



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 05:33 AM GMT

PDB ID : 2R8V
Title : Native structure of N-acetylglutamate synthase from *Neisseria gonorrhoeae*
Authors : Shi, D.; Sagar, V.; Jin, Z.; Yu, X.; Caldovic, L.; Morizono, H.; Allewell, N.M.;
Tuchman, M.
Deposited on : 2007-09-11
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
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

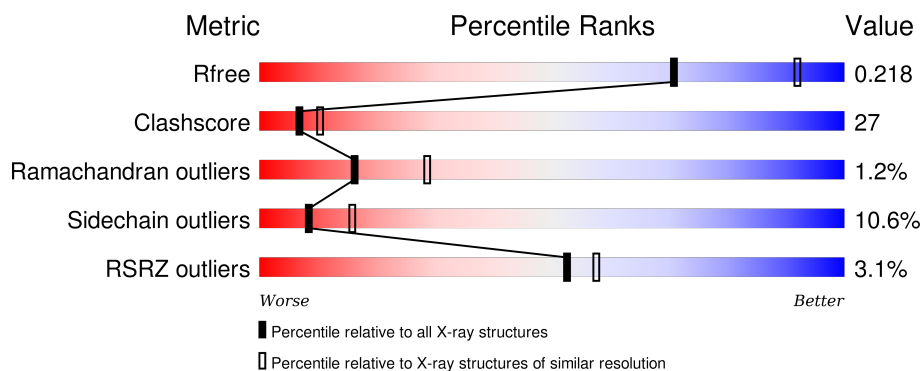
1 Overall quality at a glance

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))
R_{free}	91344	3553 (2.50-2.50)
Clashscore	102246	4242 (2.50-2.50)
Ramachandran outliers	100387	4156 (2.50-2.50)
Sidechain outliers	100360	4158 (2.50-2.50)
RSRZ outliers	91569	3562 (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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	456	<div> <div>3%</div> <div>57%</div> <div>30%</div> <div>5%</div> <div>7%</div> </div>

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
2	ACO	A	601	X	-	-	-

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 3395 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.

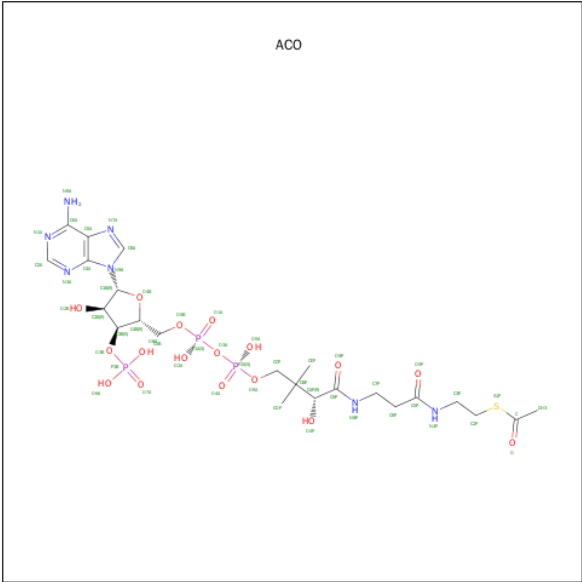
- Molecule 1 is a protein called Putative acetylglutamate synthase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	424	Total	C	N	O	S	0	0	0
			3227	2012	595	611	9			

