W O R L D W I D E
wwPDB
PROTEIN DATA BANK

Full wwPDB X-ray Structure Validation Report (i)

Feb 1, 2016 – 04:40 AM GMT

PDB ID	:	2NTJ
Title	:	Mycobacterium tuberculosis InhA bound with PTH-NAD adduct
Authors	:	Wang, F.; Sacchettini, J.C.
Deposited on	:	2006-11-07
Resolution	:	2.50 Å(reported)

The following versions of software and data (see references (i)) 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
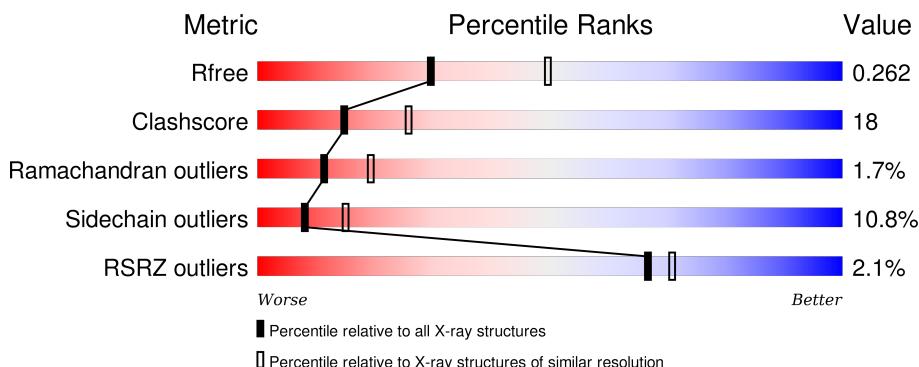
1 Overall quality at a glance (i)

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	Percentile Ranks	Value
Rfree		0.262
Clashscore		18
Ramachandran outliers		1.7%
Sidechain outliers		10.8%
RSRZ outliers		2.1%

Worse — *Better*

■ Percentile relative to all X-ray structures
▯ Percentile relative to X-ray structures of similar resolution

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 <=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	268	79% · · · 17% ·
1	B	268	4% · 69% · · · 23% · 7% ·

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 4181 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.
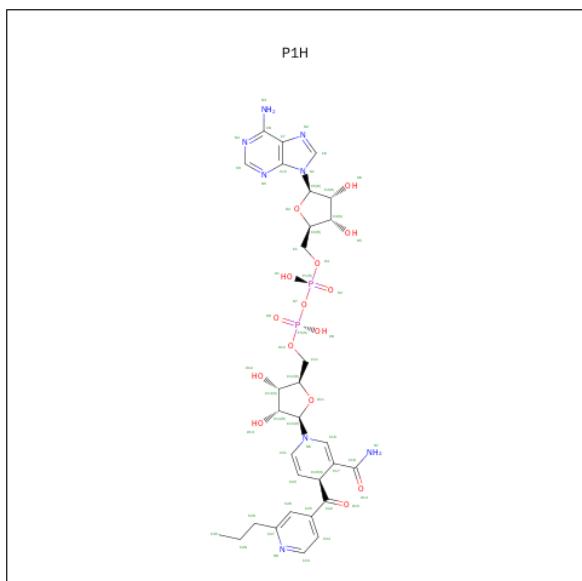
- Molecule 1 is a protein called Enoyl-[acyl-carrier-protein] reductase [NADH.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	268	Total 1994	C 1263	N 348	O 373	S 10	0	0	0
1	B	268	Total 1994	C 1263	N 348	O 373	S 10	0	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	2	ALA	ASP	ENGINEERED	UNP P0A5Y6
B	2	ALA	ASP	ENGINEERED	UNP P0A5Y6

