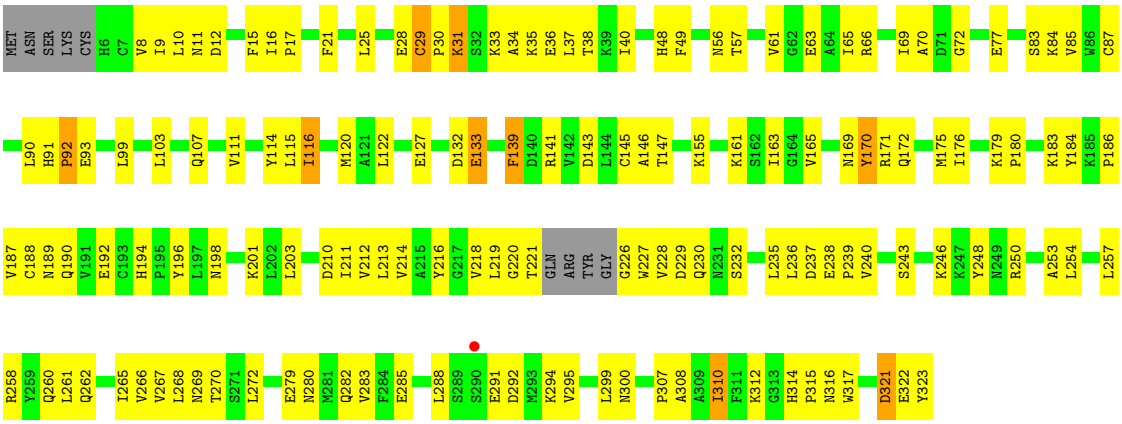
• Molecule 1: Aldo-keto reductase family 1, member C21

Chain B:



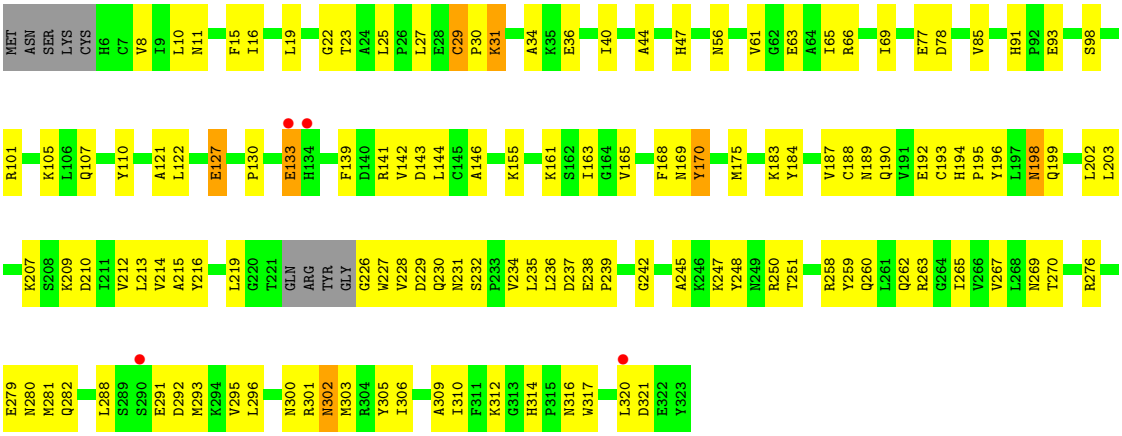
• Molecule 1: Aldo-keto reductase family 1, member C21

Chain C:



- Molecule 1: Aldo-keto reductase family 1, member C21

Chain D:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	56.48Å 166.76Å 69.55Å 90.00° 97.60° 90.00°	Depositor
Resolution (Å)	19.91 – 2.90 19.91 – 2.90	Depositor EDS
% Data completeness (in resolution range)	99.2 (19.91-2.90) 99.3 (19.91-2.90)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	3.09 (at 2.88Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.218 , 0.279 0.210 , 0.270	Depositor DCC
R_{free} test set	1403 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å^2)	44.8	Xtriage
Anisotropy	0.360	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.26 , 47.8	EDS
L-test for twinning[2]	$< \|L\| > = 0.43$, $< L^2 > = 0.26$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.90	EDS
Total number of atoms	10489	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 7.80% 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: NDP, ACT, BME

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	0.39	0/2615	0.62	0/3537
1	B	0.40	0/2615	0.62	0/3537
1	C	0.41	0/2577	0.63	1/3485 (0.0%)
1	D	0.40	0/2577	0.63	0/3485
All	All	0.40	0/10384	0.62	1/14044 (0.0%)

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

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	C	116	ILE	N-CA-C	-5.08	97.28	111.00

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	224	TYR	Sidechain

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	2555	0	2552	118	0
1	B	2555	0	2552	155	0
1	C	2519	0	2518	140	0
1	D	2519	0	2518	115	0
2	A	48	0	26	6	0
2	B	48	0	26	5	0
2	C	48	0	26	5	0
2	D	48	0	26	4	0
3	C	4	0	3	2	0
3	D	4	0	3	3	0
4	C	4	0	6	1	0
5	A	46	0	0	3	0
5	B	29	0	0	5	0
5	C	35	0	0	2	0
5	D	27	0	0	2	0
All	All	10489	0	10256	503	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 24.