There are 23 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	MET	-	EXPRESSION TAG	UNP Q5FAK7
A	-18	GLY	-	EXPRESSION TAG	UNP Q5FAK7
A	-17	SER	-	EXPRESSION TAG	UNP Q5FAK7
A	-16	SER	-	EXPRESSION TAG	UNP Q5FAK7
A	-15	HIS	-	EXPRESSION TAG	UNP Q5FAK7
A	-14	HIS	-	EXPRESSION TAG	UNP Q5FAK7
A	-13	HIS	-	EXPRESSION TAG	UNP Q5FAK7
A	-12	HIS	-	EXPRESSION TAG	UNP Q5FAK7
A	-11	HIS	-	EXPRESSION TAG	UNP Q5FAK7
A	-10	HIS	-	EXPRESSION TAG	UNP Q5FAK7
A	-9	SER	-	EXPRESSION TAG	UNP Q5FAK7
A	-8	SER	-	EXPRESSION TAG	UNP Q5FAK7
A	-7	GLY	-	EXPRESSION TAG	UNP Q5FAK7
A	-6	LEU	-	EXPRESSION TAG	UNP Q5FAK7
A	-5	VAL	-	EXPRESSION TAG	UNP Q5FAK7
A	-4	PRO	-	EXPRESSION TAG	UNP Q5FAK7
A	-3	ARG	-	EXPRESSION TAG	UNP Q5FAK7
A	-2	GLY	-	EXPRESSION TAG	UNP Q5FAK7
A	-1	SER	-	EXPRESSION TAG	UNP Q5FAK7
A	0	HIS	-	EXPRESSION TAG	UNP Q5FAK7
A	312	ILE	VAL	ENGINEERED	UNP Q5FAK7
A	336	ASN	ASP	ENGINEERED	UNP Q5FAK7
A	427	SER	PRO	ENGINEERED	UNP Q5FAK7

- Molecule 2 is ACETYL COENZYME *A (three-letter code: ACO) (formula: C₂₃H₃₈N₇O₁₇P₃S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	
2	A	1	Total	C	N	O	P	S	0	0
			51	23	7	17	3	1		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	117	Total	O	0	0
			117	117		

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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 ($\text{RSRZ} > 2$). 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.

Chain A:

Row 1	Row 2	Row 3	Row 4
L337	V253	T153	MET
Y338	H254	D154	GLY
G339	R255	T155	GLY
C340	V256	L158	SER
K344	Q257	R159	SER
D350	L258	N166	HIS
E353	G265	M170	HIS
I354	S266	P171	HIS
S360	L267	P172	HIS
P361	L268	L173	SER
Q362	Q269	L177	GLY
K363	E270	S176	LEU
D365	R274	F182	VAL
R371	V275	D185	PRO
L372	G276	Q188	ARG
L373	L277	E200	GLY
A374	R278	K201	SER
E375	F286	L202	HIS
I376	S287	T206	MET
D378	G288	L207	ASN
L388	T289	R213	ALA
T393	Q291	P214	ALA
N394	A292	D215	PRO
T395	H293	G216	P5
G396	S294	T217	V8
E397	L297	E220	F11
R402	A301	S223	A12
G403	I304	A224	A13
F404	R305	Q225	A14
A405	E308	E226	A15
T406	G311	A227	P16
A408	L312	A231	P17
E409	L313	E232	M21
L412	L314	S236	T24
R417	R316	E237	T25
K418	S317	T238	L26
R425	R318	R239	T30
I429	E319	M144	D31
L430	V320	E145	R33
V431	L321	Y146	I34
H435	E322	V246	L35
R436	N323	L249	G38
	H324	E250	T39
	T330		L40
			R41
			K42
			L43
			G48
			L49
			I50
			S51

4 Data and refinement statistics

Property	Value	Source
Space group	P 3 1 2	Depositor
Cell constants a, b, c, α , β , γ	98.66 Å 98.66 Å 89.75 Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	20.00 – 2.50 19.87 – 2.50	Depositor EDS
% Data completeness (in resolution range)	98.9 (20.00-2.50) 99.1 (19.87-2.50)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.55 (at 2.50 Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.192 , 0.252 0.191 , 0.218	Depositor DCC
R_{free} test set	835 reflections (5.08%)	DCC
Wilson B-factor (Å ²)	54.3	Xtriage
Anisotropy	0.346	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.27 , 49.5	EDS
Estimated twinning fraction	0.053 for -h,-k,l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 17270 reflections	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	3395	wwPDB-VP
Average B, all atoms (Å ²)	27.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.56% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 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: ACO

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	0.57	0/3280	1.01	6/4433 (0.1%)

There are no bond length outliers.

