



# Full wwPDB X-ray Structure Validation Report ⓘ

Mar 10, 2018 – 07:33 pm GMT

PDB ID : 3HQ4  
Title : Crystal Structure of C151S mutant of Glyceraldehyde-3-phosphate dehydrogenase 1 (GAPDH1) complexed with NAD from Staphylococcus aureus MRSA252 at 2.2 angstrom resolution  
Authors : Mukherjee, S.; Dutta, D.; Saha, B.; Das, A.K.  
Deposited on : 2009-06-05  
Resolution : 2.20 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](mailto: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.

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

MolProbity : 4.02b-467  
Mogul : 1.7.3 (157068), CSD as539be (2018)  
Xtriage (Phenix) : 1.13  
EDS : trunk30967  
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)  
Refmac : 5.8.0158  
CCP4 : 7.0 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk30967

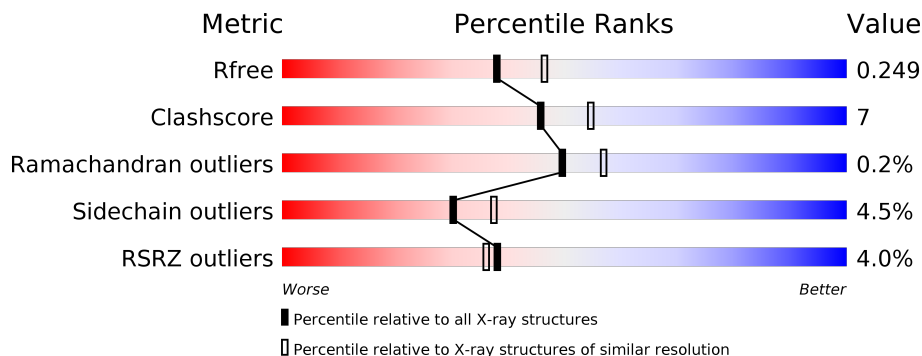
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.20 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))
$R_{free}$	111664	4343 (2.20-2.20)
Clashscore	122126	5027 (2.20-2.20)
Ramachandran outliers	120053	4952 (2.20-2.20)
Sidechain outliers	120020	4953 (2.20-2.20)
RSRZ outliers	108989	4245 (2.20-2.20)

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  $\geq 3$ , 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	O	336	<div> <div>2%</div> <div> <div></div> <div>84%</div> <div>14%</div> <div>..</div> </div> </div>
1	P	336	<div> <div>3%</div> <div> <div></div> <div>85%</div> <div>13%</div> <div>..</div> </div> </div>
1	Q	336	<div> <div>9%</div> <div> <div></div> <div>80%</div> <div>17%</div> <div>..</div> </div> </div>
1	R	336	<div> <div>2%</div> <div> <div></div> <div>88%</div> <div>10%</div> <div>..</div> </div> </div>

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 10707 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 Glyceraldehyde-3-phosphate dehydrogenase 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	R	334	Total	C	N	O	S	0	0	0
			2531	1576	435	511	9			
1	O	334	Total	C	N	O	S	6	2	0
			2540	1583	436	512	9			
1	P	334	Total	C	N	O	S	0	1	0
			2537	1579	436	513	9			
1	Q	334	Total	C	N	O	S	0	0	0
			2531	1576	435	511	9			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
R	151	SER	CYS	ENGINEERED	UNP Q6GIL8
O	151	SER	CYS	ENGINEERED	UNP Q6GIL8
P	151	SER	CYS	ENGINEERED	UNP Q6GIL8
Q	151	SER	CYS	ENGINEERED	UNP Q6GIL8

- Molecule 2 is NICOTINAMIDE-ADENINE-DINUCLEOTIDE (three-letter code: NAD) (formula: C<sub>21</sub>H<sub>27</sub>N<sub>7</sub>O<sub>14</sub>P<sub>2</sub>).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	R	1	Total 44	C 21	N 7	O 14	P 2	0	0
2	O	1	Total 44	C 21	N 7	O 14	P 2	0	0
2	P	1	Total 44	C 21	N 7	O 14	P 2	0	0
2	Q	1	Total 44	C 21	N 7	O 14	P 2	0	0