All (503) 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:C:262:GLN:HE22	1:C:288:LEU:H	1.06	1.01
1:B:258:ARG:HE	1:B:262:GLN:NE2	1.64	0.93
1:B:258:ARG:NE	1:B:262:GLN:HE21	1.64	0.93
1:A:262:GLN:HE22	1:A:288:LEU:H	1.14	0.92
1:A:258:ARG:HE	1:A:262:GLN:HE21	0.95	0.92
1:D:262:GLN:HE22	1:D:288:LEU:H	1.17	0.91
1:C:258:ARG:HE	1:C:262:GLN:HE21	0.93	0.90
1:D:198:ASN:ND2	1:D:300:ASN:HB2	1.88	0.89
1:A:84:LYS:HE2	2:A:401:NDP:H71N	1.41	0.86
1:B:171:ARG:HH22	1:C:180:PRO:HG3	1.38	0.85
1:A:258:ARG:HE	1:A:262:GLN:NE2	1.72	0.85
1:A:27:LEU:HB2	1:C:230:GLN:HE21	1.44	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:258:ARG:HE	1:C:262:GLN:NE2	1.77	0.81
1:A:258:ARG:NE	1:A:262:GLN:HE21	1.77	0.79
1:D:66:ARG:HH12	1:D:107:GLN:NE2	1.79	0.79
1:A:230:GLN:CA	1:A:230:GLN:HE21	1.96	0.79
1:D:258:ARG:HE	1:D:262:GLN:HE21	1.28	0.78
1:A:91:HIS:CE1	1:A:142:VAL:HG22	2.17	0.78
1:C:258:ARG:NE	1:C:262:GLN:HE21	1.76	0.77
1:A:221:THR:OG1	1:A:223:ARG:HB2	1.83	0.77
1:A:65:ILE:O	1:A:69:ILE:HG13	1.83	0.77
1:A:223:ARG:HG2	1:C:226:GLY:N	2.00	0.77
1:B:165:VAL:O	1:B:189:ASN:HA	1.85	0.77
1:C:262:GLN:NE2	1:C:288:LEU:H	1.84	0.76
1:D:269:ASN:ND2	1:D:280:ASN:OD1	2.20	0.75
1:A:230:GLN:HE21	1:A:230:GLN:N	1.85	0.75
1:C:269:ASN:ND2	1:C:280:ASN:OD1	2.20	0.74
1:D:91:HIS:HB3	1:D:93:GLU:OE2	1.87	0.74
1:D:262:GLN:HE22	1:D:288:LEU:N	1.85	0.74
1:C:31:LYS:HE3	1:C:31:LYS:HA	1.70	0.73
1:C:262:GLN:HE22	1:C:288:LEU:N	1.83	0.73
1:A:221:THR:HB	5:A:431:HOH:O	1.87	0.73
1:A:221:THR:HG21	1:A:306:ILE:HD11	1.69	0.73
1:B:91:HIS:HB3	1:B:93:GLU:OE2	1.89	0.72
1:C:36:GLU:O	1:C:40:ILE:HG12	1.90	0.71
1:C:253:ALA:O	1:C:257:LEU:HG	1.91	0.70
1:A:223:ARG:HG3	1:A:224:TYR:H	1.56	0.70
1:C:93:GLU:H	1:C:93:GLU:CD	1.95	0.70
1:C:66:ARG:HH11	1:C:107:GLN:NE2	1.89	0.70
1:D:188:CYS:HB2	1:D:212:VAL:O	1.92	0.70
1:A:91:HIS:HB3	1:A:93:GLU:OE2	1.92	0.69
1:D:196:TYR:OH	1:D:238:GLU:HB2	1.92	0.69
1:C:63:GLU:HA	1:C:66:ARG:HH21	1.58	0.69
1:B:155:LYS:NZ	1:B:161:LYS:O	2.26	0.69
1:A:245:ALA:HB1	1:A:250:ARG:O	1.93	0.68
1:C:91:HIS:HB3	1:C:93:GLU:OE2	1.93	0.68
1:D:36:GLU:O	1:D:40:ILE:HG12	1.93	0.68
1:A:31:LYS:HA	1:A:31:LYS:HE3	1.74	0.68
1:B:28:GLU:CD	1:B:28:GLU:H	1.97	0.68
1:B:66:ARG:HH11	1:B:107:GLN:NE2	1.92	0.68
1:D:194:HIS:HD2	1:D:196:TYR:H	1.41	0.68
1:C:63:GLU:CA	1:C:66:ARG:HH21	2.06	0.68
1:A:269:ASN:ND2	1:A:280:ASN:OD1	2.27	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:118:TYR:OH	1:D:228:VAL:HG21	1.94	0.67
1:C:163:ILE:O	1:C:187:VAL:HG22	1.94	0.67
1:D:192:GLU:HB2	1:D:216:TYR:CE1	2.29	0.67
1:C:218:VAL:HG22	5:C:531:HOH:O	1.93	0.67
1:B:320:LEU:HD23	1:B:320:LEU:O	1.95	0.67
1:C:221:THR:HB	2:C:401:NDP:H51A	1.77	0.66
1:A:103:LEU:HD21	1:A:111:VAL:HG13	1.77	0.66
1:A:84:LYS:HE2	2:A:401:NDP:N7N	2.11	0.66
1:B:223:ARG:HB2	1:D:226:GLY:N	2.11	0.66
1:D:213:LEU:O	1:D:265:ILE:HG23	1.94	0.66
1:A:96:ARG:O	1:A:100:GLU:HG3	1.96	0.65
1:B:141:ARG:HG2	1:B:141:ARG:HH11	1.61	0.65
1:C:196:TYR:OH	1:C:238:GLU:HB2	1.97	0.65
1:D:198:ASN:HD21	1:D:300:ASN:HB2	1.59	0.64
1:D:65:ILE:O	1:D:69:ILE:HG12	1.97	0.64
1:B:198:ASN:ND2	1:B:300:ASN:HB2	2.11	0.64
1:C:31:LYS:HD3	1:C:56:ASN:O	1.98	0.64
1:B:171:ARG:NH2	1:C:180:PRO:HG3	2.13	0.63
1:B:262:GLN:HE22	1:B:288:LEU:H	1.45	0.63
1:A:36:GLU:O	1:A:40:ILE:HG12	1.99	0.63
1:C:291:GLU:O	1:C:295:VAL:HG23	1.98	0.63
1:B:269:ASN:ND2	1:B:280:ASN:OD1	2.32	0.62
1:C:143:ASP:O	1:C:146:ALA:HB3	2.00	0.61
1:C:213:LEU:O	1:C:265:ILE:HG23	1.98	0.61
1:D:260:GLN:OE1	1:D:265:ILE:HD12	2.00	0.61
1:C:240:VAL:HG21	1:C:299:LEU:HD21	1.82	0.61
1:A:28:GLU:H	1:A:28:GLU:CD	2.03	0.61
1:A:228:VAL:HG22	3:C:324:ACT:H2	1.81	0.61
1:B:38:THR:O	1:B:42:ILE:HG13	2.00	0.61
1:C:194:HIS:HD2	1:C:196:TYR:H	1.48	0.61
1:A:198:ASN:ND2	1:A:300:ASN:HB2	2.16	0.61
1:B:248:TYR:OH	1:B:292:ASP:OD2	2.15	0.61
1:A:58:GLU:HG2	1:A:81:TYR:OH	2.00	0.60
1:B:77:GLU:H	1:B:77:GLU:CD	2.02	0.60
1:B:36:GLU:O	1:B:40:ILE:HG12	2.01	0.60
1:B:111:VAL:O	1:B:160:THR:HA	2.01	0.60
1:D:141:ARG:O	1:D:142:VAL:HG23	2.02	0.60
1:C:219:LEU:HD22	1:C:236:LEU:HD21	1.84	0.60
1:A:27:LEU:H	1:C:230:GLN:NE2	2.00	0.60
1:C:248:TYR:O	1:C:250:ARG:HG2	2.01	0.60
1:B:171:ARG:HH22	1:C:180:PRO:CG	2.13	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:262:GLN:NE2	1:D:288:LEU:H	1.92	0.60
1:A:22:GLY:HA3	2:A:401:NDP:H4D	1.83	0.60
1:B:66:ARG:NH1	1:B:107:GLN:NE2	2.50	0.59
1:C:66:ARG:NH1	1:C:107:GLN:NE2	2.50	0.59
1:D:77:GLU:CD	1:D:77:GLU:H	2.06	0.59
1:B:137:LEU:HD12	1:B:310:ILE:HG13	1.85	0.59
1:D:234:VAL:HG22	1:D:237:ASP:CG	2.23	0.59
1:A:9:ILE:HB	1:A:15:PHE:CE2	2.37	0.59
1:B:225:GLY:HA3	1:B:229:ASP:HB2	1.83	0.59
1:A:27:LEU:CB	1:C:230:GLN:HE21	2.14	0.58
1:A:132:ASP:OD2	1:A:136:LYS:HB2	2.02	0.58
1:D:66:ARG:NH1	1:D:107:GLN:NE2	2.50	0.58
1:B:65:ILE:O	1:B:69:ILE:HG13	2.03	0.58
1:B:245:ALA:HB1	1:B:250:ARG:O	2.03	0.58
1:D:196:TYR:CD2	1:D:235:LEU:HD13	2.37	0.58
1:B:222:GLN:HG3	1:B:230:GLN:HE22	1.68	0.58
1:B:212:VAL:HG12	1:B:213:LEU:N	2.17	0.58
1:C:38:THR:HG23	1:C:49:PHE:CE2	2.38	0.58
1:A:172:GLN:O	1:A:176:ILE:HG12	2.03	0.58
1:B:203:LEU:HD13	1:B:213:LEU:HD13	1.85	0.58
1:D:291:GLU:O	1:D:295:VAL:HG23	2.04	0.58
1:B:253:ALA:O	1:B:256:ALA:HB3	2.03	0.58
1:D:47:HIS:HB3	1:D:78:ASP:O	2.03	0.58
1:D:63:GLU:HA	1:D:66:ARG:HH21	1.69	0.57
1:B:262:GLN:HE22	1:B:288:LEU:N	2.02	0.57
1:C:77:GLU:CD	1:C:77:GLU:H	2.08	0.57
1:C:171:ARG:NH1	1:C:321:ASP:OD2	2.37	0.57
1:A:17:PRO:HB2	1:A:48:HIS:HB2	1.86	0.57
1:D:247:LYS:HE2	5:D:426:HOH:O	2.03	0.57
1:A:77:GLU:CD	1:A:77:GLU:H	2.06	0.57
1:D:258:ARG:HE	1:D:262:GLN:NE2	1.99	0.57
1:A:223:ARG:CG	1:A:224:TYR:H	2.18	0.57
