



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 21, 2024 – 10:20 am BST

PDB ID : 2BH9
Title : X-RAY STRUCTURE OF A DELETION VARIANT OF HUMAN GLUCOSE 6-PHOSPHATE DEHYDROGENASE COMPLEXED WITH STRUCTURAL AND COENZYME NADP
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Deposited on : 2005-01-08
Resolution : 2.50 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 : 4.02b-467
Mogul : 1.8.4, CSD as541be (2020)
Xtrriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36.2

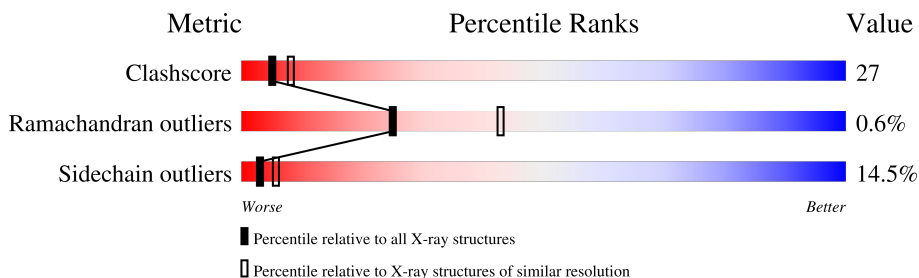
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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))
Clashscore	141614	5346 (2.50-2.50)
Ramachandran outliers	138981	5231 (2.50-2.50)
Sidechain outliers	138945	5233 (2.50-2.50)

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 $\leq 5\%$

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	489	

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 4241 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 GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	489	3971	2535	690	726	20	0	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	27	VAL	HIS	engineered mutation	UNP P11413

- Molecule 2 is NADP NICOTINAMIDE-ADENINE-DINUCLEOTIDE PHOSPHATE (three-letter code: NAP) (formula: C₂₁H₂₈N₇O₁₇P₃).



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

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	C O	0	0
			6	3 3		
3	A	1	Total	C O	0	0
			6	3 3		

- Molecule 4 is water.

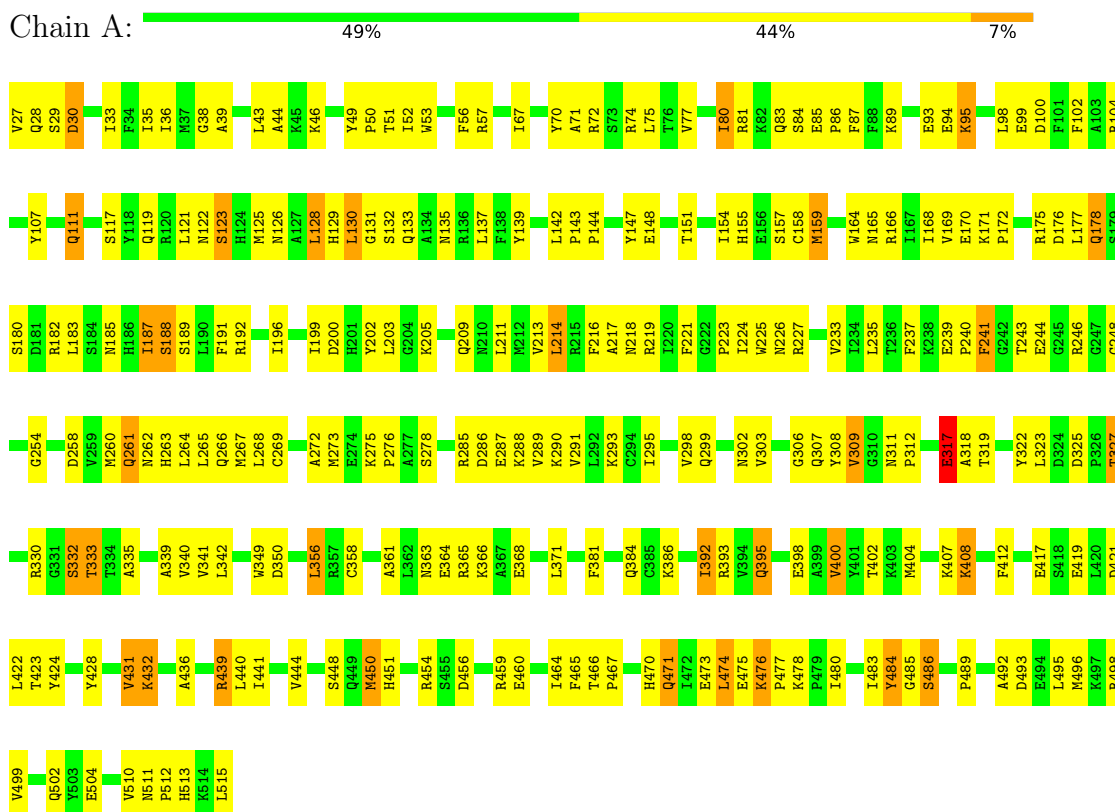
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	162	Total	O	0	0
			162	162		

3 Residue-property plots

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. 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. 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.