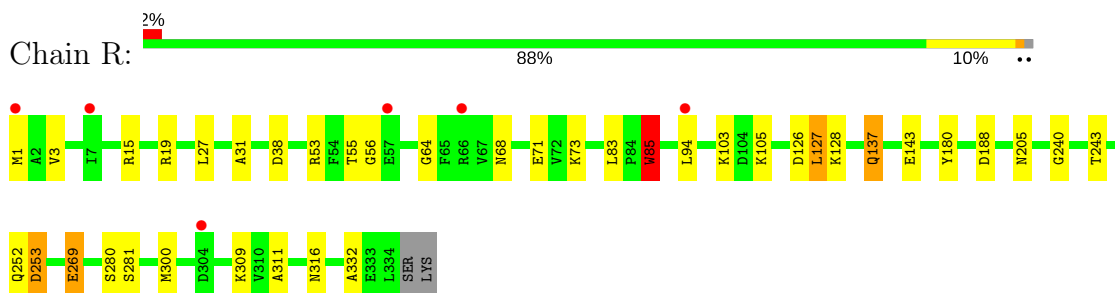
- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	R	112	Total O 112 112	0	0
3	O	111	Total O 111 111	0	0
3	P	98	Total O 98 98	0	0
3	Q	71	Total O 71 71	0	0

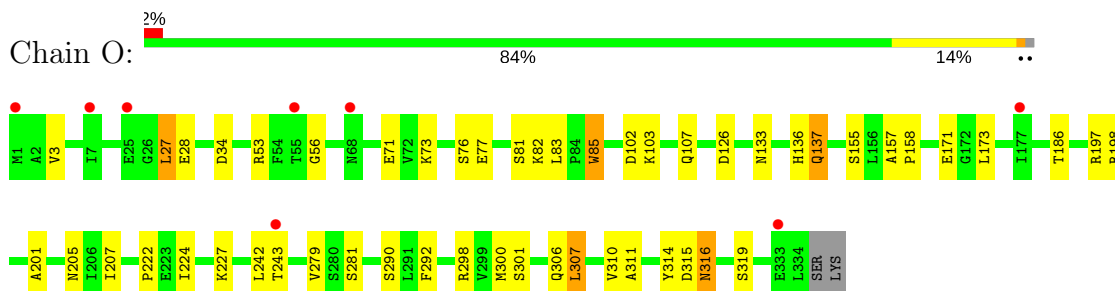
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ( $RSRZ > 2$ ). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

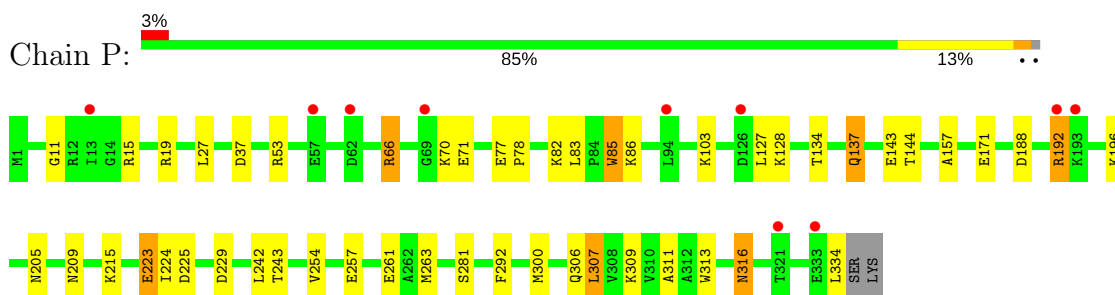
- Molecule 1: Glyceraldehyde-3-phosphate dehydrogenase 1



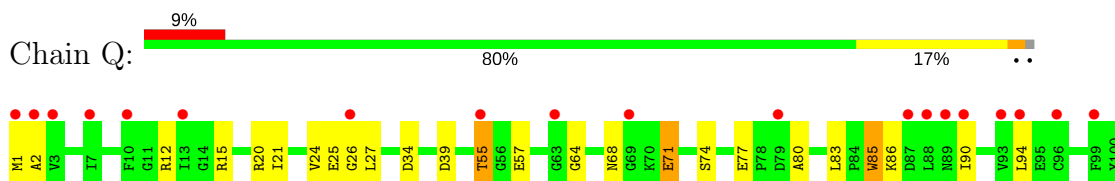
- Molecule 1: Glyceraldehyde-3-phosphate dehydrogenase 1

