



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 09:10 PM GMT

PDB ID : 1NPY
Title : Structure of shikimate 5-dehydrogenase-like protein HI0607
Authors : Korolev, S.; Koroleva, O.; Zarembinski, T.; Collart, F.; Joachimiak, A.; Midwest Center for Structural Genomics (MCSG)
Deposited on : 2003-01-20
Resolution : 1.75 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

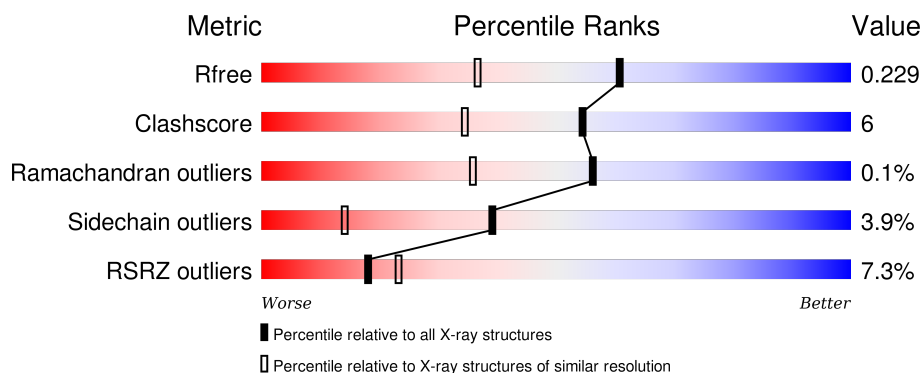
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.75 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	1609 (1.76-1.76)
Clashscore	102246	1730 (1.76-1.76)
Ramachandran outliers	100387	1711 (1.76-1.76)
Sidechain outliers	100360	1711 (1.76-1.76)
RSRZ outliers	91569	1610 (1.76-1.76)

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	271	<div> <div>2%</div> <div>86%</div> <div>12%</div> <div>••</div> </div>
1	B	271	<div> <div>2%</div> <div>88%</div> <div>11%</div> <div>•</div> </div>
1	C	271	<div> <div>4%</div> <div>88%</div> <div>10%</div> <div>•</div> </div>
1	D	271	<div> <div>21%</div> <div>82%</div> <div>17%</div> <div>•</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	ACE	C	2003	-	-	-	X
2	ACE	D	2002	-	-	X	X

2 Entry composition [i](#)

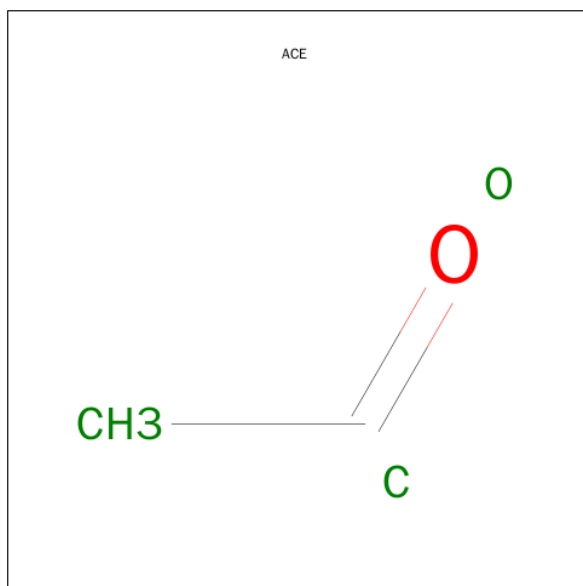
There are 3 unique types of molecules in this entry. The entry contains 9521 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Hypothetical shikimate 5-dehydrogenase-like protein HI0607.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	269	Total	C	N	O	S	0	0	0
			2087	1337	353	386	11			
1	B	270	Total	C	N	O	S	0	0	0
			2096	1343	355	387	11			
1	C	270	Total	C	N	O	S	0	0	0
			2092	1340	354	387	11			
1	D	270	Total	C	N	O	S	0	0	0
			2088	1338	353	387	10			

- Molecule 2 is ACETYL GROUP (three-letter code: ACE) (formula: C₂H₄O).