Note EDS was not executed.

- Molecule 1: GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE



4 Data and refinement statistics

Xtrriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	F 2 2 2	Depositor
Cell constants a, b, c, α , β , γ	60.76Å 172.48Å 217.22Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.70 – 2.50	Depositor
% Data completeness (in resolution range)	73.0 (29.70-2.50)	Depositor
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	BUSTER-TNT	Depositor
R, R_{free}	0.196 , 0.296	Depositor
Estimated twinning fraction	No twinning to report.	Xtrriage
Total number of atoms	4241	wwPDB-VP
Average B, all atoms (Å ²)	32.0	wwPDB-VP

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: GOL, NAP

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	1/4067 (0.0%)	0.63	0/5500

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	432	LYS	CB-CG	5.38	1.67	1.52

There are no bond angle outliers.

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	3971	0	3919	213	0
2	A	96	0	50	14	0
3	A	12	0	16	0	0
4	A	162	0	0	4	0
All	All	4241	0	3985	218	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 27.

All (218) 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:428:TYR:HB3	1:A:431:VAL:HG11	1.41	1.02
1:A:480:ILE:HG21	1:A:489:PRO:HB3	1.46	0.97
1:A:187:ILE:HD11	1:A:196:ILE:HD13	1.50	0.94
1:A:428:TYR:HB3	1:A:431:VAL:CG1	1.99	0.92
1:A:227:ARG:HE	1:A:350:ASP:HB3	1.37	0.89
1:A:81:ARG:HG3	1:A:102:PHE:CZ	2.09	0.87
1:A:311:ASN:HD22	1:A:312:PRO:HD2	1.41	0.84
1:A:311:ASN:ND2	1:A:312:PRO:HD2	1.95	0.81
1:A:187:ILE:HD11	1:A:196:ILE:CD1	2.12	0.80
1:A:170:GLU:CB	2:A:799:NAP:H1D	2.12	0.80
1:A:168:ILE:HD11	1:A:444:VAL:HG11	1.64	0.79
1:A:227:ARG:HG3	1:A:227:ARG:HH11	1.48	0.79
1:A:122:ASN:OD1	1:A:158:CYS:HA	1.83	0.78
1:A:265:LEU:HD22	1:A:465:PHE:HE2	1.51	0.74
1:A:142:LEU:HB3	1:A:143:PRO:HD2	1.70	0.73
1:A:480:ILE:CG2	1:A:489:PRO:HB3	2.19	0.73
1:A:81:ARG:HG3	1:A:102:PHE:CE2	2.24	0.72
1:A:27:VAL:C	1:A:28:GLN:HG2	2.09	0.71
1:A:144:PRO:HG3	1:A:172:PRO:HD2	1.73	0.71
1:A:287:GLU:OE1	1:A:290:LYS:HE2	1.90	0.71
1:A:260:MET:HE3	1:A:465:PHE:HE1	1.56	0.71
1:A:125:MET:O	1:A:128:LEU:HB2	1.90	0.70
1:A:471:GLN:HG2	4:A:2162:HOH:O	1.90	0.70
1:A:243:THR:HG23	1:A:308:TYR:OH	1.92	0.68
1:A:227:ARG:HG3	1:A:227:ARG:NH1	2.06	0.68
1:A:298:VAL:HG22	1:A:342:LEU:HD21	1.76	0.68
1:A:233:VAL:HG22	1:A:371:LEU:CD2	2.23	0.68
1:A:318:ALA:HB1	1:A:484:TYR:CD1	2.29	0.67
1:A:57:ARG:HD2	1:A:94:GLU:OE2	1.95	0.67
1:A:408:LYS:HE2	1:A:412:PHE:CE1	2.30	0.67
1:A:240:PRO:HD2	1:A:241:PHE:CD1	2.31	0.66
1:A:269:CYS:O	1:A:273:MET:HB3	1.95	0.66
1:A:100:ASP:O	1:A:104:ARG:HG3	1.95	0.66
1:A:164:TRP:CE3	1:A:166:ARG:HG3	2.32	0.65