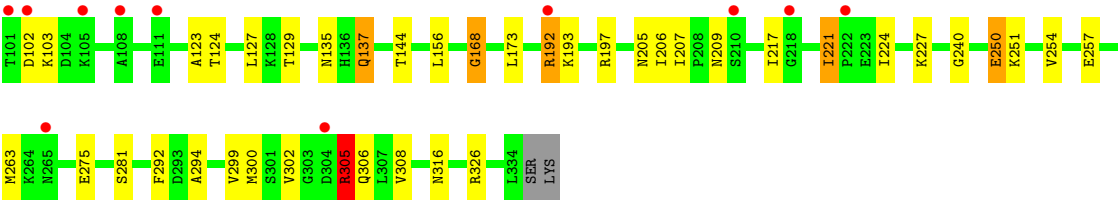


- Molecule 1: Glyceraldehyde-3-phosphate dehydrogenase 1



- Molecule 1: Glyceraldehyde-3-phosphate dehydrogenase 1





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	68.67Å 105.92Å 91.37Å 90.00° 108.00° 90.00°	Depositor
Resolution (Å)	29.01 – 2.20 29.01 – 2.20	Depositor EDS
% Data completeness (in resolution range)	96.0 (29.01-2.20) 96.0 (29.01-2.20)	Depositor EDS
$R_{merge}$	0.05	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.81 (at 2.20Å)	Xtriage
Refinement program	REFMAC	Depositor
R, $R_{free}$	0.184 , 0.244 0.191 , 0.249	Depositor DCC
$R_{free}$ test set	3076 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	34.6	Xtriage
Anisotropy	0.032	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 31.5	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.51$ , $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	10707	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	31.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.97% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

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

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	O	0.92	0/2580	0.86	1/3494 (0.0%)
1	P	0.90	0/2571	0.86	4/3483 (0.1%)
1	Q	0.88	0/2565	0.87	4/3475 (0.1%)
1	R	0.96	1/2565 (0.0%)	0.93	7/3475 (0.2%)
All	All	0.92	1/10281 (0.0%)	0.88	16/13927 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	R	85	TRP	CB-CG	5.04	1.59	1.50

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	R	53	ARG	NE-CZ-NH1	8.63	124.62	120.30
1	R	188	ASP	CB-CG-OD1	6.93	124.54	118.30
1	R	15	ARG	NE-CZ-NH1	6.46	123.53	120.30
1	P	19	ARG	NE-CZ-NH2	-6.45	117.08	120.30
1	R	252	GLN	C-N-CA	-6.39	105.72	121.70
1	P	188	ASP	CB-CG-OD1	6.37	124.03	118.30
1	P	37	ASP	CB-CG-OD1	5.93	123.63	118.30
1	R	94	LEU	CA-CB-CG	5.83	128.72	115.30
1	Q	20	ARG	NE-CZ-NH2	-5.80	117.40	120.30
1	P	53	ARG	NE-CZ-NH2	-5.73	117.43	120.30
1	R	19	ARG	NE-CZ-NH2	-5.63	117.49	120.30
1	O	53	ARG	NE-CZ-NH2	-5.54	117.53	120.30
1	Q	326	ARG	NE-CZ-NH1	5.31	122.96	120.30
1	Q	305	ARG	NE-CZ-NH1	5.17	122.88	120.30
1	R	53	ARG	NE-CZ-NH2	-5.12	117.74	120.30
1	Q	20	ARG	CG-CD-NE	-5.07	101.15	111.80



There are no chirality outliers.

There are no planarity outliers.

## 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	O	2540	0	2530	46	0
1	P	2537	0	2516	37	0
1	Q	2531	0	2512	55	0
1	R	2531	0	2512	28	0
2	O	44	0	26	2	0
2	P	44	0	26	0	0
2	Q	44	0	26	1	0
2	R	44	0	26	2	0
3	O	111	0	0	6	0
3	P	98	0	0	5	0
3	Q	71	0	0	9	0
3	R	112	0	0	5	0
All	All	10707	0	10174	142	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 7.