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

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

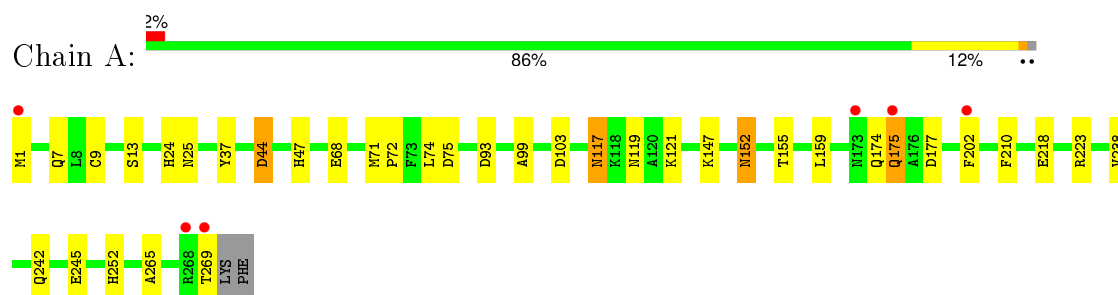
- Molecule 3 is water.

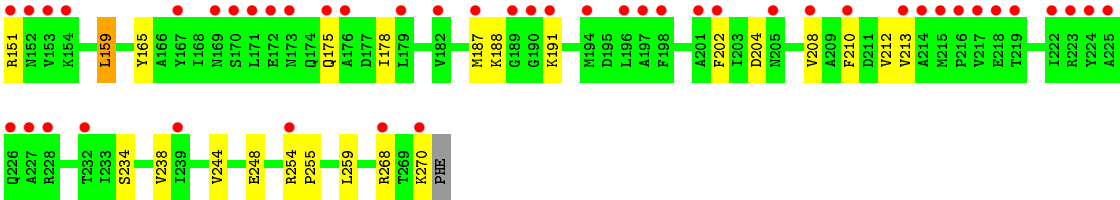
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	332	Total	O	0	0
			332	332		
3	B	325	Total	O	0	0
			325	325		
3	C	300	Total	O	0	0
			300	300		
3	D	192	Total	O	0	0
			192	192		

3 Residue-property plots [i](#)

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.

- Molecule 1: Hypothetical shikimate 5-dehydrogenase-like protein HI0607





4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	90.58Å 66.58Å 96.92Å 90.00° 109.56° 90.00°	Depositor
Resolution (Å)	30.00 – 1.75 42.68 – 1.75	Depositor EDS
% Data completeness (in resolution range)	98.4 (30.00-1.75) 98.4 (42.68-1.75)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.91 (at 1.75Å)	Xtriage
Refinement program	REFMAC 5.1.24	Depositor
R, R_{free}	0.179 , 0.219 0.191 , 0.229	Depositor DCC
R_{free} test set	5394 reflections (5.25%)	DCC
Wilson B-factor (Å ²)	14.4	Xtriage
Anisotropy	0.221	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.40 , 58.7	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Outliers	0 of 108130 reflections	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	9521	wwPDB-VP
Average B, all atoms (Å ²)	19.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 34.44 % of the origin peak, indicating pseudo translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo translational symmetry is equal to 6.8180e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹ Intensities estimated from amplitudes.

² Theoretical 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

5.1 Standard geometry

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

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	0.38	0/2128	0.90	4/2877 (0.1%)
1	B	0.41	0/2137	0.90	0/2888
1	C	0.40	0/2133	0.88	1/2884 (0.0%)
1	D	0.34	0/2128	0.85	4/2877 (0.1%)
All	All	0.38	0/8526	0.88	9/11526 (0.1%)

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	B	0	2

There are no bond length outliers.