1:A:67:ILE:HD12	1:A:67:ILE:N	2.12	0.64
1:A:273:MET:HE3	1:A:287:GLU:HB2	1.79	0.64
1:A:85:GLU:N	1:A:86:PRO:HD2	2.12	0.64
1:A:170:GLU:HB3	2:A:799:NAP:H1D	1.79	0.64
1:A:219:ARG:O	1:A:223:PRO:HD2	1.97	0.64
1:A:254:GLY:O	1:A:258:ASP:HB2	1.97	0.64
1:A:209:GLN:HE22	1:A:439:ARG:HD2	1.61	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:51:THR:HG21	1:A:441:ILE:HD12	1.80	0.64
1:A:233:VAL:HG22	1:A:371:LEU:HD23	1.79	0.63
1:A:264:LEU:HB3	1:A:356:LEU:HD13	1.80	0.63
1:A:170:GLU:HB2	4:A:2057:HOH:O	1.98	0.63
1:A:30:ASP:OD1	1:A:30:ASP:N	2.32	0.62
1:A:72:ARG:HH21	2:A:799:NAP:C2A	2.12	0.62
1:A:240:PRO:HD2	1:A:241:PHE:HD1	1.64	0.62
1:A:239:GLU:OE1	1:A:365:ARG:HG3	1.99	0.62
1:A:289:VAL:HG23	1:A:460:GLU:HG3	1.82	0.61
1:A:276:PRO:HB2	1:A:278:SER:O	2.01	0.61
1:A:248:GLY:N	1:A:327:THR:HG23	2.15	0.61
1:A:70:TYR:CD1	1:A:121:LEU:HD22	2.36	0.60
1:A:35:ILE:HD12	1:A:35:ILE:H	1.67	0.60
1:A:95:LYS:O	1:A:99:GLU:HG2	2.02	0.60
1:A:466:THR:HB	1:A:467:PRO:HD3	1.84	0.60
1:A:470:HIS:O	1:A:473:GLU:HB2	2.02	0.59
1:A:187:ILE:CD1	1:A:196:ILE:HD13	2.31	0.59
1:A:70:TYR:OH	1:A:117:SER:HB3	2.03	0.58
1:A:365:ARG:NH2	1:A:395:GLN:HG3	2.17	0.58
1:A:49:TYR:N	1:A:50:PRO:HD2	2.18	0.58
1:A:303:VAL:HG22	1:A:340:VAL:HG22	1.84	0.58
1:A:408:LYS:HB3	1:A:412:PHE:HB2	1.84	0.58
1:A:144:PRO:HA	1:A:147:TYR:CE2	2.39	0.57
1:A:363:ASN:HB3	1:A:485:GLY:O	2.04	0.57
1:A:77:VAL:HG23	4:A:2013:HOH:O	2.02	0.57
1:A:213:VAL:O	1:A:217:ALA:HB3	2.04	0.57
1:A:187:ILE:HD11	1:A:196:ILE:CG1	2.35	0.56
1:A:243:THR:HG21	1:A:322:TYR:CD1	2.40	0.56
1:A:365:ARG:HH21	1:A:395:GLN:HG3	1.70	0.56
1:A:272:ALA:HA	1:A:349:TRP:CZ2	2.41	0.56
1:A:177:LEU:HB3	1:A:178:GLN:NE2	2.21	0.56
1:A:137:LEU:HD21	1:A:444:VAL:HG12	1.87	0.56
1:A:27:VAL:HG12	1:A:27:VAL:O	2.06	0.55
1:A:81:ARG:O	1:A:85:GLU:HB2	2.07	0.55
1:A:214:LEU:HD23	1:A:392:ILE:CD1	2.36	0.55
1:A:137:LEU:CD2	1:A:444:VAL:HG12	2.37	0.55
1:A:265:LEU:HD22	1:A:465:PHE:CE2	2.38	0.55
1:A:330:ARG:HA	1:A:330:ARG:NE	2.22	0.55
1:A:263:HIS:O	1:A:267:MET:HG3	2.06	0.55
1:A:119:GLN:HE22	1:A:157:SER:HB2	1.70	0.55
1:A:144:PRO:HA	1:A:147:TYR:CZ	2.42	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:183:LEU:O	1:A:187:ILE:HG23	2.07	0.55
1:A:456:ASP:O	1:A:460:GLU:HG2	2.07	0.54
1:A:248:GLY:H	1:A:327:THR:CG2	2.20	0.54
1:A:408:LYS:HD3	1:A:412:PHE:CG	2.42	0.54
1:A:51:THR:CG2	1:A:441:ILE:HD12	2.38	0.54
1:A:244:GLU:O	1:A:244:GLU:HG3	2.07	0.54
1:A:260:MET:CE	1:A:465:PHE:HE1	2.19	0.54
1:A:248:GLY:N	1:A:327:THR:CG2	2.71	0.54
1:A:123:SER:HA	1:A:126:ASN:HD22	1.71	0.53
1:A:43:LEU:HD22	2:A:799:NAP:O4D	2.08	0.53
1:A:474:LEU:HG	1:A:475:GLU:HG2	1.90	0.53
1:A:71:ALA:HB3	1:A:107:TYR:OH	2.09	0.53
1:A:170:GLU:HB2	2:A:799:NAP:H1D	1.90	0.53
1:A:178:GLN:HE21	1:A:178:GLN:N	2.07	0.53