All (142) 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:Q:300:MET:HE3	1:Q:302:VAL:HG23	1.28	1.13
1:Q:300:MET:CE	1:Q:302:VAL:HG23	1.85	1.07
1:Q:300:MET:CE	1:Q:302:VAL:CG2	2.42	0.97
1:Q:305:ARG:HG3	1:Q:305:ARG:HH11	1.29	0.97
1:R:309:LYS:HE2	3:R:387:HOH:O	1.67	0.95
1:O:137:GLN:HB2	3:O:343:HOH:O	1.67	0.93
1:O:205:ASN:HD21	1:P:281[B]:SER:HB2	1.39	0.88
1:O:133:ASN:H	1:O:136:HIS:HD2	1.26	0.82
1:P:309:LYS:HG2	3:P:413:HOH:O	1.83	0.79
1:O:133:ASN:H	1:O:136:HIS:CD2	2.03	0.76
1:Q:137:GLN:HG3	3:Q:356:HOH:O	1.87	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Q:193:LYS:HE3	3:Q:397:HOH:O	1.89	0.72
1:P:254:VAL:H	1:P:306:GLN:HE22	1.41	0.69
1:O:205:ASN:ND2	1:P:281[B]:SER:HB2	2.08	0.68
1:R:103:LYS:HE2	1:R:126:ASP:O	1.93	0.68
1:R:3:VAL:HG21	1:R:332:ALA:HB1	1.76	0.67
1:R:137:GLN:HB2	3:R:352:HOH:O	1.93	0.66
1:O:107:GLN:HG3	3:O:348:HOH:O	1.95	0.65
1:O:307:LEU:HD22	1:P:171:GLU:HG3	1.79	0.65
1:P:103:LYS:HB2	1:P:127:LEU:HD23	1.78	0.64
1:Q:2:ALA:HA	1:Q:26:GLY:HA2	1.80	0.64
1:Q:55:THR:HB	3:Q:385:HOH:O	1.97	0.64
1:O:197:ARG:HB3	1:O:207:ILE:HG23	1.80	0.64
1:P:223:GLU:HG2	3:P:423:HOH:O	1.97	0.64
1:P:83:LEU:HD13	1:P:85:TRP:CZ2	2.33	0.63
1:R:56:GLY:HA3	1:R:68:ASN:HD21	1.62	0.63
1:O:171:GLU:HG3	1:P:307:LEU:HD22	1.80	0.63
1:Q:24:VAL:HG11	1:Q:27:LEU:HD22	1.80	0.63
1:Q:221:ILE:HG12	1:Q:224:ILE:HG12	1.79	0.62
1:Q:305:ARG:HG3	1:Q:305:ARG:NH1	2.00	0.61
1:Q:137:GLN:CG	3:Q:356:HOH:O	2.47	0.61
1:O:205:ASN:HD21	1:P:281[B]:SER:CB	2.12	0.60
1:O:281:SER:H	1:P:205:ASN:HD22	1.50	0.59
1:O:103:LYS:HD2	1:O:126:ASP:O	2.03	0.59
1:O:34:ASP:HA	2:O:0:NAD:H8A	1.84	0.59
1:P:257:GLU:O	1:P:261:GLU:HG3	2.02	0.59
1:Q:300:MET:HE2	1:Q:302:VAL:CG2	2.32	0.58
1:O:34:ASP:HA	2:O:0:NAD:C8A	2.34	0.58
1:Q:299:VAL:HG22	1:Q:308:VAL:HG22	1.85	0.58
1:O:34:ASP:O	1:O:76:SER:HA	2.04	0.57
1:R:3:VAL:HB	1:R:27:LEU:HD23	1.85	0.57
1:O:28:GLU:HG3	3:O:377:HOH:O	2.04	0.57
1:R:105:LYS:HD3	3:R:433:HOH:O	2.06	0.55
1:P:128:LYS:NZ	1:P:143:GLU:OE2	2.39	0.55
1:Q:85:TRP:CE3	1:Q:90:ILE:HG13	2.43	0.54
1:Q:168:GLY:HA3	1:Q:250:GLU:HG3	1.89	0.54
1:Q:156:LEU:HD23	1:Q:217:ILE:HD13	1.90	0.53
1:Q:103:LYS:HD2	1:Q:127:LEU:HD23	1.91	0.53
1:P:66:ARG:NH1	1:P:71:GLU:HB2	2.24	0.53