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	93	ASP	CB-CG-OD2	7.10	124.69	118.30
1	C	44	ASP	CB-CG-OD1	6.79	124.41	118.30
1	A	44	ASP	CB-CG-OD1	6.14	123.83	118.30
1	A	177	ASP	CB-CG-OD2	6.11	123.80	118.30
1	D	75	ASP	CB-CG-OD2	5.67	123.40	118.30
1	D	53	ARG	NE-CZ-NH1	5.49	123.04	120.30
1	D	204	ASP	CB-CG-OD2	5.36	123.12	118.30
1	D	44	ASP	CB-CG-OD1	5.32	123.09	118.30
1	A	75	ASP	CB-CG-OD2	5.28	123.05	118.30

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	172	GLU	Peptide
1	B	174	GLN	Peptide

5.2 Too-close contacts ⓘ

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	2087	0	2095	28	0
1	B	2096	0	2108	25	0
1	C	2092	0	2097	29	0
1	D	2088	0	2096	24	0
2	B	3	0	3	1	0
2	C	3	0	3	1	0
2	D	3	0	3	2	0
3	A	332	0	0	11	0
3	B	325	0	0	9	0
3	C	300	0	0	16	0
3	D	192	0	0	12	0
All	All	9521	0	8405	107	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 6.

All (107) 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:245:GLU:HG3	3:A:569:HOH:O	1.49	1.12
1:D:93:ASP:HB3	3:D:2077:HOH:O	1.56	1.04
1:C:231:GLN:HG2	3:C:2265:HOH:O	1.82	0.78
1:A:7:GLN:HG2	3:A:584:HOH:O	1.83	0.77
1:D:208:VAL:CG2	3:D:2167:HOH:O	2.34	0.75
1:D:244:VAL:O	1:D:248:GLU:HG3	1.88	0.74
1:B:187:MET:HG3	3:B:2247:HOH:O	1.88	0.72
2:D:2002:ACE:H2	3:D:2005:HOH:O	1.88	0.72
1:D:208:VAL:HG21	3:D:2167:HOH:O	1.90	0.71
1:B:18:ASN:HD22	1:B:270:LYS:HD3	1.54	0.71
1:A:25:ASN:HD21	1:A:37:TYR:H	1.36	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:242:GLN:CG	3:A:445:HOH:O	2.38	0.71
1:B:147:LYS:NZ	1:B:174:GLN:OE1	2.21	0.70
1:A:242:GLN:HG3	3:A:445:HOH:O	1.91	0.70
1:B:25:ASN:HD21	1:B:37:TYR:H	1.41	0.69
2:C:2003:ACE:H3	3:C:2052:HOH:O	1.93	0.67
1:C:24:HIS:HD2	3:C:2018:HOH:O	1.76	0.67
1:D:13:SER:HB3	1:D:63:SER:HB2	1.79	0.65
2:B:2001:ACE:H2	3:B:2192:HOH:O	1.96	0.65
1:C:25:ASN:HD21	1:C:37:TYR:H	1.45	0.64
1:B:139:LYS:HE3	3:B:2306:HOH:O	1.97	0.64
1:D:178:ILE:HD11	3:D:2114:HOH:O	1.95	0.64
1:A:121:LYS:NZ	1:A:175:GLN:HG3	2.14	0.63
1:D:47:HIS:HE1	3:D:2073:HOH:O	1.82	0.63
1:B:173:ASN:HB3	1:C:121:LYS:NZ	2.14	0.62
1:C:67:LYS:CE	3:C:2288:HOH:O	2.47	0.61
1:A:7:GLN:CG	3:A:584:HOH:O	2.46	0.61
1:A:252:HIS:HE1	3:A:375:HOH:O	1.83	0.61
1:B:8:LEU:HD23	1:B:57:ILE:HD12	1.83	0.61
1:C:131:ALA:HB2	1:C:182:VAL:HG21	1.82	0.60
1:A:147:LYS:NZ	1:A:174:GLN:OE1	2.28	0.60
1:B:18:ASN:ND2	1:B:270:LYS:HD3	2.17	0.60
1:C:121:LYS:HE3	3:C:2254:HOH:O	2.01	0.59
1:B:44:ASP:OD2	1:B:47:HIS:HD2	1.85	0.59
1:B:191:LYS:HD3	3:B:2305:HOH:O	2.03	0.59
1:A:68:GLU:HG2	3:A:587:HOH:O	2.02	0.59
1:A:7:GLN:OE1	3:A:584:HOH:O	2.17	0.57
1:D:44:ASP:OD2	1:D:47:HIS:HD2	1.89	0.56
1:C:68:GLU:HG2	3:C:2251:HOH:O	2.06	0.56
1:A:24:HIS:HD2	3:A:286:HOH:O	1.88	0.56
1:C:175:GLN:HB3	3:C:2254:HOH:O	2.06	0.55
1:C:117:ASN:ND2	1:C:119:ASN:H	2.05	0.55
1:B:24:HIS:HD2	3:B:2030:HOH:O	1.89	0.55
1:B:109:LYS:HG2	3:B:2175:HOH:O	2.06	0.54
1:A:44:ASP:OD2	1:A:47:HIS:HD2	1.90	0.54
1:D:30:LYS:HB2	1:D:259:LEU:HD21	1.90	0.54