- Molecule 2 is {(2R,3S,4R,5R)-5-[(4S)-3-(AMINOCARBONYL)-4-(2-PROPYLISONICOT INOYL)PYRIDIN-1(4H)-YL]-3,4-DIHYDROXYTETRAHYDROFURAN-2-YL}METHYL L [(2R,3S,4R,5R)-5-(6-AMINO-9H-PURIN-9-YL)-3,4-DIHYDROXYTETRAHYDROFU RAN-2-YL]METHYL DIHYDROGEN DIPHOSPHATE (three-letter code: P1H) (formula: $C_{30}H_{38}N_8O_{15}P_2$).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total 55	C 30	N 8	O 15	P 2	0	0
2	B	1	Total 55	C 30	N 8	O 15	P 2	0	0
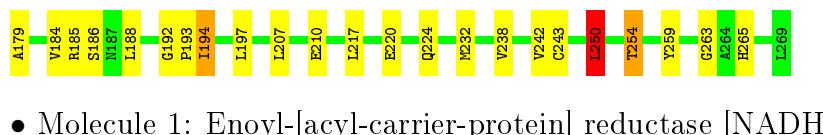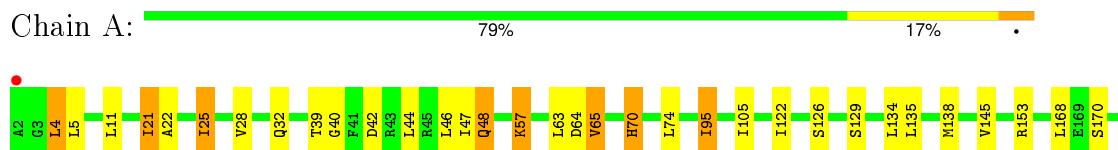
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	45	Total 45	O 45	0	0
3	B	38	Total 38	O 38	0	0

3 Residue-property plots ⓘ

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 (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: Enoyl-[acyl-carrier-protein] reductase [NADH

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4   Data and refinement statistics (i)

Property	Value	Source
Space group	I 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	91.59Å 100.52Å 186.50Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.99 – 2.50 40.67 – 2.50	Depositor EDS
% Data completeness (in resolution range)	99.5 (19.99-2.50) 99.4 (40.67-2.50)	Depositor EDS
R_{merge}	0.15	Depositor
R_{sym}	0.10	Depositor
$<I/\sigma(I)>$ [1]	1.57 (at 2.51Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.216 , 0.268 0.211 , 0.262	Depositor DCC
R_{free} test set	1522 reflections (5.35%)	DCC
Wilson B-factor (Å^2)	37.3	Xtriage
Anisotropy	0.293	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.35 , 37.4	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning[2]	$<\lvert L\rvert> = 0.48$, $<L^2> = 0.31$	Xtriage
Outliers	0 of 29979 reflections	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	4181	wwPDB-VP
Average B, all atoms (Å^2)	33.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.78% of the height of the origin peak. No significant pseudotranslation is detected.*

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[1]Intensities estimated from amplitudes.

[2]Theoretical values of $<\lvert L\rvert>$, $<L^2>$ 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: P1H

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	0.70	1/2032 (0.0%)	0.83	1/2758 (0.0%)
1	B	0.73	0/2032	0.90	3/2758 (0.1%)
All	All	0.71	1/4064 (0.0%)	0.86	4/5516 (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	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	210	GLU	CG-CD	5.35	1.59	1.51

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	41	PHE	CB-CG-CD2	12.89	129.82	120.80
1	B	41	PHE	CB-CG-CD1	-11.75	112.58	120.80
1	A	250	LEU	CA-CB-CG	6.77	130.88	115.30
1	B	135	LEU	CA-CB-CG	5.07	126.96	115.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	211	ALA	Peptide

5.2 Too-close contacts (i)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1994	0	2011	51	1
1	B	1994	0	2011	98	0
2	A	55	0	36	4	0
2	B	55	0	36	13	0
3	A	45	0	0	5	0
3	B	38	0	0	10	0
All	All	4181	0	4094	145	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 18.