1:A:93:GLU:CD	1:A:93:GLU:H	2.12	0.52
1:A:170:GLU:HB3	2:A:799:NAP:H6N	1.92	0.52
1:A:129:HIS:CE1	1:A:130:LEU:HD22	2.44	0.52
1:A:33:ILE:HD13	1:A:125:MET:HB3	1.91	0.52
1:A:368:GLU:HG3	1:A:393:ARG:HA	1.91	0.51
1:A:423:THR:HG22	1:A:423:THR:O	2.10	0.51
1:A:216:PHE:CD1	1:A:275:LYS:HG3	2.45	0.51
1:A:203:LEU:HB3	1:A:451:HIS:HB3	1.92	0.51
1:A:38:GLY:CA	1:A:142:LEU:HD21	2.41	0.51
1:A:159:MET:HG3	1:A:165:ASN:ND2	2.26	0.51
1:A:227:ARG:NE	1:A:350:ASP:HB3	2.17	0.51
1:A:237:PHE:O	1:A:358:CYS:HA	2.09	0.51
1:A:330:ARG:HA	1:A:330:ARG:HE	1.76	0.51
1:A:72:ARG:HG2	1:A:111:GLN:HA	1.92	0.51
1:A:325:ASP:OD1	1:A:327:THR:HB	2.11	0.50
1:A:400:VAL:HG13	1:A:422:LEU:HD23	1.94	0.50
1:A:125:MET:O	1:A:131:GLY:HA3	2.12	0.50
1:A:361:ALA:O	1:A:485:GLY:N	2.45	0.50
1:A:218:ASN:HD22	1:A:221:PHE:HD2	1.59	0.50
1:A:81:ARG:NH2	1:A:98:LEU:HD23	2.26	0.50
1:A:154:ILE:HG22	1:A:155:HIS:N	2.27	0.50
1:A:448:SER:HB3	1:A:450:MET:CE	2.41	0.50
1:A:285:ARG:NH1	1:A:454:ARG:CB	2.75	0.49
1:A:309:VAL:HG23	1:A:483:ILE:HD13	1.95	0.49
1:A:319:THR:HG22	1:A:319:THR:O	2.12	0.49
1:A:187:ILE:HG13	1:A:188:SER:N	2.23	0.49
1:A:493:ASP:HA	1:A:496:MET:HE2	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:85:GLU:N	1:A:86:PRO:CD	2.77	0.48
1:A:81:ARG:HG3	1:A:102:PHE:CE1	2.48	0.48
1:A:510:VAL:HG23	1:A:510:VAL:O	2.13	0.48
1:A:273:MET:HE3	1:A:287:GLU:CB	2.42	0.48
1:A:291:VAL:O	1:A:295:ILE:HD12	2.14	0.48
1:A:289:VAL:O	1:A:293:LYS:HG3	2.13	0.47
2:A:811:NAP:H3D	2:A:811:NAP:O1N	2.13	0.47
1:A:35:ILE:HD12	1:A:35:ILE:N	2.27	0.47
1:A:38:GLY:HA3	1:A:142:LEU:CD2	2.44	0.47
1:A:235:LEU:HD11	1:A:268:LEU:HA	1.96	0.47
1:A:243:THR:CG2	1:A:322:TYR:CD1	2.97	0.47
1:A:147:TYR:O	1:A:151:THR:HG23	2.14	0.47
1:A:178:GLN:NE2	1:A:178:GLN:H	2.13	0.47
1:A:224:ILE:HG13	1:A:224:ILE:O	2.15	0.47
1:A:285:ARG:O	1:A:289:VAL:HG12	2.14	0.47
2:A:799:NAP:H2N	2:A:799:NAP:C3D	2.44	0.47
1:A:237:PHE:CD1	1:A:237:PHE:C	2.88	0.47
1:A:323:LEU:O	1:A:330:ARG:NH1	2.48	0.47
1:A:67:ILE:N	1:A:67:ILE:CD1	2.78	0.47
1:A:241:PHE:CD1	1:A:241:PHE:N	2.83	0.46
1:A:260:MET:CE	1:A:465:PHE:CE1	2.99	0.46
1:A:298:VAL:HG22	1:A:342:LEU:CD2	2.44	0.46
1:A:476:LYS:O	1:A:476:LYS:HG2	2.16	0.46
1:A:39:ALA:O	1:A:44:ALA:HB3	2.16	0.46
1:A:421:ASP:OD1	2:A:811:NAP:N7N	2.49	0.46
1:A:139:TYR:CE2	1:A:168:ILE:HG21	2.51	0.46
1:A:128:LEU:O	1:A:131:GLY:N	2.48	0.46
1:A:49:TYR:N	1:A:50:PRO:CD	2.80	0.45
1:A:402:THR:O	1:A:419:GLU:HB2	2.14	0.45
1:A:456:ASP:N	1:A:456:ASP:OD1	2.47	0.45
1:A:175:ARG:HB3	1:A:175:ARG:NH1	2.32	0.45
1:A:148:GLU:HB2	4:A:2052:HOH:O	2.17	0.45
1:A:285:ARG:HH11	1:A:454:ARG:HB2	1.82	0.45
1:A:261:GLN:HE21	1:A:261:GLN:HB3	1.56	0.45
1:A:298:VAL:HG23	1:A:464:ILE:O	2.17	0.45
1:A:178:GLN:HE21	1:A:178:GLN:H	1.65	0.45