1:C:44:ASP:OD2	1:C:47:HIS:HD2	1.90	0.54
1:D:74:LEU:HD13	1:D:99:ALA:HB2	1.89	0.53
1:C:13:SER:HB3	1:C:63:SER:HB2	1.89	0.53
1:C:77:ILE:HD11	3:C:2050:HOH:O	2.07	0.53
1:A:24:HIS:HE1	3:A:332:HOH:O	1.92	0.53
1:B:30:LYS:HG3	1:B:259:LEU:HD11	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:242:GLN:OE1	3:C:2274:HOH:O	2.19	0.53
1:B:24:HIS:HE1	3:B:2094:HOH:O	1.91	0.53
1:A:103:ASP:OD1	1:A:242:GLN:CD	2.47	0.52
1:B:173:ASN:HB3	1:C:121:LYS:HZ3	1.76	0.51
1:B:139:LYS:CE	3:B:2306:HOH:O	2.57	0.51
1:D:24:HIS:HD2	3:D:2024:HOH:O	1.93	0.50
1:A:74:LEU:HD13	1:A:99:ALA:HB2	1.94	0.50
1:A:121:LYS:HZ1	1:A:175:GLN:HG3	1.76	0.50
1:B:215:MET:HE1	3:B:2318:HOH:O	2.12	0.49
1:C:30:LYS:HE2	3:C:2287:HOH:O	2.12	0.49
1:D:187:MET:HG3	1:D:213:VAL:HG13	1.93	0.49
1:B:74:LEU:HD13	1:B:99:ALA:HB2	1.93	0.49
1:A:218:GLU:OE1	1:A:223:ARG:HG2	2.13	0.49
1:C:131:ALA:CB	1:C:182:VAL:HG21	2.43	0.48
1:D:178:ILE:CD1	3:D:2114:HOH:O	2.55	0.48
1:C:33:LEU:HD11	3:C:2013:HOH:O	2.13	0.48
1:D:93:ASP:OD1	3:D:2052:HOH:O	2.19	0.48
1:B:8:LEU:HD23	1:B:57:ILE:CD1	2.44	0.48
1:D:103:ASP:O	1:D:107:ILE:HG12	2.14	0.47
1:D:130:MET:HE1	1:D:238:VAL:HG11	1.95	0.47
1:C:204:ASP:OD1	1:C:228:ARG:CZ	2.63	0.47
1:D:71:MET:N	1:D:72:PRO:CD	2.77	0.47
1:D:139:LYS:HA	1:D:165:TYR:OH	2.14	0.47
1:C:231:GLN:HA	1:C:231:GLN:OE1	2.16	0.46
1:C:254:ARG:HG2	3:C:2232:HOH:O	2.14	0.46
1:D:9:CYS:O	1:D:37:TYR:HA	2.15	0.46
1:C:68:GLU:CG	3:C:2251:HOH:O	2.63	0.45
1:A:265:ALA:O	1:A:269:THR:HG23	2.16	0.45
1:D:116:LEU:HB3	3:D:2114:HOH:O	2.17	0.44
1:C:151:ARG:NE	3:C:2300:HOH:O	2.50	0.44
1:D:132:LYS:HG3	1:D:159:LEU:HD21	1.99	0.44
1:A:9:CYS:O	1:A:37:TYR:HA	2.17	0.44
1:D:117:ASN:N	3:D:2114:HOH:O	2.49	0.44
1:A:223:ARG:HD3	3:A:595:HOH:O	2.17	0.44
1:B:8:LEU:HB3	1:B:57:ILE:HD12	1.99	0.44
1:C:24:HIS:HE1	3:C:2037:HOH:O	2.00	0.44
1:B:173:ASN:HB3	1:C:121:LYS:HZ1	1.81	0.44
1:C:9:CYS:O	1:C:37:TYR:HA	2.17	0.43
1:D:30:LYS:CB	1:D:259:LEU:HD21	2.48	0.43
2:D:2002:ACE:CH3	3:D:2005:HOH:O	2.58	0.43
1:A:152:ASN:ND2	1:A:155:THR:H	2.17	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:175:GLN:CG	1:B:176:ALA:H	2.32	0.42
1:C:13:SER:CB	1:C:63:SER:HB2	2.49	0.42
1:B:9:CYS:O	1:B:37:TYR:HA	2.19	0.42
1:A:117:ASN:ND2	1:A:119:ASN:H	2.17	0.42
1:D:130:MET:HE3	1:D:212:VAL:HG13	2.02	0.42
1:A:152:ASN:HD22	1:A:152:ASN:C	2.22	0.41
1:B:131:ALA:HB2	1:B:182:VAL:HG21	2.01	0.41
1:A:238:VAL:HG12	1:A:242:GLN:OE1	2.20	0.41
1:B:87:VAL:HG11	1:B:90:ILE:HD11	2.03	0.41
1:A:71:MET:N	1:A:72:PRO:CD	2.83	0.41
1:A:159:LEU:HA	1:A:159:LEU:HD23	1.88	0.41
1:C:154:LYS:NZ	3:C:2262:HOH:O	2.47	0.41
1:A:121:LYS:HE2	1:A:175:GLN:O	2.21	0.40
1:C:218:GLU:OE1	1:C:226:GLN:OE1	2.38	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	267/271 (98%)	265 (99%)	2 (1%)	0	100	100
1	B	268/271 (99%)	265 (99%)	2 (1%)	1 (0%)	39	19
1	C	268/271 (99%)	264 (98%)	4 (2%)	0	100	100
1	D	268/271 (99%)	263 (98%)	5 (2%)	0	100	100
All	All	1071/1084 (99%)	1057 (99%)	13 (1%)	1 (0%)	56	36