All (145) 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:B:202:ILE:CG2	1:B:203:VAL:HG12	1.75	1.15
1:B:203:VAL:HG23	1:B:207:LEU:O	1.51	1.10
1:B:202:ILE:HG22	1:B:203:VAL:CG1	1.83	1.07
1:B:204:GLY:O	1:B:206:ALA:HA	1.55	1.06
1:B:202:ILE:HG22	1:B:203:VAL:HG12	1.08	1.06
1:B:203:VAL:HA	1:B:204:GLY:C	1.74	1.03
1:A:57:LYS:HD2	1:A:57:LYS:H	1.27	0.98
1:A:254:THR:HG21	3:A:338:HOH:O	1.63	0.97
1:B:64:ASP:H	1:B:70:HIS:HD2	1.16	0.92
1:A:95:ILE:CD1	1:A:122:ILE:HG23	2.06	0.85
1:B:64:ASP:H	1:B:70:HIS:CD2	1.95	0.85
1:A:64:ASP:H	1:A:70:HIS:HD2	1.27	0.82
1:B:103:MET:O	1:B:105:ILE:N	2.14	0.81
1:B:41:PHE:HB2	2:B:400:P1H:N5	1.96	0.79
1:A:186:SER:H	1:A:254:THR:CG2	1.95	0.78
1:B:3:GLY:O	1:B:32:GLN:OE1	2.00	0.77
1:B:105:ILE:HA	1:B:207:LEU:HD13	1.65	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:45:ARG:HB2	3:B:407:HOH:O	1.85	0.75
1:B:211:ALA:HB1	1:B:214:GLN:H	1.53	0.74
1:B:205:GLY:HA2	3:B:429:HOH:O	1.87	0.74
1:B:41:PHE:CD1	2:B:400:P1H:N4	2.55	0.74
1:A:4:LEU:H	1:A:32:GLN:HE21	1.35	0.73
1:A:95:ILE:HD11	1:A:122:ILE:HG23	1.69	0.73
1:B:210:GLU:HB2	3:B:423:HOH:O	1.88	0.72
1:B:149:PHE:HB3	2:B:400:P1H:H20	1.71	0.71
1:A:57:LYS:CD	1:A:57:LYS:H	2.01	0.70
1:B:45:ARG:HA	1:B:45:ARG:HE	1.56	0.70
1:A:186:SER:H	1:A:254:THR:HG22	1.56	0.70
1:A:194:ILE:H	2:A:300:P1H:HN72	1.39	0.69
1:A:192:GLY:O	1:A:194:ILE:HD12	1.92	0.69
1:A:39:THR:HG22	3:A:342:HOH:O	1.93	0.69
1:B:101:THR:HG21	1:B:115:ASP:OD2	1.93	0.68
1:B:41:PHE:HB2	2:B:400:P1H:C9	2.24	0.68
1:B:105:ILE:HG12	1:B:106:ASN:N	2.10	0.67
1:A:39:THR:HG23	1:A:63:LEU:HB3	1.77	0.66
1:B:131:ALA:O	1:B:135:LEU:HB2	1.96	0.66
1:A:64:ASP:H	1:A:70:HIS:CD2	2.11	0.65
1:A:25:ILE:CD1	1:A:242:VAL:HG21	2.27	0.65
1:A:95:ILE:CD1	1:A:122:ILE:CG2	2.75	0.64
1:B:65:VAL:HG21	1:B:126:SER:HB2	1.78	0.64
1:B:41:PHE:CD1	2:B:400:P1H:C9	2.81	0.63
1:B:39:THR:HG23	1:B:63:LEU:HB3	1.79	0.63
1:A:4:LEU:H	1:A:32:GLN:NE2	1.97	0.63
1:B:206:ALA:HB1	1:B:207:LEU:HA	1.81	0.63
1:B:194:ILE:H	2:B:400:P1H:HN72	1.46	0.62
1:B:3:GLY:O	1:B:4:LEU:HB2	1.98	0.62
1:B:105:ILE:HA	1:B:207:LEU:CD1	2.31	0.61
1:A:259:TYR:O	1:B:253:THR:HB	2.00	0.61
1:B:253:THR:HG22	3:B:401:HOH:O	2.00	0.61
1:A:57:LYS:N	1:A:57:LYS:HD2	2.10	0.60
1:B:211:ALA:HB1	1:B:214:GLN:N	2.17	0.60
1:B:216:GLN:O	1:B:220:GLU:HG2	2.01	0.60
1:B:65:VAL:CG2	1:B:126:SER:HB2	2.32	0.60
1:B:98:MET:CE	1:B:119:GLY:HA3	2.32	0.60
1:B:64:ASP:HB3	1:B:67:ASN:HB2	1.85	0.59
1:B:211:ALA:HB3	1:B:214:GLN:HG2	1.84	0.59
1:B:201:ALA:O	1:B:205:GLY:O	2.20	0.59
1:A:194:ILE:N	2:A:300:P1H:N7	2.46	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:39:THR:CG2	3:A:342:HOH:O	2.51	0.59
1:A:134:LEU:O	1:A:138:MET:HG3	2.02	0.58
1:A:95:ILE:HD11	1:A:122:ILE:O	2.04	0.58
1:B:74:LEU:HD13	1:B:134:LEU:HD21	1.87	0.57
1:B:39:THR:HG22	3:B:426:HOH:O	2.05	0.56
1:B:203:VAL:HA	1:B:204:GLY:O	2.02	0.56
1:B:203:VAL:CA	1:B:204:GLY:C	2.63	0.55
1:A:185:ARG:HA	1:A:254:THR:HG23	1.88	0.55
1:B:209:GLU:O	1:B:210:GLU:C	2.45	0.55
1:B:45:ARG:HA	1:B:45:ARG:NE	2.21	0.55
1:B:64:ASP:N	1:B:70:HIS:HD2	1.96	0.55
1:B:201:ALA:O	1:B:202:ILE:C	2.45	0.55
1:A:39:THR:HG21	1:A:63:LEU:HD23	1.89	0.55
1:B:202:ILE:HG23	1:B:203:VAL:HG12	1.80	0.54
1:A:186:SER:H	1:A:254:THR:HG23	1.70	0.54