1:R:205:ASN:HD22	1:Q:281:SER:H	1.55	0.53
1:P:192:ARG:CD	3:P:427:HOH:O	2.56	0.52
1:Q:102:ASP:OD1	1:Q:124:THR:OG1	2.20	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:R:300:MET:HB2	1:Q:173:LEU:HD21	1.91	0.52
1:Q:123:ALA:HB3	1:Q:127:LEU:HD12	1.90	0.52
1:Q:257:GLU:HB3	3:Q:354:HOH:O	2.10	0.52
1:O:155:SER:HA	1:O:290:SER:HB2	1.92	0.51
1:O:224:ILE:HA	1:O:227:LYS:HD2	1.91	0.51
1:O:316:ASN:H	1:O:316:ASN:ND2	2.09	0.51
1:R:128:LYS:NZ	1:R:143:GLU:OE2	2.44	0.51
1:Q:57:GLU:H	1:Q:68:ASN:HD21	1.60	0.50
1:Q:192:ARG:HG3	3:Q:346:HOH:O	2.11	0.50
1:O:242:LEU:HD11	1:O:311:ALA:HB1	1.94	0.49
1:Q:71:GLU:HG2	3:Q:355:HOH:O	2.12	0.49
1:O:205:ASN:HD22	1:P:281[B]:SER:H	1.60	0.49
1:Q:57:GLU:H	1:Q:68:ASN:ND2	2.11	0.49
1:R:280:SER:HB3	1:Q:206:ILE:HB	1.94	0.48
1:O:243:THR:O	1:O:311:ALA:HA	2.14	0.48
1:P:11:GLY:O	1:P:15:ARG:HG3	2.14	0.48
1:Q:34:ASP:OD1	2:Q:0:NAD:H1B	2.14	0.48
1:O:157:ALA:N	1:O:158:PRO:HD2	2.29	0.48
1:Q:240:GLY:H	1:Q:316:ASN:HD21	1.60	0.48
1:R:180:TYR:CE1	1:O:186:THR:HG22	2.48	0.48
1:R:240:GLY:H	1:R:316:ASN:ND2	2.12	0.48
1:Q:129:THR:O	1:Q:135:ASN:ND2	2.47	0.48
1:R:240:GLY:H	1:R:316:ASN:HD21	1.61	0.47
1:Q:197:ARG:HB3	1:Q:207:ILE:HG23	1.96	0.47
1:O:3:VAL:HB	1:O:27:LEU:HD12	1.97	0.47
1:Q:224:ILE:HA	1:Q:227:LYS:HD2	1.96	0.47
1:O:205:ASN:HD22	1:P:281[A]:SER:H	1.62	0.47
1:Q:305:ARG:HH11	1:Q:305:ARG:CG	2.15	0.47
1:O:298:ARG:HG3	3:O:357:HOH:O	2.15	0.47
1:Q:299:VAL:HG12	3:Q:399:HOH:O	2.14	0.47
1:O:316:ASN:HD22	1:O:316:ASN:H	1.63	0.46
1:P:263:MET:HG3	1:P:292:PHE:CZ	2.50	0.46
1:O:205:ASN:ND2	1:P:281[B]:SER:CB	2.75	0.46
1:P:192:ARG:HD3	3:P:427:HOH:O	2.17	0.45
1:O:71:GLU:OE2	1:O:73:LYS:HE2	2.17	0.45
1:Q:300:MET:HE1	1:Q:302:VAL:CG2	2.41	0.45
1:Q:64:GLY:HA2	1:Q:74:SER:HB3	1.98	0.45
1:O:28:GLU:CG	3:O:377:HOH:O	2.63	0.45
1:P:137:GLN:HB2	3:P:345:HOH:O	2.17	0.45
1:Q:240:GLY:H	1:Q:316:ASN:ND2	2.13	0.45
1:Q:275:GLU:HG2	1:Q:294:ALA:HB3	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Q:263:MET:HG3	1:Q:292:PHE:CZ	2.52	0.45
1:Q:12:ARG:HH11	1:Q:15:ARG:NH2	2.14	0.44
1:R:269:GLU:CG	3:R:424:HOH:O	2.65	0.44
1:Q:21:ILE:HG23	1:Q:27:LEU:HB3	1.99	0.44
1:Q:80:ALA:HA	1:Q:83:LEU:HD12	1.99	0.44