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	402	ARG	NE-CZ-NH2	-7.46	116.57	120.30
1	A	259	LEU	CB-CG-CD2	-6.73	99.55	111.00
1	A	110	LEU	CA-CB-CG	5.51	127.97	115.30
1	A	425	ARG	NE-CZ-NH1	-5.40	117.60	120.30
1	A	431	VAL	CB-CA-C	-5.17	101.58	111.40
1	A	151	ARG	NE-CZ-NH1	-5.02	117.79	120.30

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	3227	0	3208	172	1
2	A	51	0	34	12	0
3	A	117	0	0	27	1
All	All	3395	0	3242	175	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 27.

All (175) 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:304:ILE:HD11	1:A:313:LEU:CD1	1.55	1.35
1:A:304:ILE:CD1	1:A:313:LEU:HD12	1.78	1.12
1:A:316:ARG:HG2	1:A:317:SER:N	1.57	1.11
1:A:82:ARG:HH11	1:A:82:ARG:HG2	0.94	1.06
1:A:239:ARG:NH2	1:A:243:SER:HB2	1.71	1.04
1:A:320:TYR:OH	1:A:344:LYS:HE2	1.58	1.04
1:A:64:TYR:HB2	3:A:440:HOH:O	1.59	1.01
1:A:239:ARG:HH21	1:A:243:SER:HB2	0.87	1.01
1:A:82:ARG:NH1	1:A:82:ARG:HG2	1.69	0.96
1:A:304:ILE:HD11	1:A:313:LEU:HD12	0.97	0.95
1:A:320:TYR:CE1	1:A:324:HIS:CE1	2.55	0.95
1:A:393:THR:HG23	1:A:394:ASN:ND2	1.85	0.92
1:A:259:LEU:HD21	1:A:270:GLU:HG3	1.50	0.92
1:A:254:HIS:HB3	3:A:508:HOH:O	1.70	0.91
1:A:425:ARG:HB2	3:A:503:HOH:O	1.71	0.90
1:A:151:ARG:HG3	1:A:151:ARG:HH11	1.35	0.89
1:A:24:THR:HG23	3:A:500:HOH:O	1.71	0.88
1:A:103:ARG:HH21	1:A:127:SER:HB2	1.37	0.87
1:A:301:ALA:O	1:A:305:ARG:HG3	1.74	0.86
1:A:304:ILE:HD11	1:A:313:LEU:HD13	1.56	0.84
1:A:103:ARG:HD3	3:A:479:HOH:O	1.77	0.84
1:A:320:TYR:CZ	1:A:324:HIS:ND1	2.45	0.84
1:A:316:ARG:HG2	1:A:317:SER:H	1.41	0.83
1:A:350:ASP:HB2	3:A:489:HOH:O	1.78	0.83
1:A:239:ARG:HH21	1:A:243:SER:CB	1.82	0.82
1:A:265:GLY:C	3:A:487:HOH:O	2.18	0.81
1:A:286:PHE:O	1:A:286:PHE:HD1	1.62	0.81
1:A:265:GLY:HA2	3:A:487:HOH:O	1.81	0.80
1:A:213:ARG:HB3	1:A:214:PRO:HD2	1.62	0.79
1:A:313:LEU:HD21	2:A:601:ACO:H22	1.67	0.76
1:A:31:ASP:OD2	1:A:33:ARG:HD3	1.85	0.76
1:A:82:ARG:HH11	1:A:82:ARG:CG	1.83	0.76
1:A:313:LEU:HD21	2:A:601:ACO:C2P	2.15	0.76
1:A:407:ALA:HB3	1:A:429:ILE:HD11	1.67	0.76
1:A:377:ILE:HD12	1:A:377:ILE:C	2.06	0.75