1:B:208:GLY:O	1:B:209:GLU:HB2	2.07	0.54
1:B:204:GLY:O	1:B:206:ALA:CA	2.43	0.54
1:A:95:ILE:HD11	1:A:122:ILE:CG2	2.36	0.53
1:B:225:ARG:HG3	3:B:403:HOH:O	2.08	0.53
1:B:245:LEU:HD11	1:B:258:ILE:HD13	1.89	0.53
1:B:41:PHE:CE1	2:B:400:P1H:N4	2.77	0.53
1:B:204:GLY:O	1:B:207:LEU:O	2.27	0.53
1:A:25:ILE:HD13	1:A:242:VAL:HG21	1.90	0.53
1:B:105:ILE:HG12	1:B:106:ASN:H	1.73	0.52
1:B:203:VAL:CG2	1:B:207:LEU:O	2.43	0.52
1:A:22:ALA:HA	1:A:25:ILE:HG13	1.91	0.51
1:A:65:VAL:CG2	1:A:126:SER:HB2	2.40	0.51
1:A:48:GLN:HA	1:A:48:GLN:OE1	2.09	0.51
1:A:11:LEU:HD23	1:A:11:LEU:C	2.31	0.51
1:B:102:GLY:O	1:B:159:ASN:HB2	2.11	0.51
1:B:44:LEU:HD21	1:B:62:GLU:HG3	1.93	0.51
1:B:203:VAL:HA	1:B:205:GLY:N	2.25	0.50
1:B:193:PRO:HA	2:B:400:P1H:HN71	1.75	0.50
1:B:219:GLU:CA	1:B:232:MET:HE1	2.41	0.50
1:B:41:PHE:CG	2:B:400:P1H:C9	2.94	0.50
2:A:300:P1H:O8	2:A:300:P1H:H161	2.11	0.50
1:A:250:LEU:HD12	1:B:241:THR:HG23	1.93	0.50
1:B:66:GLN:HE22	1:B:118:LYS:HE2	1.77	0.50
1:A:65:VAL:HG21	1:A:126:SER:HB2	1.93	0.50
1:B:208:GLY:HA3	3:B:423:HOH:O	2.11	0.50
1:A:259:TYR:CG	1:A:265:HIS:CE1	3.01	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:207:LEU:CB	1:B:208:GLY:HA2	2.43	0.49
1:B:49:ARG:HH11	1:B:49:ARG:HB3	1.77	0.49
1:A:193:PRO:HA	2:A:300:P1H:HN71	1.78	0.49
1:B:211:ALA:CB	1:B:214:GLN:HG2	2.43	0.48
1:B:135:LEU:N	1:B:136:PRO:CD	2.76	0.48
1:B:104:GLY:HA2	1:B:157:ALA:HA	1.96	0.48
1:B:41:PHE:CB	2:B:400:P1H:C9	2.91	0.48
1:A:185:ARG:CA	1:A:254:THR:HG23	2.44	0.48
1:B:63:LEU:O	2:B:400:P1H:H9	2.13	0.48
1:A:179:ALA:HB1	1:A:184:VAL:HG12	1.95	0.48
1:A:21:ILE:HD11	1:A:25:ILE:HD11	1.95	0.47
1:B:145:VAL:HA	1:B:187:ASN:O	2.13	0.47
1:A:105:ILE:HG22	1:A:207:LEU:O	2.15	0.46
1:B:202:ILE:N	3:B:409:HOH:O	2.49	0.46
1:B:39:THR:CG2	3:B:426:HOH:O	2.62	0.45
1:B:66:GLN:NE2	1:B:118:LYS:HE2	2.31	0.45
1:A:254:THR:OG1	1:B:228:ILE:HG12	2.17	0.45
1:B:232:MET:HB2	1:B:232:MET:HE3	1.80	0.45
1:B:161:MET:CE	1:B:165:LYS:HE2	2.47	0.45
1:B:3:GLY:O	1:B:4:LEU:CB	2.65	0.44
1:B:218:LEU:HD11	2:B:400:P1H:H301	1.99	0.44
1:B:100:GLN:O	1:B:105:ILE:HG23	2.17	0.44
1:B:202:ILE:CG2	1:B:203:VAL:CG1	2.62	0.44
1:B:15:ILE:HD13	1:B:23:PHE:HA	2.00	0.44
1:A:185:ARG:HA	1:A:254:THR:CG2	2.48	0.44
1:B:161:MET:HE3	1:B:165:LYS:HE2	1.99	0.44
1:A:40:GLY:HA3	1:A:47:ILE:HD13	1.99	0.43
1:B:93:HIS:O	1:B:146:GLY:HA2	2.19	0.43
1:A:185:ARG:NH1	3:A:324:HOH:O	2.52	0.43
1:A:21:ILE:HD13	1:A:238:VAL:HG11	2.00	0.43
1:B:150:ASP:HA	1:B:151:PRO:HD3	1.70	0.43
1:B:149:PHE:HB3	2:B:400:P1H:C20	2.46	0.43
1:B:193:PRO:O	1:B:232:MET:HG3	2.19	0.43
1:A:28:VAL:HG12	1:A:243:CYS:SG	2.58	0.42
1:A:21:ILE:CD1	1:A:25:ILE:HD11	2.49	0.42
1:A:220:GLU:O	1:A:224:GLN:HG3	2.19	0.42
1:B:219:GLU:HA	1:B:232:MET:CE	2.49	0.42
1:B:219:GLU:N	1:B:232:MET:HE1	2.34	0.42
1:B:105:ILE:CA	1:B:207:LEU:HD13	2.43	0.41
1:B:256:ASP:HB2	1:B:257:ILE:H	1.40	0.41
1:B:104:GLY:O	1:B:105:ILE:O	2.39	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:263:GLY:HA3	1:B:254:THR:HG22	2.03	0.41
1:A:232:MET:HG2	3:A:326:HOH:O	2.20	0.41
1:B:209:GLU:HA	3:B:429:HOH:O	2.22	0.40
1:A:250:LEU:CD1	1:B:241:THR:HG23	2.50	0.40
1:B:193:PRO:HG2	1:B:232:MET:HE2	2.04	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:153:ARG:NH2	1:A:153:ARG:NH2[6_545]	2.10	0.10