1:A:386:LYS:HE3	1:A:504:GLU:OE1	2.16	0.45
1:A:159:MET:CE	1:A:191:PHE:CE2	3.00	0.44
1:A:302:ASN:OD1	1:A:498:ARG:NH2	2.51	0.44
1:A:307:GLN:HB2	1:A:335:ALA:HA	2.00	0.44
1:A:306:GLY:O	1:A:335:ALA:HB1	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:424:TYR:HD1	1:A:424:TYR:H	1.65	0.44
1:A:474:LEU:HG	1:A:474:LEU:O	2.17	0.44
1:A:476:LYS:N	1:A:477:PRO:CD	2.80	0.44
1:A:144:PRO:HG3	1:A:172:PRO:CD	2.45	0.44
1:A:285:ARG:NH1	1:A:454:ARG:HB2	2.32	0.44
1:A:137:LEU:HD22	1:A:444:VAL:CG1	2.47	0.44
1:A:203:LEU:HD11	1:A:266:GLN:HG3	2.00	0.44
2:A:811:NAP:H71N	2:A:811:NAP:H4N	1.55	0.44
1:A:248:GLY:H	1:A:327:THR:HG23	1.81	0.43
1:A:339:ALA:HA	1:A:356:LEU:O	2.18	0.43
1:A:480:ILE:HG21	1:A:489:PRO:CB	2.32	0.43
1:A:480:ILE:HG22	1:A:489:PRO:HG3	2.00	0.43
1:A:169:VAL:HG12	1:A:170:GLU:N	2.33	0.43
1:A:275:LYS:HA	1:A:276:PRO:HD3	1.89	0.43
1:A:428:TYR:O	1:A:431:VAL:HG13	2.17	0.43
1:A:400:VAL:CG1	1:A:422:LEU:HD23	2.49	0.43
1:A:492:ALA:O	1:A:496:MET:HG3	2.19	0.43
1:A:436:ALA:O	1:A:440:LEU:HG	2.18	0.43
1:A:46:LYS:HG2	1:A:87:PHE:CE1	2.54	0.43
1:A:366:LYS:HA	1:A:395:GLN:O	2.18	0.43
1:A:476:LYS:O	1:A:476:LYS:CG	2.67	0.43
1:A:36:ILE:HG22	1:A:39:ALA:HA	2.01	0.42
1:A:159:MET:HG3	1:A:165:ASN:CG	2.39	0.42
1:A:363:ASN:ND2	1:A:364:GLU:HG2	2.34	0.42
1:A:43:LEU:HB3	2:A:799:NAP:H52N	2.00	0.42
1:A:511:ASN:OD1	1:A:512:PRO:CD	2.68	0.42
1:A:119:GLN:NE2	1:A:157:SER:HB2	2.34	0.42
2:A:799:NAP:H8A	2:A:799:NAP:O5B	2.20	0.42
1:A:53:TRP:O	1:A:56:PHE:HB3	2.19	0.42
1:A:287:GLU:O	1:A:291:VAL:HG23	2.20	0.42
1:A:323:LEU:HD21	1:A:332:SER:H	1.84	0.42
1:A:175:ARG:HB3	1:A:175:ARG:HH11	1.84	0.41
1:A:318:ALA:CB	1:A:484:TYR:CE1	3.03	0.41
1:A:202:TYR:CE1	1:A:205:LYS:NZ	2.81	0.41
2:A:799:NAP:O2N	2:A:799:NAP:H3D	2.20	0.41
1:A:171:LYS:HB2	1:A:171:LYS:HE3	1.85	0.41
1:A:333:THR:HG23	1:A:333:THR:O	2.19	0.41
1:A:185:ASN:O	1:A:189:SER:HB3	2.21	0.41
1:A:330:ARG:HE	1:A:330:ARG:CA	2.32	0.41
1:A:341:VAL:HG11	1:A:499:VAL:HG11	2.03	0.41
1:A:512:PRO:HB2	1:A:515:LEU:HD21	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:80:ILE:HD12	1:A:80:ILE:HA	1.76	0.41
1:A:243:THR:HG21	1:A:322:TYR:CE1	2.55	0.41
1:A:72:ARG:NH2	2:A:799:NAP:C2A	2.83	0.41
1:A:135:ASN:HB3	1:A:164:TRP:CE2	2.55	0.41
1:A:273:MET:CE	1:A:287:GLU:HB2	2.48	0.41
1:A:317:GLU:H	1:A:317:GLU:HG3	1.55	0.41
1:A:381:PHE:O	1:A:384:GLN:HG3	2.20	0.41
1:A:38:GLY:CA	1:A:142:LEU:CD2	3.00	0.40
1:A:386:LYS:CE	1:A:504:GLU:OE1	2.70	0.40
1:A:200:ASP:OD1	1:A:202:TYR:HB2	2.21	0.40
1:A:211:LEU:HD23	1:A:392:ILE:HD12	2.03	0.40
1:A:166:ARG:NH1	1:A:444:VAL:O	2.53	0.40
1:A:381:PHE:O	1:A:384:GLN:CG	2.70	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	487/489 (100%)	440 (90%)	44 (9%)	3 (1%)	25	43