1:B:122:LEU:HD23	1:B:139:PHE:HA	1.84	0.57
1:B:31:LYS:HE3	1:B:31:LYS:HA	1.86	0.57
1:B:222:GLN:HG3	1:B:230:GLN:NE2	2.19	0.57
1:B:231:ASN:CG	1:D:27:LEU:HD13	2.25	0.57
1:A:66:ARG:HH12	1:A:107:GLN:NE2	2.01	0.57
1:B:203:LEU:HD22	1:B:265:ILE:HD11	1.86	0.57
1:D:133:GLU:CD	1:D:133:GLU:H	2.06	0.57
1:C:216:TYR:CE1	2:C:401:NDP:H41N	2.41	0.56
1:D:229:ASP:HA	1:D:232:SER:OG	2.05	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:192:GLU:HG2	1:A:197:LEU:HD23	1.86	0.56
1:B:54:VAL:HG22	1:D:227:TRP:HH2	1.69	0.56
1:B:315:PRO:HG3	1:C:171:ARG:HG2	1.87	0.56
1:A:66:ARG:HH11	1:A:107:GLN:HB2	1.69	0.56
1:C:183:LYS:HE2	1:C:184:TYR:CZ	2.41	0.56
1:C:132:ASP:HB2	1:C:133:GLU:OE2	2.06	0.56
1:C:145:CYS:SG	4:C:501:BME:H11	2.46	0.56
1:A:54:VAL:HG22	1:C:227:TRP:HH2	1.70	0.55
1:D:122:LEU:HD23	1:D:139:PHE:HA	1.86	0.55
1:D:139:PHE:CD1	1:D:314:HIS:HD2	2.24	0.55
1:C:63:GLU:HA	1:C:66:ARG:NH2	2.21	0.55
1:B:240:VAL:HG21	1:B:299:LEU:HD21	1.89	0.55
1:D:203:LEU:HD13	1:D:213:LEU:HD13	1.89	0.55
1:A:232:SER:HB2	1:C:310:ILE:HD13	1.88	0.55
1:C:238:GLU:OE1	1:C:239:PRO:HD2	2.06	0.55
1:C:268:LEU:O	1:C:269:ASN:HB2	2.07	0.55
1:B:103:LEU:HD21	1:B:111:VAL:HG13	1.89	0.55
1:B:141:ARG:HD3	1:C:323:TYR:OH	2.07	0.55
1:B:111:VAL:HG23	1:B:160:THR:OG1	2.07	0.54
1:A:171:ARG:NH1	1:A:321:ASP:OD2	2.40	0.54
1:B:228:VAL:HG22	3:D:324:ACT:CH3	2.38	0.54
1:D:219:LEU:O	1:D:235:LEU:HD23	2.08	0.54
1:B:134:HIS:HA	1:D:301:ARG:NH2	2.23	0.54
1:A:228:VAL:HG22	3:C:324:ACT:CH3	2.38	0.54
1:A:270:THR:O	2:A:401:NDP:H8A	2.08	0.54
1:C:169:ASN:HB2	1:C:323:TYR:O	2.08	0.54
1:A:194:HIS:HD2	1:A:196:TYR:H	1.54	0.54
1:B:137:LEU:CD1	1:B:310:ILE:HG13	2.38	0.53
1:A:149:GLU:HG3	1:A:179:LYS:HE3	1.89	0.53
1:D:31:LYS:HE3	1:D:31:LYS:HA	1.90	0.53
1:D:320:LEU:HD23	1:D:320:LEU:O	2.09	0.53
1:D:165:VAL:O	1:D:189:ASN:HA	2.08	0.53
1:C:260:GLN:HA	1:C:260:GLN:OE1	2.08	0.53
1:A:221:THR:C	1:A:223:ARG:N	2.62	0.53
1:D:19:LEU:HD12	1:D:267:VAL:HG23	1.90	0.53
1:C:270:THR:O	2:C:401:NDP:H8A	2.09	0.52
1:C:8:VAL:HG22	1:C:9:ILE:N	2.24	0.52
1:B:221:THR:HB	5:B:415:HOH:O	2.09	0.52
1:B:225:GLY:HA3	1:B:229:ASP:CB	2.38	0.52
1:A:10:LEU:HD21	1:A:16:ILE:HG21	1.90	0.52
1:A:99:LEU:O	1:A:103:LEU:HG	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:306:ILE:HG22	1:A:306:ILE:O	2.10	0.52
1:B:226:GLY:O	1:B:229:ASP:N	2.41	0.52
1:B:276:ARG:HD2	2:B:401:NDP:O3X	2.10	0.52
1:C:194:HIS:CD2	1:C:196:TYR:HB2	2.45	0.52
1:A:54:VAL:HG22	1:C:227:TRP:CH2	2.44	0.52
1:D:183:LYS:HE2	1:D:184:TYR:CZ	2.45	0.52
1:D:216:TYR:CZ	2:D:401:NDP:H41N	2.45	0.52
1:D:305:TYR:C	1:D:306:ILE:HG13	2.30	0.52
1:D:258:ARG:HG3	1:D:262:GLN:HE21	1.74	0.52
1:A:155:LYS:NZ	1:A:161:LYS:O	2.41	0.51
1:C:282:GLN:HG2	1:C:285:GLU:OE2	2.10	0.51
1:A:230:GLN:CA	1:A:230:GLN:NE2	2.67	0.51
1:B:251:THR:HG21	1:B:279:GLU:OE1	2.11	0.51
1:D:66:ARG:NH1	1:D:107:GLN:CD	2.63	0.51
1:D:144:LEU:HD12	1:D:175:MET:CE	2.41	0.51
1:B:301:ARG:HD3	5:B:412:HOH:O	2.10	0.51
1:D:219:LEU:HD22	1:D:236:LEU:HD21	1.91	0.51
1:B:141:ARG:NH1	1:C:323:TYR:OH	2.42	0.51
1:B:235:LEU:O	1:B:237:ASP:N	2.44	0.51
1:B:228:VAL:HG22	3:D:324:ACT:H2	1.92	0.51
1:C:238:GLU:OE1	1:C:239:PRO:CD	2.59	0.51
1:B:93:GLU:CD	1:B:93:GLU:H	2.14	0.51
1:B:133:GLU:CD	1:B:133:GLU:H	2.12	0.51
1:B:106:LEU:O	1:B:107:GLN:HB2	2.11	0.51
1:B:222:GLN:HG3	1:B:222:GLN:O	2.10	0.51
1:D:25:LEU:HD11	1:D:34:ALA:HB2	1.92	0.51
1:A:148:TRP:O	1:A:152:GLU:HG3	2.10	0.51
1:A:314:HIS:CG	1:A:315:PRO:HD2	2.45	0.51
1:B:149:GLU:O	1:B:153:LYS:HG3	2.10	0.51
1:B:103:LEU:CD1	1:B:159:LEU:HD22	2.41	0.50
1:C:214:VAL:HG22	1:C:266:VAL:HB	1.94	0.50
1:D:276:ARG:HG2	1:D:276:ARG:HH11	1.76	0.50
1:A:221:THR:O	1:A:223:ARG:N	2.44	0.50
1:A:212:VAL:HG12	1:A:213:LEU:N	2.26	0.50
1:B:237:ASP:O	1:B:238:GLU:C	2.50	0.50
1:D:199:GLN:NE2	1:D:202:LEU:HB3	2.27	0.50
1:D:248:TYR:OH	1:D:292:ASP:OD2	2.25	0.50
1:A:9:ILE:HD12	1:A:15:PHE:CZ	2.46	0.50
1:C:192:GLU:HA	1:C:216:TYR:O	2.12	0.50
1:D:155:LYS:HD3	1:D:184:TYR:CE2	2.46	0.50
1:C:188:CYS:HB2	1:C:212:VAL:O	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:115:LEU:HA	1:A:164:GLY:O	2.11	0.50
1:A:133:GLU:CD	1:A:133:GLU:H	2.15	0.50
1:B:23:THR:HG21	1:B:61:VAL:HG21	1.92	0.50
1:B:260:GLN:OE1	1:B:260:GLN:HA	2.12	0.50
1:C:66:ARG:NH1	1:C:107:GLN:CD	2.65	0.50
1:D:216:TYR:CE1	2:D:401:NDP:H41N	2.46	0.49
3:D:324:ACT:C	2:D:401:NDP:H42N	2.42	0.49
1:B:70:ALA:C	1:B:72:GLY:H	2.15	0.49
1:B:322:GLU:O	1:B:323:TYR:HB3	2.12	0.49
1:B:63:GLU:CA	1:B:66:ARG:HH21	2.25	0.49
1:B:33:LYS:HD2	1:B:37:LEU:HD11	1.93	0.49
1:C:261:LEU:HD12	1:C:283:VAL:HG22	1.95	0.49
1:B:75:ARG:NH1	1:B:77:GLU:HG3	2.28	0.49
1:B:9:ILE:HD11	1:B:13:GLY:HA2	1.94	0.49
1:B:143:ASP:HB3	1:B:146:ALA:HB2	1.95	0.49
1:A:251:THR:HG21	1:A:279:GLU:OE1	2.13	0.49
1:B:31:LYS:HD3	1:B:56:ASN:O	2.13	0.49
1:B:198:ASN:O	1:B:200:MET:N	2.46	0.49
1:C:90:LEU:O	1:C:147:THR:OG1	2.21	0.49
1:C:316:ASN:O	1:C:317:TRP:C	2.49	0.49
1:D:251:THR:HG21	1:D:279:GLU:OE1	2.12	0.49
1:A:259:TYR:CE1	1:A:296:LEU:HB2	2.48	0.48
1:D:250:ARG:NH1	1:D:282:GLN:OE1	2.46	0.48
1:A:155:LYS:HD3	1:A:184:TYR:CE2	2.47	0.48
1:D:144:LEU:HD12	1:D:175:MET:HE1	1.94	0.48
1:A:12:ASP:CG	1:A:14:ASN:HD22	2.16	0.48
1:C:85:VAL:HG12	1:C:116:ILE:HA	1.94	0.48
1:B:194:HIS:O	1:B:197:LEU:C	2.52	0.48
1:C:17:PRO:HB2	1:C:48:HIS:HB2	1.95	0.48
1:C:291:GLU:HA	1:C:294:LYS:CE	2.44	0.48
1:D:63:GLU:CA	1:D:66:ARG:HH21	2.26	0.48
1:D:199:GLN:NE2	1:D:202:LEU:HD23	2.28	0.48
1:B:141:ARG:HG2	1:B:141:ARG:NH1	2.26	0.48
1:D:91:HIS:CE1	1:D:142:VAL:HG22	2.49	0.48
1:D:258:ARG:NE	1:D:262:GLN:HE21	2.04	0.48
1:A:27:LEU:HB2	1:C:230:GLN:NE2	2.22	0.48