1:A:151:ARG:HG3	1:A:151:ARG:NH1	1.95	0.75
1:A:246:VAL:O	1:A:250:GLU:HG3	1.87	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:265:GLY:CA	3:A:487:HOH:O	2.35	0.74
1:A:418:LYS:HD2	3:A:541:HOH:O	1.88	0.73
1:A:376:ILE:HD11	1:A:388:LEU:HD11	1.71	0.72
1:A:159:ARG:HD3	3:A:499:HOH:O	1.91	0.71
1:A:103:ARG:HH21	1:A:127:SER:CB	2.04	0.70
1:A:74:GLN:HB3	1:A:76:ARG:HG3	1.73	0.70
1:A:185:ASP:OD1	1:A:188:GLN:HG2	1.92	0.69
1:A:231:ALA:HB1	1:A:239:ARG:HD2	1.74	0.69
1:A:320:TYR:CE1	1:A:324:HIS:ND1	2.60	0.69
1:A:84:LEU:HD13	1:A:136:ILE:CD1	2.24	0.67
1:A:151:ARG:CG	1:A:151:ARG:HH11	2.04	0.66
1:A:68:ASP:OD2	1:A:80:TYR:OH	2.14	0.65
1:A:286:PHE:O	1:A:286:PHE:CD1	2.48	0.65
1:A:159:ARG:NE	3:A:499:HOH:O	2.29	0.64
1:A:318:ARG:HG2	1:A:322:GLU:OE2	1.97	0.64
1:A:320:TYR:CE1	1:A:324:HIS:HE1	2.10	0.64
1:A:159:ARG:CD	3:A:499:HOH:O	2.45	0.64
1:A:52:GLN:HA	1:A:52:GLN:NE2	2.13	0.64
1:A:82:ARG:NH1	1:A:82:ARG:CG	2.49	0.64
1:A:274:ARG:HG2	1:A:274:ARG:NH1	2.12	0.63
1:A:24:THR:CG2	3:A:500:HOH:O	2.34	0.63
1:A:151:ARG:HD3	1:A:152:LYS:HG3	1.81	0.61
1:A:38:GLY:HA2	3:A:480:HOH:O	2.00	0.61
1:A:407:ALA:HB3	1:A:429:ILE:CD1	2.30	0.61
1:A:316:ARG:CB	3:A:546:HOH:O	2.48	0.61
1:A:316:ARG:CG	1:A:317:SER:N	2.46	0.61
1:A:92:LEU:C	1:A:92:LEU:HD13	2.21	0.60
1:A:406:THR:HG23	1:A:406:THR:O	1.99	0.60
1:A:8:VAL:HB	3:A:491:HOH:O	2.01	0.60
1:A:33:ARG:NH1	1:A:207:LEU:HD13	2.17	0.59
1:A:354:ILE:HD12	1:A:376:ILE:HG12	1.84	0.59
1:A:35:LEU:HD13	1:A:102:VAL:HG13	1.82	0.59
1:A:228:GLN:HE22	1:A:239:ARG:HH12	1.51	0.59
1:A:292:ALA:HB2	1:A:330:ILE:HG23	1.84	0.59
1:A:76:ARG:HH22	1:A:91:SER:HB3	1.68	0.58
1:A:274:ARG:HH11	1:A:274:ARG:HG2	1.67	0.58
1:A:274:ARG:HH11	1:A:274:ARG:CG	2.17	0.58
1:A:316:ARG:HG2	1:A:317:SER:O	2.04	0.58
1:A:81:CYS:C	1:A:83:GLY:N	2.55	0.57
1:A:319:GLU:N	1:A:319:GLU:OE2	2.37	0.57
1:A:313:LEU:HD21	2:A:601:ACO:H21	1.86	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:316:ARG:HB2	3:A:546:HOH:O	2.05	0.56
1:A:70:LEU:O	1:A:74:GLN:HB2	2.04	0.56
1:A:290:ARG:HD3	3:A:481:HOH:O	2.05	0.56
1:A:373:LEU:O	1:A:377:ILE:HG23	2.06	0.56