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	317	GLU
1	A	484	TYR
1	A	486	SER

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	429/429 (100%)	367 (86%)	62 (14%)	3 6

All (62) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	29	SER
1	A	30	ASP
1	A	52	ILE
1	A	74	ARG
1	A	75	LEU
1	A	80	ILE
1	A	83	GLN
1	A	84	SER
1	A	89	LYS
1	A	95	LYS
1	A	111	GLN
1	A	123	SER
1	A	128	LEU
1	A	130	LEU
1	A	132	SER
1	A	133	GLN
1	A	159	MET
1	A	176	ASP
1	A	178	GLN
1	A	180	SER
1	A	182	ARG
1	A	187	ILE
1	A	188	SER
1	A	192	ARG
1	A	199	ILE
1	A	214	LEU
1	A	225	TRP
1	A	226	ASN
1	A	241	PHE
1	A	246	ARG

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Mol	Chain	Res	Type
1	A	261	GLN
1	A	262	ASN
1	A	286	ASP
1	A	288	LYS
1	A	299	GLN
1	A	309	VAL
1	A	317	GLU
1	A	327	THR
1	A	332	SER
1	A	333	THR
1	A	356	LEU
1	A	392	ILE
1	A	395	GLN
1	A	398	GLU
1	A	400	VAL
1	A	404	MET
1	A	407	LYS
1	A	408	LYS
1	A	417	GLU
1	A	431	VAL
1	A	432	LYS
1	A	439	ARG
1	A	450	MET
1	A	459	ARG
1	A	471	GLN
1	A	474	LEU
1	A	476	LYS
1	A	478	LYS
1	A	486	SER
1	A	495	LEU
1	A	502	GLN
1	A	513	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	83	GLN
1	A	111	GLN
1	A	119	GLN
1	A	126	ASN
1	A	129	HIS
1	A	178	GLN

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Mol	Chain	Res	Type
1	A	218	ASN
1	A	229	ASN
1	A	261	GLN
1	A	301	ASN
1	A	311	ASN
1	A	388	ASN
1	A	471	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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

4 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	$\# Z > 2$
3	GOL	A	1516	-	5,5,5	0.55	0	5,5,5	0.42	0
2	NAP	A	811	-	45,52,52	1.34	3 (6%)	56,80,80	1.60	12 (21%)
3	GOL	A	1517	-	5,5,5	0.47	0	5,5,5	0.26	0
2	NAP	A	799	-	45,52,52	1.36	6 (13%)	56,80,80	1.75	11 (19%)

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
3	GOL	A	1516	-	-	2/4/4/4	-
2	NAP	A	811	-	-	2/31/67/67	0/5/5/5
3	GOL	A	1517	-	-	2/4/4/4	-
2	NAP	A	799	-	-	13/31/67/67	0/5/5/5

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	799	NAP	C2N-N1N	-4.94	1.28	1.35
2	A	811	NAP	C2N-N1N	-4.85	1.29	1.35
2	A	811	NAP	C2N-C3N	-3.36	1.33	1.39
2	A	799	NAP	C2N-C3N	-2.67	1.34	1.39
2	A	799	NAP	C2D-C3D	-2.61	1.46	1.53
2	A	799	NAP	C7N-N7N	2.52	1.37	1.33
2	A	799	NAP	C6N-N1N	-2.47	1.29	1.35
2	A	799	NAP	C4N-C3N	-2.28	1.35	1.39
2	A	811	NAP	C6A-C5A	-2.16	1.35	1.43