1:B:27:LEU:H	1:D:230:GLN:NE2	2.11	0.48
1:D:98:SER:O	1:D:101:ARG:HB3	2.14	0.48
1:B:25:LEU:HD11	1:B:34:ALA:HB2	1.95	0.48
1:B:194:HIS:HB2	1:B:195:PRO:HD2	1.96	0.48
1:D:194:HIS:CD2	1:D:196:TYR:HB2	2.49	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:103:LEU:HD21	1:C:111:VAL:HG13	1.95	0.48
1:D:127:GLU:O	1:D:130:PRO:HD3	2.14	0.48
1:A:223:ARG:CG	1:C:226:GLY:N	2.72	0.48
1:B:33:LYS:HD2	1:B:37:LEU:CD1	2.43	0.48
1:B:242:GLY:HA2	1:B:252:PRO:HG3	1.96	0.48
1:C:133:GLU:CD	1:C:133:GLU:H	2.16	0.47
1:C:250:ARG:NH1	5:C:502:HOH:O	2.47	0.47
1:A:262:GLN:HE22	1:A:288:LEU:N	1.95	0.47
1:B:82:THR:OG1	1:B:113:LEU:HB3	2.14	0.47
1:B:119:PRO:HB3	1:B:168:PHE:CE1	2.49	0.47
1:C:10:LEU:HB3	1:C:187:VAL:HB	1.96	0.47
1:C:165:VAL:O	1:C:189:ASN:HA	2.13	0.47
1:D:276:ARG:HD3	2:D:401:NDP:C5A	2.44	0.47
1:B:17:PRO:HB2	1:B:48:HIS:HB2	1.97	0.47
1:C:198:ASN:ND2	1:C:300:ASN:HB2	2.29	0.47
1:D:85:VAL:HG13	1:D:85:VAL:O	2.14	0.47
1:A:231:ASN:O	1:A:232:SER:C	2.51	0.47
1:B:167:ASN:HA	1:B:191:VAL:HG12	1.97	0.47
1:B:292:ASP:O	1:B:295:VAL:HB	2.15	0.47
1:D:44:ALA:O	1:D:281:MET:HG3	2.14	0.47
1:D:121:ALA:O	1:D:122:LEU:HD23	2.14	0.47
1:C:28:GLU:CD	1:C:28:GLU:H	2.17	0.47
1:B:148:TRP:O	1:B:152:GLU:HG3	2.14	0.47
1:C:183:LYS:HE2	1:C:184:TYR:OH	2.15	0.47
1:C:186:PRO:O	1:C:211:ILE:HG12	2.15	0.47
1:C:243:SER:O	1:C:246:LYS:N	2.48	0.47
1:D:259:TYR:CD1	1:D:296:LEU:HD12	2.50	0.47
1:A:66:ARG:NH1	1:A:107:GLN:CD	2.68	0.46
1:A:93:GLU:CD	1:A:93:GLU:H	2.18	0.46
1:B:22:GLY:O	1:B:270:THR:HG22	2.14	0.46
1:A:85:VAL:HG13	1:A:85:VAL:O	2.15	0.46
1:A:223:ARG:NH1	1:A:230:GLN:OE1	2.48	0.46
1:A:223:ARG:CB	1:C:226:GLY:N	2.79	0.46
1:B:270:THR:O	2:B:401:NDP:H8A	2.14	0.46
1:C:99:LEU:HD13	1:C:114:TYR:CE1	2.51	0.46
1:C:122:LEU:HD23	1:C:139:PHE:HA	1.96	0.46
1:A:223:ARG:HD2	1:A:223:ARG:HA	1.67	0.46
1:B:244:MET:O	1:B:247:LYS:HB3	2.16	0.46
1:A:106:LEU:O	1:A:107:GLN:HB2	2.15	0.46
1:C:201:LYS:HE3	1:C:322:GLU:OE2	2.14	0.46
1:A:73:THR:O	1:A:74:VAL:HG13	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:193:CYS:O	1:A:218:VAL:HG12	2.15	0.46
1:C:70:ALA:C	1:C:72:GLY:H	2.17	0.46
1:D:194:HIS:HB2	1:D:235:LEU:HD21	1.97	0.46
1:D:259:TYR:CE1	1:D:296:LEU:HB2	2.51	0.46
1:A:21:PHE:CE1	1:A:270:THR:HA	2.50	0.46
1:A:291:GLU:O	1:A:295:VAL:HG23	2.16	0.46
1:B:306:ILE:HG22	1:B:306:ILE:O	2.15	0.46
2:B:401:NDP:H42N	5:B:406:HOH:O	2.14	0.46
1:D:238:GLU:OE2	1:D:239:PRO:HD2	2.16	0.46
1:A:231:ASN:O	1:A:232:SER:O	2.32	0.46
1:B:294:LYS:HA	1:B:297:ASP:OD2	2.15	0.46
1:D:310:ILE:O	1:D:310:ILE:HG13	2.16	0.46
1:B:291:GLU:O	1:B:295:VAL:HG23	2.16	0.46
1:D:143:ASP:O	1:D:146:ALA:HB3	2.15	0.46
1:B:166:SER:O	1:B:167:ASN:HB2	2.16	0.46
1:B:244:MET:O	1:B:248:TYR:HD1	1.98	0.46
1:D:245:ALA:HB1	1:D:250:ARG:O	2.15	0.46
1:C:280:ASN:HD21	2:C:401:NDP:H61A	1.64	0.45
1:D:219:LEU:HD13	1:D:236:LEU:HD11	1.97	0.45
1:A:213:LEU:C	1:A:213:LEU:HD23	2.36	0.45
1:C:175:MET:HB3	1:C:175:MET:HE2	1.85	0.45
1:B:207:LYS:C	1:B:209:LYS:H	2.20	0.45
1:C:57:THR:O	1:C:61:VAL:HG23	2.16	0.45
1:D:193:CYS:HB3	1:D:215:ALA:HB1	1.99	0.45
1:B:8:VAL:HG22	1:B:9:ILE:N	2.32	0.45
1:C:61:VAL:O	1:C:65:ILE:HG13	2.16	0.45
1:D:93:GLU:CD	1:D:93:GLU:H	2.20	0.45
1:D:195:PRO:HD2	1:D:235:LEU:HD21	1.98	0.45
1:D:196:TYR:HB3	1:D:303:MET:HB3	1.97	0.45
1:A:230:GLN:HE21	1:A:230:GLN:HA	1.76	0.45
1:B:99:LEU:HD21	1:B:159:LEU:HB3	1.98	0.45
1:C:9:ILE:HB	1:C:15:PHE:CE2	2.51	0.45
1:C:65:ILE:O	1:C:69:ILE:HG12	2.16	0.45
1:D:192:GLU:HA	1:D:216:TYR:O	2.16	0.45
1:B:223:ARG:O	1:B:223:ARG:NE	2.50	0.45
1:B:229:ASP:OD1	1:D:309:ALA:HB3	2.17	0.45
1:B:9:ILE:HB	1:B:15:PHE:CE2	2.52	0.44
1:C:238:GLU:OE2	1:C:299:LEU:HD22	2.17	0.44
1:D:8:VAL:O	1:D:15:PHE:HA	2.17	0.44
1:D:190:GLN:HA	1:D:214:VAL:O	2.17	0.44
1:A:245:ALA:HA	1:A:255:ILE:HD11	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:81:TYR:CE2	1:B:106:LEU:HD11	2.53	0.44
1:B:194:HIS:HB3	1:B:218:VAL:HA	1.99	0.44
1:C:203:LEU:HD22	1:C:265:ILE:HD11	1.99	0.44
1:A:278:LYS:O	1:A:280:ASN:N	2.50	0.44
1:C:172:GLN:O	1:C:176:ILE:HD13	2.16	0.44
1:A:167:ASN:HA	1:A:191:VAL:HG12	1.99	0.44
1:B:196:TYR:OH	1:B:238:GLU:HB2	2.17	0.44
1:B:282:GLN:HG2	1:B:285:GLU:OE2	2.17	0.44
1:C:99:LEU:HD13	1:C:114:TYR:CD1	2.53	0.44
1:C:216:TYR:CD1	1:C:216:TYR:C	2.91	0.44
1:A:196:TYR:HB3	1:A:303:MET:HB3	1.98	0.44
1:A:197:LEU:HD22	1:A:304:ARG:HA	1.99	0.44
1:C:12:ASP:OD2	1:C:155:LYS:NZ	2.51	0.44
1:D:234:VAL:HG22	1:D:237:ASP:OD1	2.18	0.44
1:A:291:GLU:HG2	1:A:294:LYS:HZ1	1.82	0.44
1:B:144:LEU:HD23	1:B:144:LEU:HA	1.81	0.44
1:B:135:GLY:HA3	1:D:301:ARG:NH1	2.33	0.44
1:C:141:ARG:HG2	1:C:141:ARG:HH11	1.83	0.44
1:B:40:ILE:HG23	1:B:274:GLU:HG3	2.00	0.43
1:B:99:LEU:HD13	1:B:114:TYR:CE1	2.53	0.43
1:C:37:LEU:HD11	1:C:272:LEU:CD2	2.48	0.43
1:C:235:LEU:C	1:C:237:ASP:H	2.21	0.43
1:C:248:TYR:OH	1:C:292:ASP:OD2	2.27	0.43
1:B:235:LEU:C	1:B:237:ASP:H	2.21	0.43
1:A:253:ALA:O	1:A:257:LEU:HG	2.18	0.43
1:B:216:TYR:CE1	2:B:401:NDP:H41N	2.53	0.43
1:C:314:HIS:HA	1:C:315:PRO:HD3	1.87	0.43
1:B:282:GLN:C	1:B:284:PHE:H	2.22	0.43
1:C:25:LEU:HD11	1:C:34:ALA:HB2	2.00	0.43
1:C:248:TYR:CD1	1:C:248:TYR:N	2.87	0.43
1:B:22:GLY:HA3	2:B:401:NDP:O3D	2.19	0.43
1:B:225:GLY:CA	1:B:229:ASP:HB2	2.49	0.43
1:C:161:LYS:HB3	1:C:161:LYS:HE2	1.77	0.43
1:D:165:VAL:HB	1:D:168:PHE:CD1	2.53	0.43
1:A:175:MET:O	1:A:175:MET:HG2	2.18	0.43
1:A:194:HIS:CD2	1:A:196:TYR:HB2	2.54	0.43
1:A:260:GLN:O	1:A:265:ILE:HB	2.18	0.43
1:A:216:TYR:CZ	2:A:401:NDP:H41N	2.53	0.43
1:B:225:GLY:O	1:B:229:ASP:OD2	2.37	0.43
1:D:169:ASN:O	1:D:170:TYR:C	2.57	0.43