1:A:395:THR:HG22	1:A:395:THR:O	2.06	0.55
1:A:49:LEU:HD22	1:A:53:LEU:HD11	1.89	0.55
1:A:21:MET:O	1:A:24:THR:HB	2.08	0.54
1:A:270:GLU:HA	1:A:276:GLY:HA2	1.88	0.54
1:A:80:TYR:HA	1:A:84:LEU:O	2.06	0.54
1:A:8:VAL:CB	3:A:491:HOH:O	2.56	0.54
1:A:377:ILE:HD12	1:A:378:ASP:N	2.23	0.53
1:A:397:GLU:CD	1:A:397:GLU:H	2.09	0.53
1:A:365:ASP:OD1	2:A:601:ACO:H3B	2.09	0.53
1:A:279:THR:HG22	1:A:280:SER:N	2.24	0.53
1:A:287:VAL:HG12	1:A:289:ILE:HG13	1.91	0.53
1:A:429:ILE:HD12	1:A:430:LEU:N	2.23	0.53
1:A:213:ARG:O	1:A:214:PRO:C	2.47	0.52
1:A:172:PRO:O	1:A:173:LEU:HD23	2.09	0.52
1:A:176:SER:HB3	1:A:182:PHE:HE1	1.75	0.52
1:A:320:TYR:HH	1:A:344:LYS:HE2	1.71	0.52
1:A:425:ARG:O	3:A:446:HOH:O	2.19	0.52
1:A:406:THR:O	1:A:406:THR:CG2	2.58	0.52
1:A:397:GLU:OE1	2:A:601:ACO:H2A	2.09	0.51
1:A:61:HIS:CE1	1:A:172:PRO:HD3	2.45	0.51
1:A:48:GLY:O	1:A:51:SER:HB3	2.10	0.51
1:A:26:LEU:C	1:A:26:LEU:HD23	2.31	0.51
1:A:364:GLN:HG2	3:A:494:HOH:O	2.09	0.51
1:A:259:LEU:CD2	1:A:270:GLU:HG3	2.31	0.50
1:A:393:THR:HG23	1:A:394:ASN:HD22	1.72	0.50
1:A:35:LEU:HD13	1:A:102:VAL:CG1	2.42	0.50
1:A:316:ARG:HD2	1:A:321:LEU:HG	1.95	0.49
1:A:397:GLU:OE1	2:A:601:ACO:C2A	2.61	0.49
1:A:112:GLY:O	1:A:113:SER:HB2	2.13	0.49
1:A:155:THR:HG22	1:A:159:ARG:NH2	2.27	0.49
1:A:123:VAL:HG12	1:A:124:PRO:HD2	1.95	0.49
1:A:429:ILE:HG13	1:A:429:ILE:O	2.12	0.48
1:A:123:VAL:CG1	1:A:124:PRO:HD2	2.43	0.48
1:A:33:ARG:HD2	1:A:65:HIS:CG	2.48	0.48
1:A:30:ILE:HG12	1:A:205:LEU:HD12	1.95	0.48
1:A:256:VAL:HG23	1:A:257:GLN:N	2.29	0.48
1:A:277:ILE:HD12	1:A:278:GLY:N	2.28	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:103:ARG:NH2	1:A:127:SER:HB2	2.18	0.47
1:A:412:LEU:O	1:A:417:ARG:NH1	2.47	0.47
1:A:267:LEU:N	3:A:487:HOH:O	2.48	0.47
1:A:435:HIS:HB2	3:A:534:HOH:O	2.13	0.46
1:A:70:LEU:HD23	1:A:70:LEU:HA	1.74	0.46
1:A:31:ASP:OD1	1:A:33:ARG:NH1	2.45	0.46
1:A:337:LEU:C	1:A:337:LEU:HD12	2.36	0.46
1:A:236:SER:O	1:A:239:ARG:HB3	2.14	0.46
1:A:15:ALA:N	1:A:16:PRO:CD	2.79	0.46
1:A:294:SER:HA	1:A:297:ILE:HD12	1.97	0.46
1:A:418:LYS:HD2	1:A:418:LYS:HA	1.66	0.46