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	266/268 (99%)	253 (95%)	13 (5%)	0	100	100
1	B	266/268 (99%)	241 (91%)	16 (6%)	9 (3%)	5	6
All	All	532/536 (99%)	494 (93%)	29 (6%)	9 (2%)	11	19

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	104	GLY
1	B	105	ILE
1	B	201	ALA
1	B	203	VAL
1	B	204	GLY
1	B	209	GLU
1	B	4	LEU
1	B	210	GLU

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Mol	Chain	Res	Type
1	B	202	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	203/203 (100%)	179 (88%)	24 (12%)	6	12
1	B	203/203 (100%)	183 (90%)	20 (10%)	10	18
All	All	406/406 (100%)	362 (89%)	44 (11%)	8	15

All (44) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	4	LEU
1	A	5	LEU
1	A	21	ILE
1	A	25	ILE
1	A	42	ASP
1	A	44	LEU
1	A	46	LEU
1	A	48	GLN
1	A	57	LYS
1	A	65	VAL
1	A	70	HIS
1	A	74	LEU
1	A	95	ILE
1	A	129	SER
1	A	135	LEU
1	A	145	VAL
1	A	168	LEU
1	A	170	SER
1	A	188	LEU
1	A	194	ILE
1	A	197	LEU
1	A	217	LEU