1:D:207:LYS:C	1:D:209:LYS:H	2.21	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:30:PRO:HA	5:A:404:HOH:O	2.18	0.43
1:D:105:LYS:HD3	5:D:412:HOH:O	2.18	0.43
1:A:322:GLU:O	1:A:323:TYR:HB3	2.19	0.43
1:B:213:LEU:C	1:B:213:LEU:HD23	2.39	0.43
1:B:226:GLY:O	1:B:227:TRP:C	2.56	0.43
1:B:314:HIS:CE1	1:B:316:ASN:HB2	2.54	0.43
1:C:16:ILE:HA	1:C:17:PRO:HD3	1.81	0.43
1:C:35:LYS:NZ	1:C:63:GLU:CD	2.72	0.43
1:A:230:GLN:NE2	1:A:230:GLN:HA	2.34	0.42
1:B:54:VAL:HG22	1:D:227:TRP:CH2	2.53	0.42
1:C:190:GLN:NE2	1:C:268:LEU:HD11	2.34	0.42
1:C:261:LEU:HA	1:C:261:LEU:HD23	1.81	0.42
1:B:39:LYS:O	1:B:40:ILE:C	2.57	0.42
1:B:194:HIS:CE1	1:B:197:LEU:HB3	2.54	0.42
1:B:222:GLN:HE22	1:B:234:VAL:HG12	1.84	0.42
1:B:321:ASP:N	1:B:321:ASP:OD1	2.53	0.42
1:A:236:LEU:HG	5:A:429:HOH:O	2.18	0.42
1:B:179:LYS:HA	1:B:180:PRO:HD3	1.95	0.42
1:B:237:ASP:O	1:B:238:GLU:O	2.38	0.42
1:D:193:CYS:HB3	1:D:215:ALA:CB	2.49	0.42
1:B:314:HIS:HA	1:B:315:PRO:HD3	1.91	0.42
1:C:176:ILE:O	1:C:179:LYS:CB	2.67	0.42
1:A:61:VAL:O	1:A:65:ILE:HG13	2.19	0.42
1:A:177:LEU:HD23	1:A:177:LEU:HA	1.82	0.42
1:B:58:GLU:O	1:B:106:LEU:HD23	2.19	0.42
1:B:91:HIS:CE1	1:B:142:VAL:HG22	2.54	0.42
1:A:177:LEU:CD2	1:A:185:LYS:HG2	2.50	0.42
1:B:290:SER:O	1:B:294:LYS:HG3	2.19	0.42
1:D:110:TYR:CE1	1:D:161:LYS:HD2	2.55	0.42
1:D:227:TRP:O	1:D:231:ASN:HB2	2.20	0.42
1:D:316:ASN:O	1:D:317:TRP:C	2.58	0.42
1:A:237:ASP:O	1:A:238:GLU:C	2.58	0.42
1:B:212:VAL:CG1	1:B:213:LEU:N	2.81	0.42
1:C:188:CYS:HA	1:C:211:ILE:HG22	2.00	0.42
1:C:216:TYR:CZ	2:C:401:NDP:H41N	2.55	0.42
1:D:259:TYR:O	1:D:263:ARG:HG3	2.19	0.42
1:B:115:LEU:HA	1:B:164:GLY:O	2.20	0.42
1:B:143:ASP:HB3	1:B:146:ALA:CB	2.50	0.42
1:C:261:LEU:HD12	1:C:283:VAL:CG2	2.50	0.42
1:C:321:ASP:OD1	1:C:321:ASP:N	2.53	0.42
1:A:141:ARG:HH11	1:A:141:ARG:HG2	1.85	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:240:VAL:CG2	1:C:299:LEU:HD21	2.48	0.42
1:D:192:GLU:HB2	1:D:216:TYR:CZ	2.54	0.42
1:B:139:PHE:HD2	1:C:171:ARG:HH21	1.68	0.42
1:C:9:ILE:HD12	1:C:15:PHE:CE1	2.55	0.42
1:C:84:LYS:HE2	1:C:190:GLN:OE1	2.19	0.42
1:C:91:HIS:O	1:C:92:PRO:C	2.58	0.42
1:D:242:GLY:O	1:D:245:ALA:HB3	2.20	0.42
1:A:221:THR:OG1	1:A:223:ARG:CB	2.64	0.41
1:B:29:CYS:HA	1:B:30:PRO:HD3	1.80	0.41
1:D:110:TYR:HE1	1:D:161:LYS:HD2	1.84	0.41
1:B:236:LEU:HD23	1:B:236:LEU:HA	1.92	0.41
1:C:176:ILE:O	1:C:179:LYS:HB3	2.20	0.41
1:D:31:LYS:HD3	1:D:56:ASN:O	2.20	0.41
1:D:226:GLY:O	1:D:229:ASP:N	2.53	0.41
1:A:48:HIS:CD2	1:A:48:HIS:C	2.93	0.41
1:B:22:GLY:O	1:B:270:THR:CG2	2.69	0.41
1:B:31:LYS:HB3	1:B:60:HIS:CD2	2.55	0.41
1:B:289:SER:OG	1:B:292:ASP:OD2	2.32	0.41
1:B:293:MET:O	1:B:297:ASP:OD2	2.37	0.41
1:D:301:ARG:O	1:D:302:ASN:HB2	2.20	0.41
1:B:28:GLU:CD	1:B:28:GLU:N	2.70	0.41
1:B:282:GLN:C	1:B:284:PHE:N	2.73	0.41
1:B:306:ILE:HG22	5:B:417:HOH:O	2.20	0.41
1:C:85:VAL:O	1:C:85:VAL:HG13	2.21	0.41
1:C:279:GLU:O	1:C:282:GLN:HB2	2.20	0.41
1:C:307:PRO:O	1:C:308:ALA:HB3	2.20	0.41
1:A:28:GLU:O	1:A:29:CYS:C	2.58	0.41
1:A:32:SER:O	1:A:33:LYS:C	2.59	0.41
1:A:85:VAL:HG12	1:A:116:ILE:HA	2.03	0.41
1:C:8:VAL:HG13	1:C:16:ILE:CG2	2.51	0.41
1:C:21:PHE:HA	1:C:269:ASN:O	2.20	0.41
1:D:163:ILE:O	1:D:187:VAL:HG22	2.21	0.41
1:A:33:LYS:HD2	1:A:37:LEU:HG	2.02	0.41
1:B:121:ALA:HB3	1:B:140:ASP:O	2.21	0.41
1:B:320:LEU:HD23	1:B:320:LEU:C	2.41	0.41
1:A:262:GLN:NE2	1:A:288:LEU:H	1.97	0.41
1:B:193:CYS:O	1:B:218:VAL:HG12	2.20	0.41
1:D:10:LEU:HD23	1:D:212:VAL:HG21	2.02	0.41
1:D:23:THR:HG21	1:D:61:VAL:HG21	2.01	0.41
1:D:288:LEU:HD12	1:D:293:MET:SD	2.61	0.41
1:B:52:ALA:HB2	1:B:84:LYS:HZ3	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:171:ARG:NH1	1:B:321:ASP:OD2	2.53	0.41
1:A:171:ARG:HH11	1:A:171:ARG:HG3	1.86	0.41
1:A:258:ARG:CG	1:A:288:LEU:HG	2.50	0.41
1:A:311:PHE:O	1:A:312:LYS:C	2.58	0.41
1:B:135:GLY:HA3	1:D:301:ARG:HH12	1.84	0.41
1:B:260:GLN:HB2	1:B:267:VAL:HG11	2.03	0.41
1:C:169:ASN:O	1:C:170:TYR:C	2.58	0.41
1:C:188:CYS:HA	1:C:211:ILE:CG2	2.51	0.41
1:C:229:ASP:HA	1:C:232:SER:OG	2.21	0.41
1:A:194:HIS:HA	1:A:260:GLN:NE2	2.36	0.41
1:B:191:VAL:O	1:B:215:ALA:HA	2.20	0.41
1:C:84:LYS:HE3	1:C:115:LEU:HD12	2.03	0.41
1:D:22:GLY:O	1:D:270:THR:CG2	2.68	0.41
1:C:169:ASN:OD1	1:C:172:GLN:HG3	2.21	0.40
1:C:258:ARG:HA	1:C:258:ARG:HD2	1.97	0.40
1:C:28:GLU:O	1:C:29:CYS:C	2.59	0.40
1:C:87:CYS:HB3	1:C:120:MET:O	2.21	0.40
1:A:31:LYS:HB3	1:A:60:HIS:CD2	2.57	0.40
1:A:307:PRO:O	1:A:308:ALA:HB3	2.21	0.40
1:B:21:PHE:HA	1:B:269:ASN:O	2.22	0.40
1:B:48:HIS:CD2	1:B:48:HIS:C	2.95	0.40
1:B:221:THR:N	5:B:415:HOH:O	2.52	0.40
1:C:29:CYS:HA	1:C:30:PRO:HD3	1.78	0.40
1:C:30:PRO:O	1:C:31:LYS:C	2.60	0.40
1:C:37:LEU:HD11	1:C:272:LEU:HD23	2.02	0.40
1:C:83:SER:O	1:C:114:TYR:HA	2.21	0.40
1:D:8:VAL:HG12	1:D:16:ILE:O	2.21	0.40
1:D:29:CYS:HA	1:D:30:PRO:HD3	1.82	0.40
1:D:141:ARG:HG2	1:D:141:ARG:HH11	1.86	0.40
1:D:194:HIS:HD2	1:D:196:TYR:N	2.14	0.40
1:A:81:TYR:CE2	1:A:106:LEU:HD11	2.56	0.40
1:A:86:TRP:HA	1:A:86:TRP:CE3	2.56	0.40
1:C:203:LEU:HA	1:C:213:LEU:HD22	2.03	0.40
1:A:276:ARG:HD2	2:A:401:NDP:O3X	2.21	0.40
1:B:40:ILE:CG2	1:B:274:GLU:HG3	2.51	0.40
1:B:161:LYS:HB3	1:B:161:LYS:HE2	1.92	0.40
1:B:262:GLN:NE2	1:B:288:LEU:H	2.16	0.40
1:C:254:LEU:HD23	1:C:257:LEU:HD12	2.03	0.40
1:C:260:GLN:OE1	1:C:265:ILE:HD12	2.21	0.40
1:D:194:HIS:HB2	1:D:195:PRO:HD2	2.03	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	316/323 (98%)	276 (87%)	32 (10%)	8 (2%)	5 21
1	B	316/323 (98%)	276 (87%)	28 (9%)	12 (4%)	3 13
1	C	310/323 (96%)	269 (87%)	33 (11%)	8 (3%)	5 20
1	D	310/323 (96%)	271 (87%)	34 (11%)	5 (2%)	9 32
All	All	1252/1292 (97%)	1092 (87%)	127 (10%)	33 (3%)	5 20