1:A:316:ARG:CG	1:A:317:SER:O	2.64	0.45
1:A:200:GLU:HB2	3:A:500:HOH:O	2.15	0.45
1:A:144:MET:HB3	1:A:147:ALA:HB3	1.98	0.45
1:A:320:TYR:CD1	1:A:324:HIS:CE1	3.02	0.45
1:A:377:ILE:CD1	1:A:377:ILE:C	2.79	0.45
2:A:601:ACO:H8A	3:A:494:HOH:O	2.16	0.45
1:A:249:LEU:HD23	1:A:253:VAL:O	2.16	0.45
1:A:374:ALA:O	1:A:377:ILE:HG13	2.17	0.45
1:A:285:ALA:O	1:A:287:VAL:HG23	2.16	0.44
1:A:223:SER:OG	1:A:226:GLU:HG3	2.17	0.44
1:A:225:GLN:O	1:A:228:GLN:HB3	2.17	0.44
1:A:213:ARG:HB3	1:A:214:PRO:CD	2.41	0.44
1:A:81:CYS:C	1:A:83:GLY:H	2.21	0.44
1:A:60:ILE:HG12	1:A:170:MET:HB2	2.00	0.43
1:A:155:THR:HG22	1:A:159:ARG:HH21	1.83	0.43
1:A:84:LEU:HD13	1:A:136:ILE:HD12	2.00	0.43
1:A:148:GLY:HA3	1:A:182:PHE:HB3	2.00	0.43
1:A:364:GLN:O	1:A:365:ASP:HB2	2.19	0.43
1:A:313:LEU:CD2	2:A:601:ACO:C2P	2.95	0.42
2:A:601:ACO:H62	2:A:601:ACO:O9P	2.18	0.42
1:A:202:LEU:HB3	1:A:256:VAL:HB	2.01	0.42
1:A:67:LEU:HD23	1:A:67:LEU:HA	1.88	0.42
1:A:8:VAL:N	3:A:491:HOH:O	1.93	0.42
1:A:259:LEU:HD21	1:A:270:GLU:CG	2.36	0.42
1:A:158:LEU:HD21	1:A:170:MET:CE	2.49	0.42
1:A:397:GLU:OE1	2:A:601:ACO:N1A	2.53	0.42
1:A:82:ARG:HA	1:A:82:ARG:HD3	1.95	0.42
1:A:316:ARG:CG	1:A:317:SER:H	2.21	0.42
1:A:255:ARG:HG2	1:A:255:ARG:NH1	2.35	0.42
1:A:354:ILE:HB	1:A:376:ILE:HD11	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:232:GLU:HG3	1:A:232:GLU:H	1.66	0.41
1:A:124:PRO:HB2	1:A:166:ASN:HD22	1.85	0.41
1:A:360:SER:HA	1:A:361:PRO:HD3	1.95	0.41
1:A:304:ILE:O	1:A:308:GLU:HG3	2.20	0.41
1:A:13:GLU:O	1:A:16:PRO:HD2	2.21	0.41
2:A:601:ACO:OAP	2:A:601:ACO:O6A	2.35	0.41
1:A:404:PHE:HB3	1:A:430:LEU:HB3	2.02	0.41
1:A:215:ASP:O	1:A:217:THR:HG22	2.21	0.41
1:A:393:THR:HG21	1:A:425:ARG:HH22	1.87	0.41
1:A:287:VAL:HG12	1:A:287:VAL:O	2.21	0.40
1:A:311:GLY:O	1:A:393:THR:HG21	2.21	0.40
1:A:287:VAL:HG21	1:A:371:ARG:HD3	2.03	0.40
1:A:408:SER:O	1:A:409:GLU:C	2.60	0.40
1:A:52:GLN:HE21	1:A:52:GLN:HA	1.81	0.40
1:A:313:LEU:CD2	2:A:601:ACO:H21	2.51	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:316:ARG:NH1	3:A:501:HOH:O[5_655]	2.16	0.04