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Mol	Chain	Res	Type
1	A	250	LEU
1	A	254	THR
1	B	4	LEU
1	B	5	LEU
1	B	39	THR
1	B	42	ASP
1	B	45	ARG
1	B	46	LEU
1	B	47	ILE
1	B	49	ARG
1	B	51	THR
1	B	57	LYS
1	B	65	VAL
1	B	70	HIS
1	B	74	LEU
1	B	135	LEU
1	B	145	VAL
1	B	155	MET
1	B	168	LEU
1	B	188	LEU
1	B	194	ILE
1	B	253	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	32	GLN
1	A	66	GLN
1	A	70	HIS
1	A	100	GLN
1	A	265	HIS
1	B	32	GLN
1	B	66	GLN
1	B	70	HIS
1	B	121	HIS

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no carbohydrates in this entry.

5.6 Ligand geometry (i)

2 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	#$|Z| > 2$	Counts	RMSZ	#$|Z| > 2$
2	P1H	A	300	-	50,60,60	4.30	19 (38%)	64,90,90	3.78	24 (37%)
2	P1H	B	400	-	50,60,60	4.48	21 (42%)	64,90,90	4.46	22 (34%)

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	P1H	A	300	-	-	0/36/86/86	0/6/6/6
2	P1H	B	400	-	-	0/36/86/86	0/6/6/6

All (40) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	400	P1H	C19-C17	-2.11	1.49	1.52
2	B	400	P1H	O4-C5	2.05	1.43	1.41
2	B	400	P1H	C25-C22	2.06	1.52	1.49
2	A	300	P1H	C7-N2	2.07	1.46	1.39
2	B	400	P1H	C21-N6	2.21	1.44	1.37
2	A	300	P1H	C21-N6	2.60	1.45	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	300	P1H	C8-N3	2.87	1.43	1.34
2	B	400	P1H	C18-N7	3.47	1.43	1.33
2	A	300	P1H	C7-C10	3.53	1.48	1.40
2	B	400	P1H	C8-N3	3.72	1.46	1.34
2	A	300	P1H	C10-N5	4.36	1.42	1.35
2	A	300	P1H	C18-N7	4.47	1.46	1.33
2	A	300	P1H	C23-N8	4.52	1.44	1.34
2	A	300	P1H	C27-N8	4.77	1.44	1.34
2	B	400	P1H	C7-C10	5.20	1.52	1.40
2	B	400	P1H	C10-N5	5.46	1.43	1.35
2	B	400	P1H	C23-N8	5.47	1.46	1.34
2	B	400	P1H	C27-N8	5.67	1.46	1.34
2	B	400	P1H	C24-C23	5.92	1.50	1.38
2	A	300	P1H	C24-C23	5.97	1.51	1.38
2	A	300	P1H	C6-N2	6.00	1.46	1.34
2	B	400	P1H	C6-N2	6.04	1.46	1.34
2	B	400	P1H	O14-C18	6.12	1.39	1.24
2	A	300	P1H	C9-N4	6.12	1.45	1.33
2	A	300	P1H	C26-C27	6.63	1.51	1.38
2	B	400	P1H	C21-C20	6.89	1.50	1.33
2	B	400	P1H	C9-N5	7.03	1.44	1.32
2	A	300	P1H	O14-C18	7.10	1.42	1.24
2	A	300	P1H	C21-C20	7.38	1.52	1.33
2	A	300	P1H	C24-C25	7.56	1.52	1.39
2	A	300	P1H	C26-C25	7.78	1.50	1.39
2	B	400	P1H	C26-C27	7.79	1.53	1.38
2	B	400	P1H	C9-N4	7.79	1.48	1.33
2	B	400	P1H	C24-C25	8.13	1.53	1.39
2	A	300	P1H	C9-N5	8.24	1.46	1.32
2	B	400	P1H	C26-C25	9.20	1.53	1.39
2	A	300	P1H	O15-C22	12.67	1.41	1.22
2	B	400	P1H	O15-C22	13.12	1.42	1.22
2	B	400	P1H	C16-C17	13.38	1.52	1.34
2	A	300	P1H	C16-C17	13.84	1.53	1.34

All (46) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	400	P1H	N5-C9-N4	-23.43	110.95	128.89
2	A	300	P1H	N5-C9-N4	-16.64	116.15	128.89
2	B	400	P1H	C17-C16-N6	-15.14	110.70	122.84
2	A	300	P1H	C17-C16-N6	-14.98	110.83	122.84