All (23) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	799	NAP	C3N-C7N-N7N	-5.80	110.79	117.75
2	A	799	NAP	C4N-C3N-C7N	-4.04	110.24	121.04
2	A	799	NAP	C2N-C3N-C7N	3.99	131.06	119.46
2	A	811	NAP	O7N-C7N-N7N	3.94	128.17	122.58
2	A	799	NAP	C3D-C2D-C1D	3.70	106.55	100.98
2	A	799	NAP	O7N-C7N-N7N	3.68	127.80	122.58
2	A	811	NAP	C3N-C2N-N1N	3.57	123.92	120.43
2	A	811	NAP	C3N-C7N-N7N	-3.43	113.63	117.75
2	A	811	NAP	C4N-C3N-C7N	-3.42	111.89	121.04
2	A	811	NAP	C3D-C2D-C1D	3.37	106.05	100.98
2	A	811	NAP	C2N-C3N-C7N	3.36	129.23	119.46
2	A	811	NAP	C6N-N1N-C2N	-3.14	119.11	121.97
2	A	799	NAP	C6N-N1N-C2N	-3.04	119.20	121.97
2	A	811	NAP	C4A-C5A-N7A	2.76	112.28	109.40
2	A	799	NAP	C5A-C6A-N6A	2.71	124.46	120.35
2	A	799	NAP	C4A-C5A-N7A	2.46	111.97	109.40
2	A	799	NAP	C3N-C2N-N1N	2.37	122.75	120.43
2	A	811	NAP	C5D-C4D-C3D	-2.33	106.44	115.18

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	811	NAP	O7N-C7N-C3N	-2.23	116.96	119.63
2	A	811	NAP	C2B-C3B-C4B	2.21	106.79	101.99
2	A	799	NAP	O2B-P2B-O1X	-2.16	101.05	109.39
2	A	811	NAP	C5A-C6A-N6A	2.16	123.63	120.35
2	A	799	NAP	C2B-C3B-C4B	2.14	106.64	101.99

There are no chirality outliers.

All (19) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	799	NAP	C2B-O2B-P2B-O3X
2	A	799	NAP	C5D-O5D-PN-O3
2	A	799	NAP	C5D-O5D-PN-O2N
2	A	799	NAP	O4D-C1D-N1N-C2N
3	A	1517	GOL	O1-C1-C2-C3
2	A	811	NAP	O4B-C4B-C5B-O5B
2	A	811	NAP	C3B-C4B-C5B-O5B
3	A	1516	GOL	O1-C1-C2-C3
3	A	1517	GOL	O1-C1-C2-O2
2	A	799	NAP	O4D-C4D-C5D-O5D
2	A	799	NAP	C4N-C3N-C7N-N7N
2	A	799	NAP	C3D-C4D-C5D-O5D
2	A	799	NAP	C2N-C3N-C7N-N7N
2	A	799	NAP	C5B-O5B-PA-O3
3	A	1516	GOL	O1-C1-C2-O2
2	A	799	NAP	C5D-O5D-PN-O1N
2	A	799	NAP	C4D-C5D-O5D-PN
2	A	799	NAP	PN-O3-PA-O1A
2	A	799	NAP	PA-O3-PN-O1N