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	173	ASN

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	218/220 (99%)	211 (97%)	7 (3%)	46	20
1	B	219/220 (100%)	215 (98%)	4 (2%)	66	46
1	C	218/220 (99%)	210 (96%)	8 (4%)	41	16
1	D	217/220 (99%)	202 (93%)	15 (7%)	19	3
All	All	872/880 (99%)	838 (96%)	34 (4%)	39	14

All (34) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	MET
1	A	13	SER
1	A	117	ASN
1	A	152	ASN
1	A	175	GLN
1	A	202	PHE
1	A	210	PHE
1	B	151	ARG
1	B	210	PHE
1	B	242	GLN
1	B	270	LYS
1	C	1	MET
1	C	33	LEU
1	C	117	ASN
1	C	154	LYS
1	C	208	VAL
1	C	210	PHE
1	C	242	GLN
1	C	268	ARG
1	D	17	SER
1	D	109	LYS
1	D	141	SER
1	D	151	ARG
1	D	159	LEU

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Mol	Chain	Res	Type
1	D	175	GLN
1	D	188	LYS
1	D	191	LYS
1	D	202	PHE
1	D	210	PHE
1	D	234	SER
1	D	254	ARG
1	D	255	PRO
1	D	268	ARG
1	D	270	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (27) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	7	GLN
1	A	24	HIS
1	A	25	ASN
1	A	47	HIS
1	A	117	ASN
1	A	152	ASN
1	A	169	ASN
1	A	173	ASN
1	A	205	ASN
1	A	252	HIS
1	B	18	ASN
1	B	24	HIS
1	B	25	ASN
1	B	47	HIS
1	B	205	ASN
1	B	226	GLN
1	B	242	GLN
1	C	24	HIS
1	C	25	ASN
1	C	47	HIS
1	C	117	ASN
1	C	242	GLN
1	D	24	HIS
1	D	47	HIS
1	D	174	GLN
1	D	205	ASN
1	D	226	GLN

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 ⓘ

3 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	ACE	B	2001	-	2,2,2	1.16	0	0,1,1	0.00	-
2	ACE	C	2003	-	2,2,2	1.35	0	0,1,1	0.00	-
2	ACE	D	2002	-	2,2,2	0.97	0	0,1,1	0.00	-