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	400	P1H	C4-C5-N1	-11.43	96.83	114.29
2	A	300	P1H	C24-C23-N8	-7.88	114.90	123.90
2	A	300	P1H	C25-C26-C27	-6.67	111.73	119.95
2	B	400	P1H	C26-C27-N8	-5.28	115.61	122.95
2	B	400	P1H	C23-C24-C25	-4.56	114.32	119.06
2	B	400	P1H	C15-N6-C21	-4.37	111.04	120.81
2	B	400	P1H	C24-C23-N8	-4.27	119.03	123.90
2	A	300	P1H	C2-O4-C5	-4.15	105.16	109.72
2	A	300	P1H	C15-N6-C21	-3.77	112.38	120.81
2	B	400	P1H	C22-C19-C17	-3.43	105.97	111.03
2	A	300	P1H	C29-C27-C26	-3.36	116.42	121.13
2	A	300	P1H	C4-C5-N1	-3.13	109.51	114.29
2	A	300	P1H	O3-C1-C2	-3.00	98.04	109.12
2	A	300	P1H	C28-C29-C27	-2.89	103.55	115.20
2	B	400	P1H	O15-C22-C25	-2.84	116.67	120.58
2	B	400	P1H	P1-O7-P2	-2.82	124.82	132.73
2	A	300	P1H	O15-C22-C25	-2.73	116.82	120.58
2	A	300	P1H	C26-C27-N8	-2.69	119.21	122.95
2	A	300	P1H	C23-C24-C25	-2.65	116.30	119.06
2	B	400	P1H	C25-C26-C27	-2.57	116.79	119.95
2	A	300	P1H	C15-N6-C16	-2.51	116.53	120.91
2	A	300	P1H	C26-C25-C22	-2.47	113.25	119.07
2	B	400	P1H	O11-C15-C14	-2.38	101.06	106.58
2	B	400	P1H	C2-O4-C5	-2.32	107.17	109.72
2	B	400	P1H	N3-C8-N4	-2.26	114.36	119.20
2	B	400	P1H	O5-C3-C4	-2.04	105.19	111.83
2	A	300	P1H	O11-C15-C14	-2.03	101.88	106.58
2	A	300	P1H	C1-C2-C3	-2.03	107.16	115.21
2	A	300	P1H	O1-P1-O2	2.26	124.78	112.53
2	A	300	P1H	C22-C19-C17	2.91	115.33	111.03
2	A	300	P1H	C9-N4-C8	3.22	124.53	118.77
2	B	400	P1H	C20-C19-C17	3.60	114.19	107.95
2	B	400	P1H	C19-C17-C16	3.89	125.73	121.80
2	A	300	P1H	C20-C19-C17	4.40	115.59	107.95
2	B	400	P1H	C24-C25-C26	4.48	124.66	119.24
2	B	400	P1H	O4-C5-N1	4.51	117.54	108.10
2	B	400	P1H	C21-N6-C16	4.72	130.68	118.52
2	A	300	P1H	C21-N6-C16	4.88	131.09	118.52
2	A	300	P1H	C24-C25-C26	5.52	125.92	119.24
2	B	400	P1H	C9-N4-C8	6.46	130.31	118.77
2	B	400	P1H	C23-N8-C27	7.68	127.90	117.36
2	A	300	P1H	C23-N8-C27	7.93	128.24	117.36

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 17 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	300	P1H	4	0
2	B	400	P1H	13	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	268/268 (100%)	-0.36	1 (0%)	93	93	18, 29, 41, 53	0
1	B	268/268 (100%)	-0.14	10 (3%)	45	50	19, 35, 60, 68	0
All	All	536/536 (100%)	-0.25	11 (2%)	67	71	18, 31, 57, 68	0

All (11) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	203	VAL	6.5
1	A	2	ALA	4.5
1	B	2	ALA	3.8
1	B	210	GLU	3.6
1	B	204	GLY	3.2
1	B	207	LEU	2.9
1	B	105	ILE	2.6
1	B	84	ALA	2.3
1	B	57	LYS	2.3
1	B	208	GLY	2.0
1	B	106	ASN	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	P1H	B	400	55/55	0.92	0.15	1.11	13,25,37,40	0
2	P1H	A	300	55/55	0.97	0.11	-0.25	15,20,24,26	0

6.5 Other polymers (i)

There are no such residues in this entry.