All (33) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	224	TYR
1	B	199	GLN
1	B	222	GLN
1	C	312	LYS
1	D	312	LYS
1	A	11	ASN
1	A	170	TYR
1	A	222	GLN
1	A	279	GLU
1	B	220	GLY
1	B	236	LEU
1	B	302	ASN
1	B	312	LYS
1	C	11	ASN
1	D	198	ASN
1	A	27	LEU
1	B	227	TRP
1	B	238	GLU
1	C	139	PHE
1	D	11	ASN
1	A	29	CYS
1	C	29	CYS

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Mol	Chain	Res	Type
1	D	29	CYS
1	D	170	TYR
1	A	232	SER
1	B	242	GLY
1	B	279	GLU
1	C	170	TYR
1	B	40	ILE
1	B	29	CYS
1	C	92	PRO
1	C	220	GLY
1	C	310	ILE

5.3.2 Protein sidechains (i)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	281/286 (98%)	270 (96%)	11 (4%)	32	66
1	B	281/286 (98%)	270 (96%)	11 (4%)	32	66
1	C	278/286 (97%)	270 (97%)	8 (3%)	42	76
1	D	278/286 (97%)	272 (98%)	6 (2%)	52	81
All	All	1118/1144 (98%)	1082 (97%)	36 (3%)	39	73

All (36) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	12	ASP
1	A	31	LYS
1	A	127	GLU
1	A	133	GLU
1	A	210	ASP
1	A	221	THR
1	A	223	ARG
1	A	228	VAL
1	A	230	GLN
1	A	232	SER

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Mol	Chain	Res	Type
1	A	321	ASP
1	B	31	LYS
1	B	33	LYS
1	B	127	GLU
1	B	133	GLU
1	B	175	MET
1	B	210	ASP
1	B	223	ARG
1	B	224	TYR
1	B	232	SER
1	B	233	PRO
1	B	321	ASP
1	C	31	LYS
1	C	33	LYS
1	C	127	GLU
1	C	133	GLU
1	C	210	ASP
1	C	228	VAL
1	C	267	VAL
1	C	321	ASP
1	D	31	LYS
1	D	127	GLU
1	D	133	GLU
1	D	210	ASP
1	D	302	ASN
1	D	321	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (43) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	6	HIS
1	A	14	ASN
1	A	60	HIS
1	A	104	GLN
1	A	107	GLN
1	A	178	ASN
1	A	190	GLN
1	A	194	HIS
1	A	199	GLN
1	A	230	GLN
1	A	262	GLN
1	A	269	ASN

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Mol	Chain	Res	Type
1	A	280	ASN
1	B	47	HIS
1	B	107	GLN
1	B	178	ASN
1	B	190	GLN
1	B	194	HIS
1	B	199	GLN
1	B	222	GLN
1	B	262	GLN
1	B	269	ASN
1	C	107	GLN
1	C	167	ASN
1	C	178	ASN
1	C	194	HIS
1	C	199	GLN
1	C	230	GLN
1	C	262	GLN
1	C	269	ASN
1	C	280	ASN
1	D	6	HIS
1	D	47	HIS
1	D	60	HIS
1	D	104	GLN
1	D	107	GLN
1	D	178	ASN
1	D	194	HIS
1	D	199	GLN
1	D	230	GLN
1	D	262	GLN
1	D	269	ASN
1	D	280	ASN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

7 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	NDP	A	401	-	47,52,52	1.39	8 (17%)	61,80,80	1.12	4 (6%)
3	ACT	D	324	-	3,3,3	2.17	1 (33%)	3,3,3	0.81	0
2	NDP	B	401	-	47,52,52	1.44	8 (17%)	61,80,80	1.14	4 (6%)
2	NDP	D	401	-	47,52,52	1.42	7 (14%)	61,80,80	1.22	3 (4%)
4	BME	C	501	-	3,3,3	0.34	0	2,2,2	0.36	0
3	ACT	C	324	-	3,3,3	2.11	1 (33%)	3,3,3	0.81	0
2	NDP	C	401	-	47,52,52	1.43	8 (17%)	61,80,80	1.14	5 (8%)