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	ACE	B	2001	-	-	0/0/0/0	0/0/0/0
2	ACE	C	2003	-	-	0/0/0/0	0/0/0/0
2	ACE	D	2002	-	-	0/0/0/0	0/0/0/0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	2001	ACE	1	0
2	C	2003	ACE	1	0
2	D	2002	ACE	2	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 ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	269/271 (99%)	-0.07	6 (2%) 65 72	8, 14, 26, 42	0
1	B	270/271 (99%)	-0.06	6 (2%) 65 72	7, 13, 26, 41	0
1	C	270/271 (99%)	0.13	10 (3%) 45 51	6, 16, 34, 45	0
1	D	270/271 (99%)	1.00	57 (21%) 1 1	9, 24, 46, 57	0
All	All	1079/1084 (99%)	0.25	79 (7%) 18 23	6, 16, 39, 57	0

All (79) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	223	ARG	7.2
1	A	269	THR	6.7
1	D	194	MET	6.7
1	D	227	ALA	6.3
1	D	198	PHE	6.1
1	D	217	VAL	6.0
1	D	187	MET	5.8
1	D	224	TYR	5.4
1	D	202	PHE	5.1
1	D	169	ASN	4.8
1	A	173	ASN	4.7
1	B	173	ASN	4.6
1	D	173	ASN	4.3
1	A	1	MET	4.2
1	D	154	LYS	4.2
1	C	270	LYS	4.1
1	D	216	PRO	4.1
1	D	153	VAL	4.1
1	D	149	TYR	4.0
1	D	189	GLY	4.0
1	D	214	ALA	4.0

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Mol	Chain	Res	Type	RSRZ
1	C	1	MET	3.9
1	D	151	ARG	3.8
1	D	215	MET	3.7
1	D	191	LYS	3.7
1	C	151	ARG	3.6
1	D	175	GLN	3.6
1	D	205	ASN	3.6
1	D	232	THR	3.5
1	D	172	GLU	3.5
1	D	210	PHE	3.4
1	D	171	LEU	3.3
1	D	254	ARG	3.2
1	D	167	TYR	3.2
1	D	176	ALA	3.2
1	B	172	GLU	3.1
1	D	225	ALA	3.1
1	D	218	GLU	3.1
1	B	175	GLN	3.1
1	A	175	GLN	3.0
1	C	173	ASN	3.0
1	D	111	ILE	3.0
1	D	152	ASN	3.0
1	D	270	LYS	3.0
1	D	201	ALA	2.9
1	C	175	GLN	2.9
1	D	239	ILE	2.9
1	A	268	ARG	2.9
1	C	172	GLU	2.8
1	D	170	SER	2.8
1	D	197	ALA	2.7
1	D	110	LEU	2.7
1	D	179	LEU	2.7
1	D	141	SER	2.6
1	C	154	LYS	2.6
1	B	269	THR	2.6
1	D	196	LEU	2.6
1	D	268	ARG	2.6
1	D	142	GLY	2.5
1	D	213	VAL	2.5
1	C	153	VAL	2.5
1	D	182	VAL	2.4
1	D	121	LYS	2.4

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Mol	Chain	Res	Type	RSRZ
1	C	189	GLY	2.4
1	D	219	THR	2.3
1	B	169	ASN	2.3
1	D	114	TYR	2.3
1	D	143	PHE	2.3
1	D	138	PHE	2.2
1	B	151	ARG	2.2
1	D	208	VAL	2.2
1	D	226	GLN	2.1
1	D	117	ASN	2.1
1	D	190	GLY	2.1
1	C	115	HIS	2.1
1	D	222	ILE	2.1
1	D	116	LEU	2.0
1	D	228	ARG	2.0
1	A	202	PHE	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(Å ²)	Q<0.9
2	ACE	C	2003	3/3	0.69	0.23	13.85	23,23,24,25	0
2	ACE	D	2002	3/3	0.92	0.26	10.46	15,15,17,21	0
2	ACE	B	2001	3/3	0.53	0.37	-	13,13,20,21	0

6.5 Other polymers [i](#)

There are no such residues in this entry.