1:O:281:SER:H	1:P:205:ASN:ND2	2.15	0.44
1:P:243:THR:O	1:P:311:ALA:HA	2.18	0.44
1:R:83:LEU:HD13	1:R:85:TRP:CZ2	2.53	0.44
1:Q:2:ALA:HA	1:Q:26:GLY:CA	2.46	0.44
1:O:197:ARG:HB3	1:O:207:ILE:CG2	2.46	0.43
1:R:205:ASN:HD21	1:Q:281:SER:CB	2.31	0.43
1:R:253:ASP:CG	1:R:253:ASP:O	2.56	0.43
1:O:133:ASN:N	1:O:136:HIS:HD2	2.04	0.43
1:O:198:ARG:NH1	3:O:369:HOH:O	2.50	0.43
1:Q:85:TRP:HA	1:Q:85:TRP:CE3	2.54	0.43
1:R:316:ASN:OD1	2:R:0:NAD:N7N	2.52	0.43
1:R:103:LYS:HB2	1:R:127:LEU:HD23	2.01	0.43
1:R:281:SER:H	1:Q:205:ASN:HD22	1.66	0.43
1:P:316:ASN:H	1:P:316:ASN:ND2	2.16	0.42
1:R:269:GLU:HG2	3:R:424:HOH:O	2.19	0.42
1:P:316:ASN:H	1:P:316:ASN:HD22	1.67	0.42
1:O:205:ASN:HD21	1:P:281[A]:SER:CB	2.30	0.42
1:O:279:VAL:HG23	1:P:205:ASN:ND2	2.35	0.42
1:P:300:MET:O	1:P:306:GLN:HA	2.19	0.42
1:R:38:ASP:OD2	1:R:64:GLY:HA2	2.20	0.42
1:O:301[A]:SER:HB3	1:O:306:GLN:HG2	2.01	0.41
1:O:85:TRP:CE3	1:O:85:TRP:HA	2.55	0.41
1:R:205:ASN:ND2	1:Q:281:SER:H	2.17	0.41
1:Q:86:LYS:HD2	3:Q:349:HOH:O	2.21	0.41
1:O:77:GLU:HG2	1:O:82:LYS:HB2	2.02	0.41
1:O:83:LEU:HD13	1:O:85:TRP:CZ2	2.55	0.41
1:Q:300:MET:CE	1:Q:302:VAL:HG22	2.44	0.41
1:P:242:LEU:HD13	1:P:313:TRP:CD2	2.55	0.41
1:P:196:LYS:NZ	1:Q:39:ASP:OD2	2.42	0.41
1:O:281:SER:CB	1:P:205:ASN:HD21	2.33	0.41
1:O:173:LEU:HD21	1:P:300:MET:HB2	2.02	0.41
1:Q:83:LEU:HD13	1:Q:85:TRP:CZ2	2.55	0.41
1:R:316:ASN:HB2	2:R:0:NAD:H71N	1.86	0.41
1:Q:85:TRP:HE3	1:Q:85:TRP:HA	1.85	0.41
1:R:31:ALA:HA	1:R:73:LYS:O	2.21	0.41
1:P:134:THR:HG21	1:P:157:ALA:HB1	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:P:77:GLU:HA	1:P:78:PRO:HD3	1.93	0.41
1:Q:263:MET:HG3	1:Q:292:PHE:CE1	2.56	0.41
1:R:281:SER:CB	1:Q:205:ASN:HD21	2.34	0.40
1:O:292:PHE:CE1	1:O:310:VAL:HB	2.56	0.40
1:O:300:MET:HE1	1:P:229:ASP:HB2	2.02	0.40
1:P:224:ILE:O	1:P:225:ASP:C	2.60	0.40
1:R:243:THR:O	1:R:311:ALA:HA	2.22	0.40
1:O:315:ASP:O	1:O:319:SER:HB2	2.21	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	O	334/336 (99%)	315 (94%)	17 (5%)	2 (1%)	27	28
1	P	333/336 (99%)	318 (96%)	15 (4%)	0	100	100
1	Q	332/336 (99%)	313 (94%)	18 (5%)	1 (0%)	43	48
1	R	332/336 (99%)	314 (95%)	18 (5%)	0	100	100
All	All	1331/1344 (99%)	1260 (95%)	68 (5%)	3 (0%)	49	57