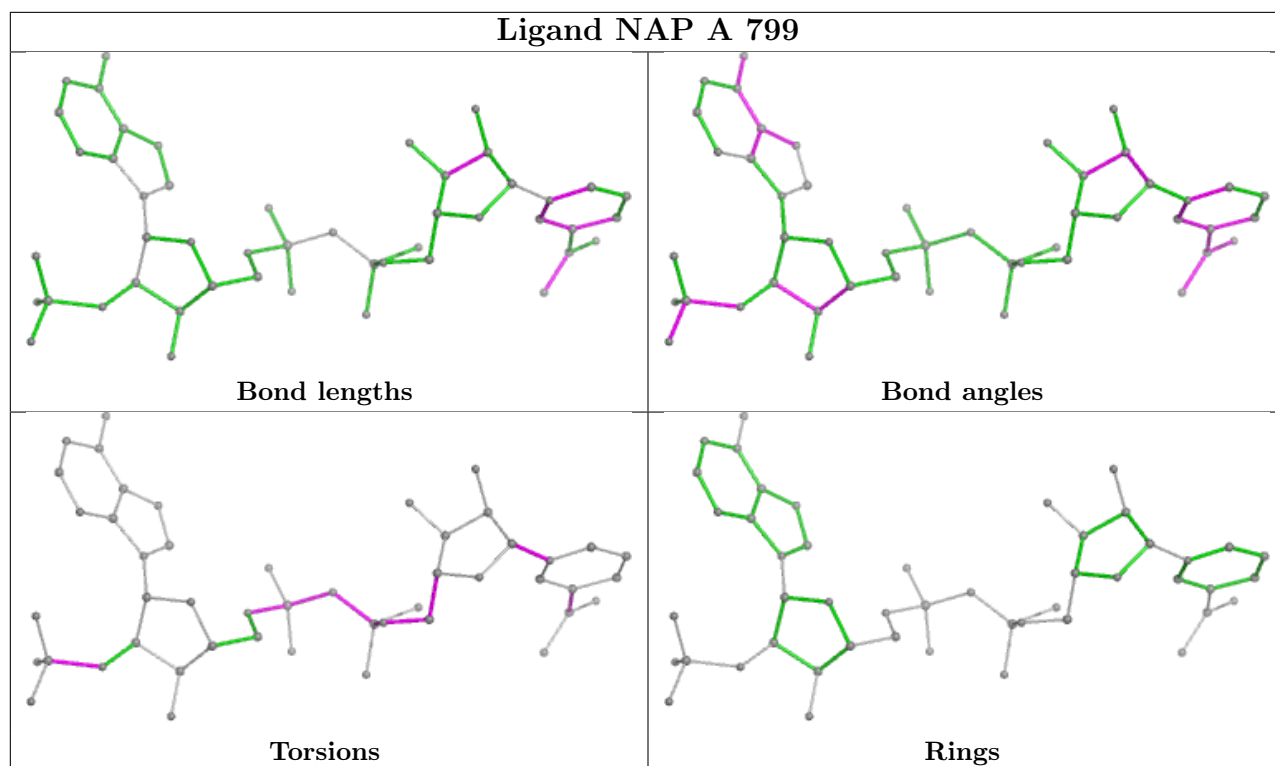
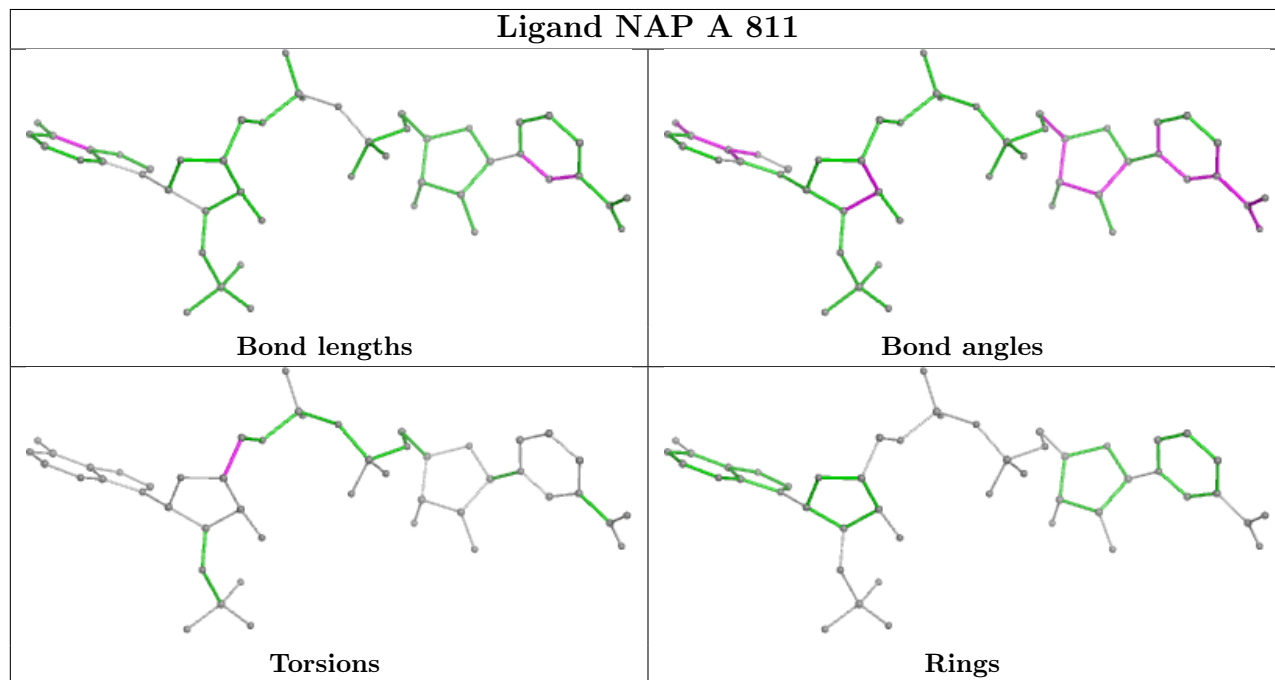
There are no ring outliers.

2 monomers are involved in 14 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	811	NAP	3	0
2	A	799	NAP	11	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 [i](#)

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

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates [i](#)

EDS was not executed - this section is therefore empty.

6.4 Ligands [i](#)

EDS was not executed - this section is therefore empty.

6.5 Other polymers [i](#)

EDS was not executed - this section is therefore empty.