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	NDP	A	401	-	-	10/30/77/77	0/5/5/5
2	NDP	B	401	-	-	10/30/77/77	0/5/5/5
2	NDP	D	401	-	-	12/30/77/77	0/5/5/5
4	BME	C	501	-	-	0/1/1/1	-
2	NDP	C	401	-	-	12/30/77/77	0/5/5/5

All (33) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	401	NDP	C2A-N3A	4.25	1.38	1.32

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	401	NDP	C4A-N3A	4.25	1.41	1.35
2	D	401	NDP	C2A-N3A	3.92	1.38	1.32
2	B	401	NDP	C4A-N3A	3.81	1.40	1.35
2	A	401	NDP	C2A-N3A	3.79	1.38	1.32
2	B	401	NDP	C2A-N3A	3.75	1.37	1.32
2	A	401	NDP	C4A-N3A	3.69	1.40	1.35
2	C	401	NDP	C4A-N3A	3.62	1.40	1.35
2	B	401	NDP	C6N-N1N	3.29	1.45	1.37
3	D	324	ACT	O-C	3.25	1.36	1.22
2	D	401	NDP	C6N-N1N	3.16	1.44	1.37
3	C	324	ACT	O-C	3.01	1.35	1.22
2	C	401	NDP	C4N-C3N	-2.98	1.44	1.50
2	A	401	NDP	C6N-N1N	2.85	1.44	1.37
2	C	401	NDP	C6N-N1N	2.78	1.44	1.37
2	C	401	NDP	C4N-C5N	-2.74	1.41	1.49
2	B	401	NDP	C6N-C5N	2.71	1.41	1.33
2	D	401	NDP	C2A-N1A	2.70	1.38	1.33
2	A	401	NDP	C2A-N1A	2.67	1.38	1.33
2	A	401	NDP	C6N-C5N	2.65	1.41	1.33
2	C	401	NDP	C2A-N1A	2.63	1.38	1.33
2	B	401	NDP	C2N-C3N	2.56	1.42	1.35
2	B	401	NDP	C2A-N1A	2.55	1.38	1.33
2	A	401	NDP	C4N-C5N	-2.43	1.42	1.49
2	D	401	NDP	C2N-C3N	2.40	1.41	1.35
2	A	401	NDP	C2N-C3N	2.38	1.41	1.35
2	D	401	NDP	C6N-C5N	2.37	1.40	1.33
2	B	401	NDP	PA-O3	2.35	1.62	1.59
2	A	401	NDP	C4N-C3N	-2.31	1.45	1.50
2	C	401	NDP	C6N-C5N	2.29	1.40	1.33
2	C	401	NDP	C2N-C3N	2.22	1.41	1.35
2	D	401	NDP	C4N-C5N	-2.13	1.43	1.49
2	B	401	NDP	C4N-C5N	-2.05	1.43	1.49

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	D	401	NDP	C4B-O4B-C1B	-4.86	105.47	109.92
2	B	401	NDP	C1D-N1N-C2N	-3.76	114.95	121.14
2	D	401	NDP	C1D-N1N-C2N	-3.51	115.35	121.14
2	C	401	NDP	C4B-O4B-C1B	-3.46	106.75	109.92
2	A	401	NDP	C1D-N1N-C2N	-3.41	115.52	121.14
2	C	401	NDP	C1D-N1N-C2N	-3.06	116.09	121.14

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	401	NDP	C4B-O4B-C1B	2.66	112.36	109.92
2	A	401	NDP	C4B-O4B-C1B	-2.32	107.80	109.92
2	B	401	NDP	N3A-C2A-N1A	-2.24	125.63	128.67
2	D	401	NDP	N3A-C2A-N1A	-2.20	125.69	128.67
2	A	401	NDP	N3A-C2A-N1A	-2.15	125.76	128.67
2	B	401	NDP	C4A-C5A-N7A	2.11	111.56	109.34
2	A	401	NDP	C4A-C5A-N7A	2.07	111.52	109.34
2	C	401	NDP	C4A-C5A-N7A	2.05	111.50	109.34
2	C	401	NDP	C3N-C2N-N1N	-2.04	120.21	123.20
2	C	401	NDP	N3A-C2A-N1A	-2.02	125.93	128.67

There are no chirality outliers.

All (44) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	401	NDP	C5B-O5B-PA-O2A
2	A	401	NDP	C5B-O5B-PA-O3
2	A	401	NDP	C5D-O5D-PN-O1N
2	B	401	NDP	C5B-O5B-PA-O1A
2	B	401	NDP	C5B-O5B-PA-O2A
2	B	401	NDP	C5B-O5B-PA-O3
2	C	401	NDP	C5D-O5D-PN-O3
2	C	401	NDP	C5D-O5D-PN-O1N
2	C	401	NDP	O4D-C4D-C5D-O5D
2	D	401	NDP	O4B-C4B-C5B-O5B
2	D	401	NDP	C3B-C4B-C5B-O5B
2	D	401	NDP	C5D-O5D-PN-O3
2	D	401	NDP	C5D-O5D-PN-O1N
2	D	401	NDP	O4D-C4D-C5D-O5D
2	D	401	NDP	O4D-C1D-N1N-C2N
2	B	401	NDP	C3B-C4B-C5B-O5B
2	C	401	NDP	O4B-C4B-C5B-O5B
2	C	401	NDP	C3B-C4B-C5B-O5B
2	D	401	NDP	C3D-C4D-C5D-O5D
2	A	401	NDP	O4D-C1D-N1N-C2N
2	C	401	NDP	O4D-C1D-N1N-C2N
2	A	401	NDP	O4D-C4D-C5D-O5D
2	B	401	NDP	O4B-C4B-C5B-O5B
2	C	401	NDP	C3D-C4D-C5D-O5D
2	A	401	NDP	C3D-C4D-C5D-O5D
2	B	401	NDP	PN-O3-PA-O5B
2	C	401	NDP	PA-O3-PN-O5D

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Mol	Chain	Res	Type	Atoms
2	D	401	NDP	PA-O3-PN-O5D
2	C	401	NDP	PN-O3-PA-O2A
2	B	401	NDP	O4D-C1D-N1N-C2N
2	A	401	NDP	C5B-O5B-PA-O1A
2	A	401	NDP	C5D-O5D-PN-O3
2	C	401	NDP	C5D-O5D-PN-O2N
2	D	401	NDP	C5D-O5D-PN-O2N
2	D	401	NDP	PN-O3-PA-O1A
2	D	401	NDP	PN-O3-PA-O2A
2	A	401	NDP	C2N-C3N-C7N-N7N
2	B	401	NDP	C2N-C3N-C7N-N7N
2	C	401	NDP	C2N-C3N-C7N-N7N
2	D	401	NDP	C2N-C3N-C7N-N7N
2	A	401	NDP	PN-O3-PA-O2A
2	B	401	NDP	PN-O3-PA-O2A
2	C	401	NDP	PN-O3-PA-O1A
2	B	401	NDP	O4D-C4D-C5D-O5D

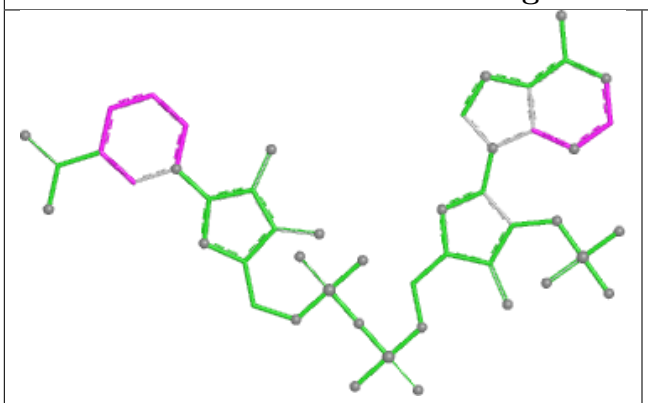
There are no ring outliers.

7 monomers are involved in 25 short contacts:

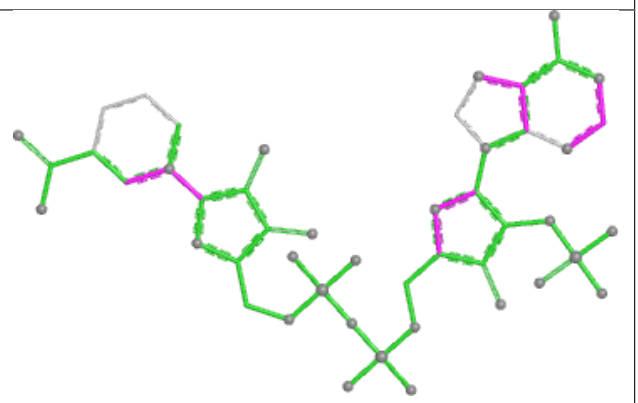
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	401	NDP	6	0
3	D	324	ACT	3	0
2	B	401	NDP	5	0
2	D	401	NDP	4	0
4	C	501	BME	1	0
3	C	324	ACT	2	0
2	C	401	NDP	5	0

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.