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	420/456 (92%)	394 (94%)	21 (5%)	5 (1%)	16	29

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	287	VAL

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Mol	Chain	Res	Type
1	A	82	ARG
1	A	145	GLU
1	A	214	PRO
1	A	277	ILE

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	330/355 (93%)	295 (89%)	35 (11%)	8 16

All (35) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	11	PHE
1	A	24	THR
1	A	40	LEU
1	A	42	LYS
1	A	43	LEU
1	A	49	LEU
1	A	76	ARG
1	A	82	ARG
1	A	101	THR
1	A	102	VAL
1	A	151	ARG
1	A	153	THR
1	A	215	ASP
1	A	217	THR
1	A	220	GLU
1	A	238	THR
1	A	267	LEU
1	A	268	LEU
1	A	274	ARG
1	A	286	PHE
1	A	291	GLN
1	A	304	ILE

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Mol	Chain	Res	Type
1	A	314	LEU
1	A	316	ARG
1	A	337	LEU
1	A	353	GLU
1	A	362	GLN
1	A	364	GLN
1	A	376	ILE
1	A	377	ILE
1	A	388	LEU
1	A	397	GLU
1	A	418	LYS
1	A	429	ILE
1	A	431	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	52	GLN
1	A	94	GLN
1	A	161	GLN
1	A	166	ASN
1	A	175	HIS
1	A	225	GLN
1	A	228	GLN
1	A	257	GLN
1	A	362	GLN
1	A	364	GLN
1	A	394	ASN
1	A	423	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

1 ligand is 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	ACO	A	601	-	43,53,53	1.05	2 (4%)	55,79,79	2.42	14 (25%)

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	ACO	A	601	-	1/1/12/14	0/47/67/67	0/3/3/3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	601	ACO	CH3-C	-2.71	1.38	1.50
2	A	601	ACO	P3B-O7A	3.49	1.62	1.51

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	601	ACO	N3A-C2A-N1A	-10.30	121.01	128.89
2	A	601	ACO	C2B-C1B-N9A	-8.76	100.91	114.29
2	A	601	ACO	C2P-C3P-N4P	-4.14	104.09	112.36
2	A	601	ACO	C7P-C6P-C5P	-4.02	105.69	112.31
2	A	601	ACO	C4B-O4B-C1B	-3.34	106.05	109.72
2	A	601	ACO	P2A-O3A-P1A	-3.06	124.13	132.73
2	A	601	ACO	O6A-P2A-O4A	-2.68	99.23	109.62

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	601	ACO	C3P-N4P-C5P	-2.46	117.95	122.79
2	A	601	ACO	O3B-C3B-C2B	-2.39	102.20	111.51
2	A	601	ACO	C6P-C5P-N4P	-2.25	112.56	116.46
2	A	601	ACO	C2A-N1A-C6A	2.10	122.51	118.77
2	A	601	ACO	CDP-CBP-CAP	2.21	113.39	109.34
2	A	601	ACO	O9A-P3B-O8A	2.42	116.60	107.38
2	A	601	ACO	N6A-C6A-N1A	2.80	125.22	119.20

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	A	601	ACO	CAP

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 12 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	601	ACO	12	0

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	424/456 (92%)	0.22	13 (3%) 52 57	8, 23, 55, 71	0

All (13) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	436	ARG	4.9
1	A	113	SER	4.1
1	A	339	GLY	3.7
1	A	274	ARG	3.0
1	A	340	CYS	2.7
1	A	5	ASP	2.7
1	A	11	PHE	2.4
1	A	17	TYR	2.2
1	A	286	PHE	2.2
1	A	202	LEU	2.1
1	A	79	HIS	2.1
1	A	256	VAL	2.0
1	A	84	LEU	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 carbohydrates 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(\AA^2)	Q<0.9
2	ACO	A	601	51/51	0.98	0.15	-0.63	20,33,48,52	0

6.5 Other polymers [i](#)

There are no such residues in this entry.