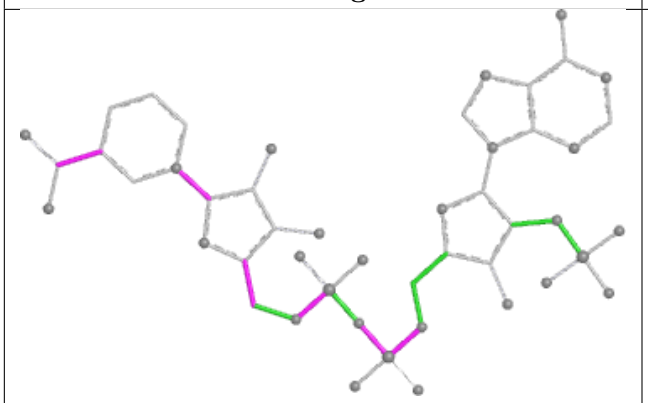
Ligand NDP A 401



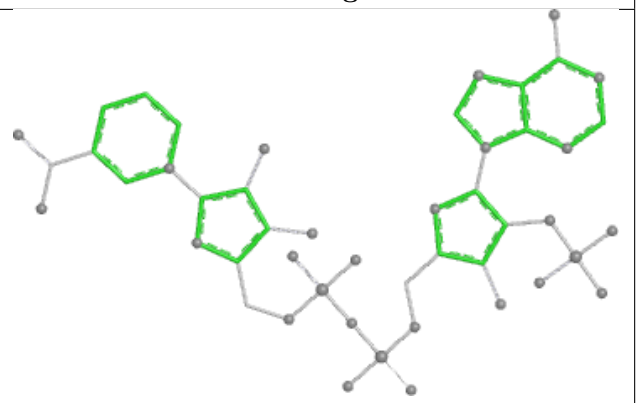
Bond lengths



Bond angles

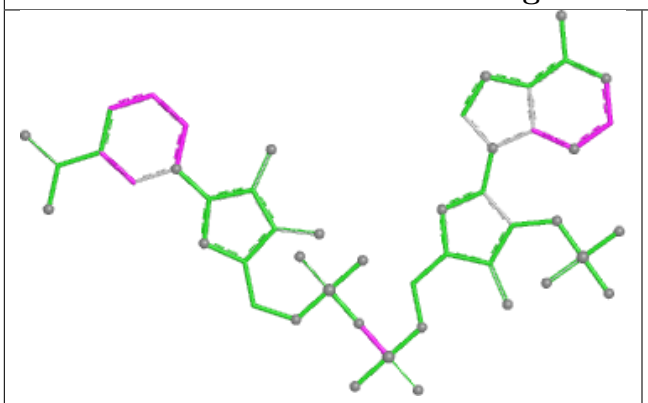


Torsions

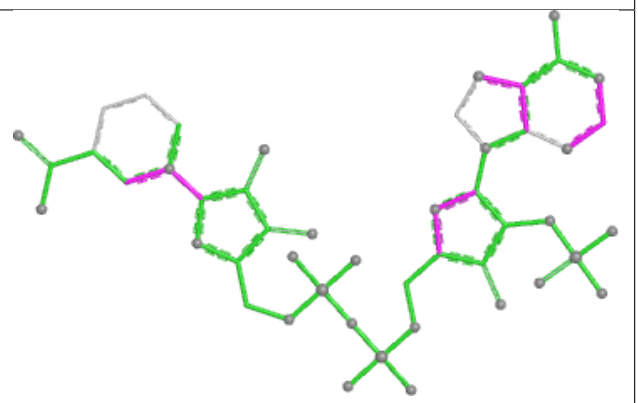


Rings

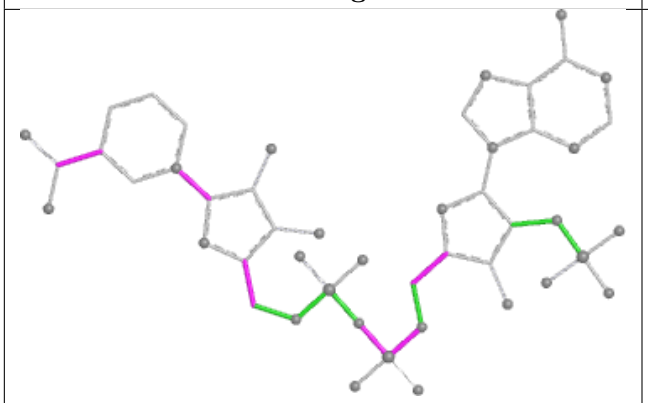
Ligand NDP B 401



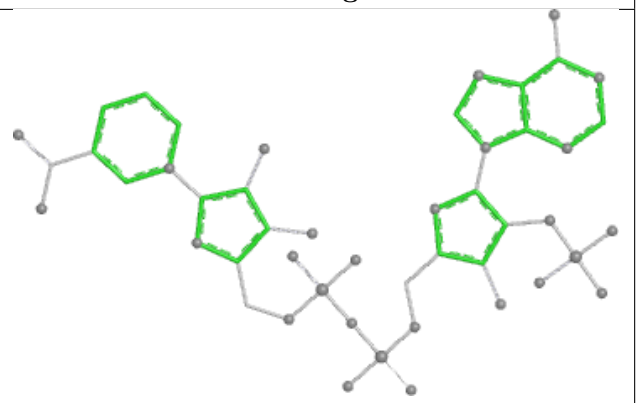
Bond lengths



Bond angles

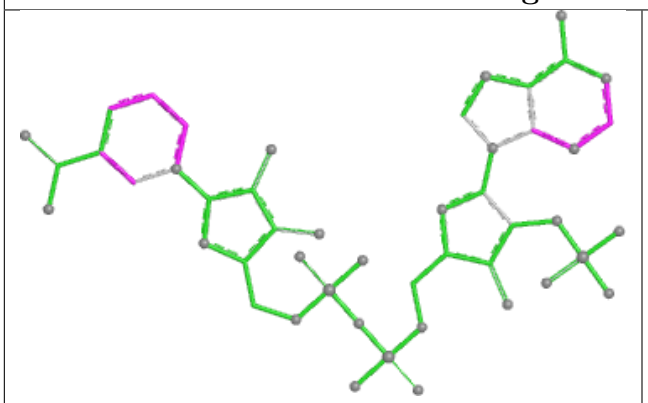


Torsions

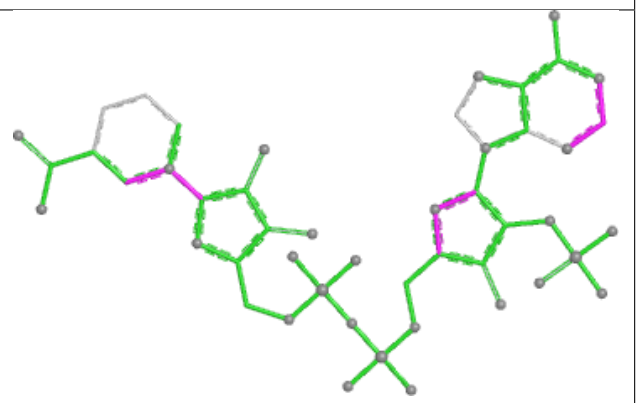


Rings

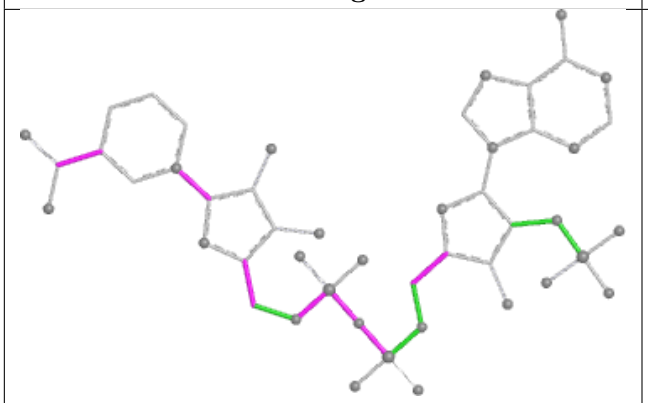
Ligand NDP D 401



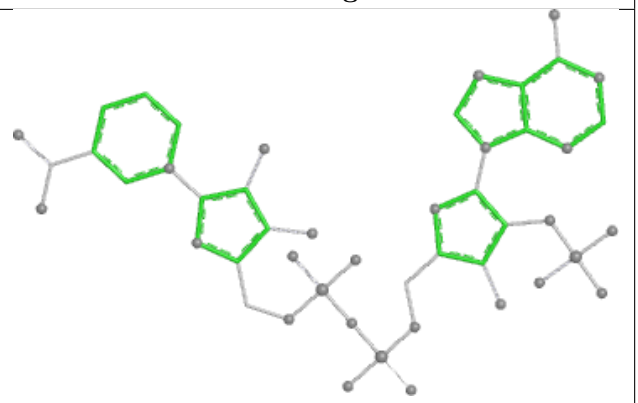
Bond lengths



Bond angles

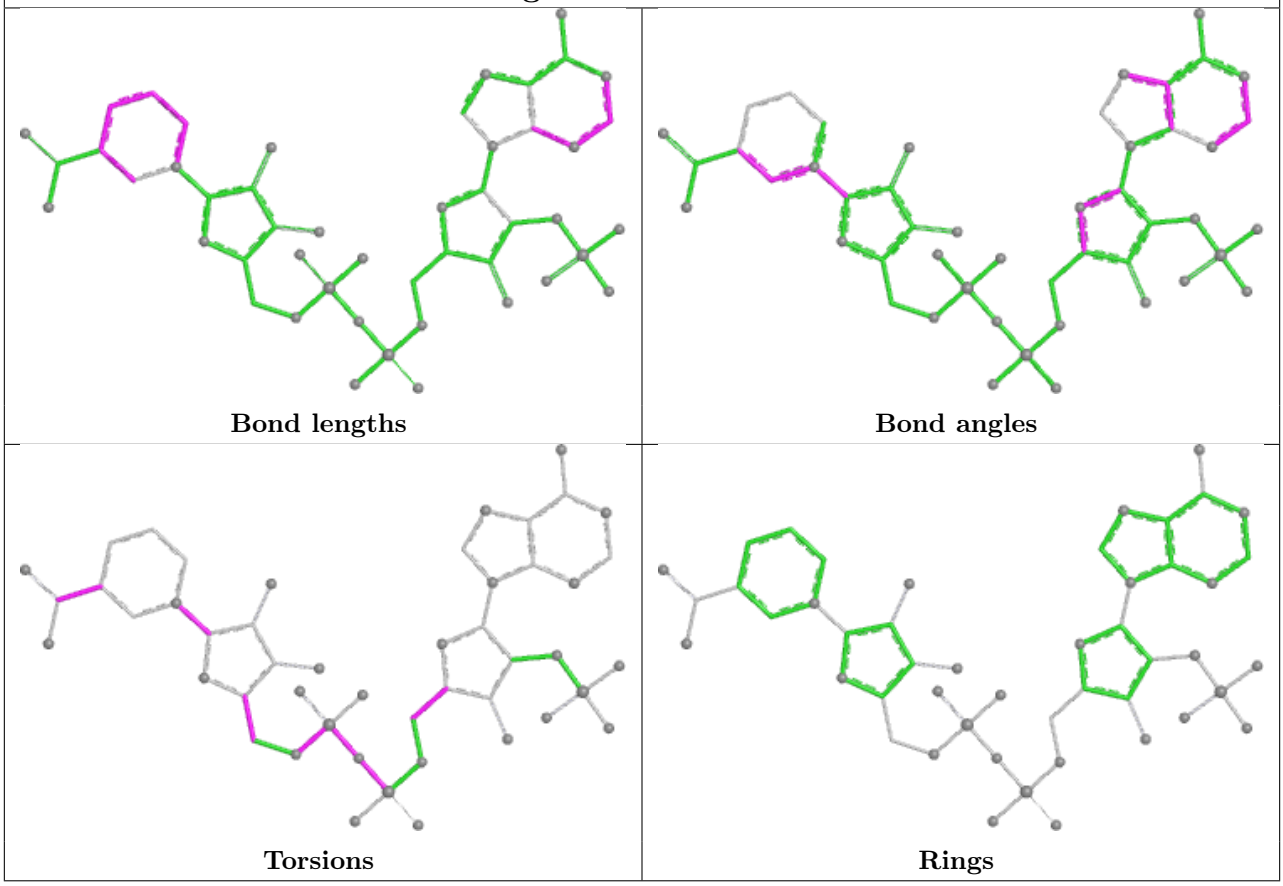


Torsions



Rings

Ligand NDP C 401



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	318/323 (98%)	-0.30	7 (2%)	62	59	15, 36, 50, 55	35 (11%)
1	B	318/323 (98%)	-0.22	7 (2%)	62	59	13, 37, 53, 59	47 (14%)
1	C	314/323 (97%)	-0.39	1 (0%)	94	94	14, 35, 51, 56	30 (9%)
1	D	314/323 (97%)	-0.34	4 (1%)	77	77	15, 36, 52, 57	34 (10%)
All	All	1264/1292 (97%)	-0.31	19 (1%)	73	73	13, 36, 52, 59	146 (11%)

All (19) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	320	LEU	3.2
1	B	249	ASN	3.1
1	B	225	GLY	3.0
1	B	237	ASP	2.8
1	A	275	GLU	2.7
1	B	275	GLU	2.6
1	D	133	GLU	2.5
1	B	243	SER	2.5
1	A	27	LEU	2.5
1	B	224	TYR	2.5
1	A	222	GLN	2.3
1	C	290	SER	2.3
1	B	6	HIS	2.2
1	A	255	ILE	2.1
1	A	32	SER	2.1
1	D	134	HIS	2.1
1	A	246	LYS	2.1
1	A	31	LYS	2.1
1	D	290	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 monosaccharides in this entry.

6.4 Ligands (i)

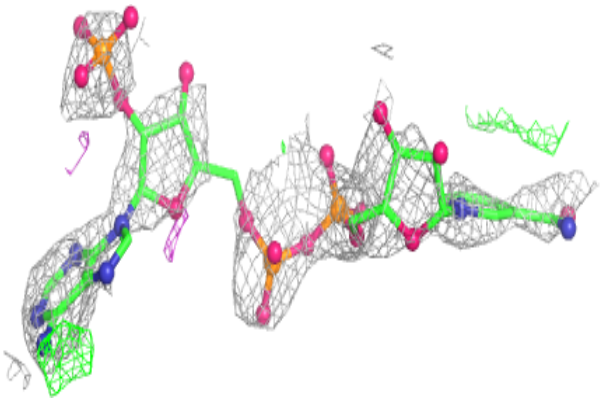
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

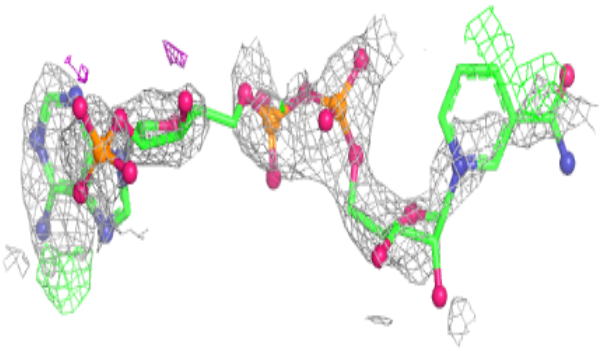
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	NDP	A	401	48/48	0.80	0.32	44,49,53,54	48
2	NDP	B	401	48/48	0.81	0.32	26,39,49,49	48
4	BME	C	501	4/4	0.89	0.16	59,60,60,61	4
3	ACT	D	324	4/4	0.93	0.21	17,19,20,20	0
2	NDP	C	401	48/48	0.94	0.16	29,43,55,57	0
2	NDP	D	401	48/48	0.94	0.17	32,46,52,53	27
3	ACT	C	324	4/4	0.96	0.14	20,22,23,23	0

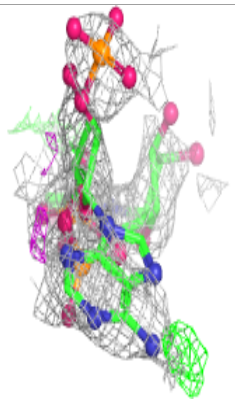
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around NDP A 401:

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

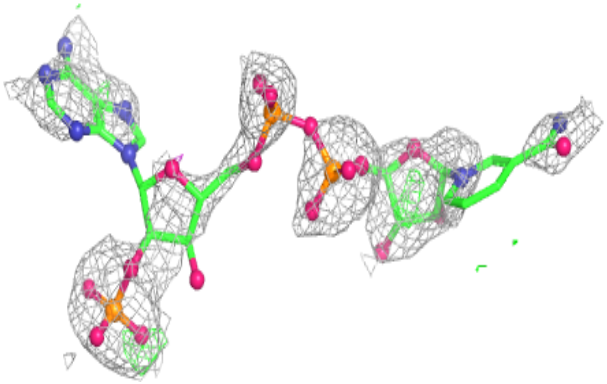


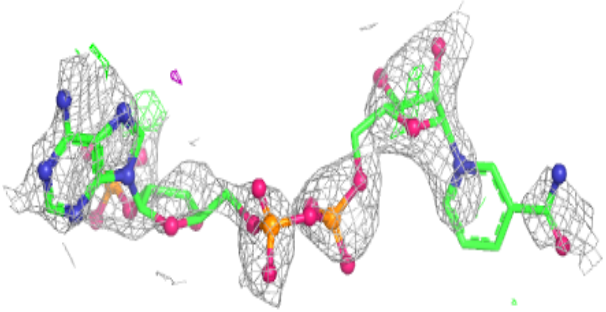


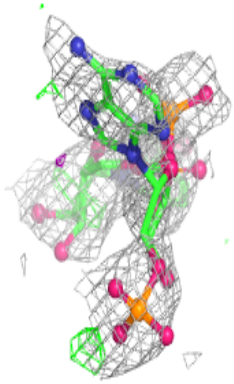


Electron density around NDP B 401:

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

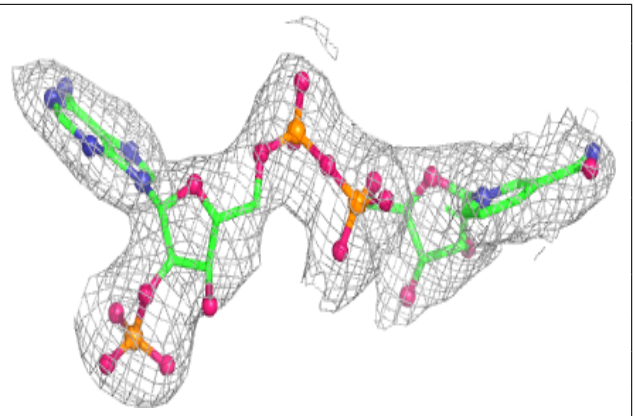


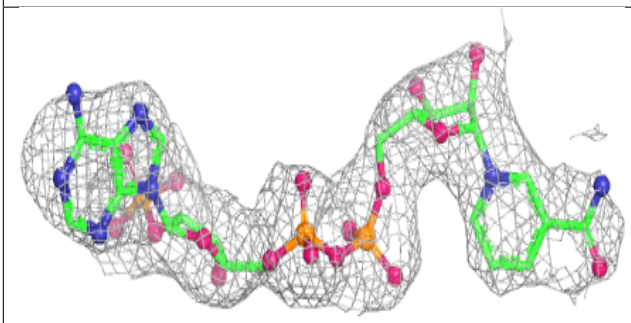


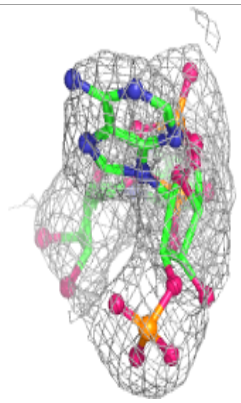


Electron density around NDP C 401:

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

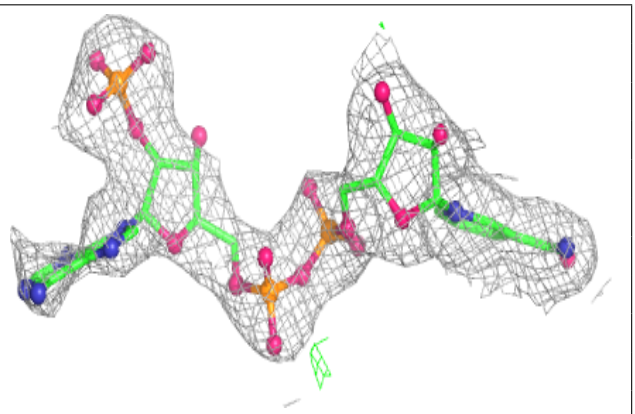


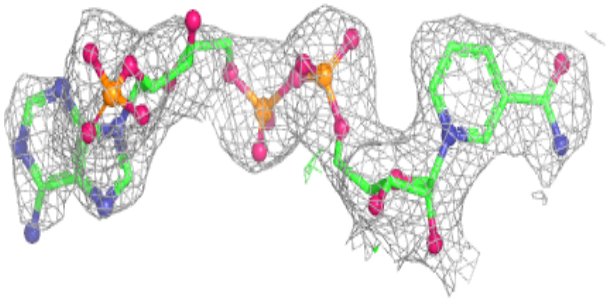


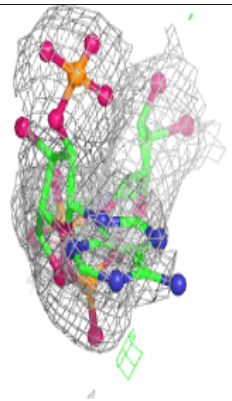


Electron density around NDP D 401:

$2mF_o$-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.