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	O	56	GLY
1	O	201	ALA
1	Q	168	GLY

### 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	O	274/274 (100%)	265 (97%)	9 (3%)	41	52
1	P	273/274 (100%)	258 (94%)	15 (6%)	24	28
1	Q	272/274 (99%)	255 (94%)	17 (6%)	20	22
1	R	272/274 (99%)	264 (97%)	8 (3%)	45	58
All	All	1091/1096 (100%)	1042 (96%)	49 (4%)	30	37

All (49) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	R	1	MET
1	R	55	THR
1	R	71	GLU
1	R	85	TRP
1	R	127	LEU
1	R	137	GLN
1	R	253	ASP
1	R	269	GLU
1	O	27	LEU
1	O	81	SER
1	O	85	TRP
1	O	102	ASP
1	O	137	GLN
1	O	222	PRO
1	O	307	LEU
1	O	314	TYR
1	O	316	ASN
1	P	27	LEU
1	P	66	ARG
1	P	70	LYS
1	P	82	LYS
1	P	85	TRP
1	P	86	LYS
1	P	137	GLN

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Mol	Chain	Res	Type
1	P	144	THR
1	P	192	ARG
1	P	209	ASN
1	P	215	LYS
1	P	223	GLU
1	P	307	LEU
1	P	316	ASN
1	P	334	LEU
1	Q	1	MET
1	Q	25	GLU
1	Q	55	THR
1	Q	71	GLU
1	Q	77	GLU
1	Q	85	TRP
1	Q	94	LEU
1	Q	137	GLN
1	Q	144	THR
1	Q	192	ARG
1	Q	209	ASN
1	Q	221	ILE
1	Q	250	GLU
1	Q	251	LYS
1	Q	254	VAL
1	Q	305	ARG
1	Q	306	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (22) such sidechains are listed below:

Mol	Chain	Res	Type
1	R	68	ASN
1	R	133	ASN
1	R	205	ASN
1	R	265	ASN
1	R	296	GLN
1	O	68	ASN
1	O	136	HIS
1	O	137	GLN
1	O	205	ASN
1	O	296	GLN
1	O	316	ASN
1	P	68	ASN
1	P	137	GLN

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Mol	Chain	Res	Type
1	P	205	ASN
1	P	265	ASN
1	P	296	GLN
1	P	306	GLN
1	Q	68	ASN
1	Q	205	ASN
1	Q	265	ASN
1	Q	296	GLN
1	Q	306	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 carbohydrates 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$
2	NAD	O	0	-	40,48,48	1.96	4 (10%)	44,73,73	2.13	10 (22%)
2	NAD	P	0	-	40,48,48	1.78	2 (5%)	44,73,73	2.19	4 (9%)
2	NAD	Q	0	-	40,48,48	1.89	3 (7%)	44,73,73	1.83	3 (6%)
2	NAD	R	0	-	40,48,48	1.84	5 (12%)	44,73,73	2.20	8 (18%)



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	NAD	O	0	-	-	0/22/62/62	0/5/5/5
2	NAD	P	0	-	-	0/22/62/62	0/5/5/5
2	NAD	Q	0	-	-	0/22/62/62	0/5/5/5
2	NAD	R	0	-	-	0/22/62/62	0/5/5/5

All (14) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	R	0	NAD	PA-O2A	-2.09	1.45	1.55
2	O	0	NAD	O4D-C1D	2.23	1.44	1.41
2	R	0	NAD	C2A-N1A	2.43	1.38	1.33
2	Q	0	NAD	C2A-N1A	2.55	1.38	1.33
2	R	0	NAD	O4D-C1D	2.95	1.45	1.41
2	P	0	NAD	C2A-N3A	3.46	1.37	1.32
2	R	0	NAD	C2A-N3A	3.70	1.38	1.32
2	O	0	NAD	C2A-N1A	4.00	1.41	1.33
2	Q	0	NAD	C2A-N3A	5.00	1.40	1.32
2	O	0	NAD	C2A-N3A	5.53	1.41	1.32
2	O	0	NAD	O7N-C7N	8.27	1.40	1.24
2	R	0	NAD	O7N-C7N	8.62	1.41	1.24
2	P	0	NAD	O7N-C7N	9.40	1.43	1.24
2	Q	0	NAD	O7N-C7N	9.46	1.43	1.24

All (25) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	P	0	NAD	N3A-C2A-N1A	-12.24	118.39	128.86
2	R	0	NAD	N3A-C2A-N1A	-11.31	119.18	128.86
2	Q	0	NAD	N3A-C2A-N1A	-10.41	119.95	128.86
2	O	0	NAD	C4B-O4B-C1B	-4.52	105.11	109.83
2	P	0	NAD	C4A-C5A-N7A	-3.66	105.87	109.41
2	O	0	NAD	C5A-C6A-N6A	-3.58	113.18	120.47
2	R	0	NAD	O7N-C7N-C3N	-3.57	115.15	119.62
2	O	0	NAD	C2A-N1A-C6A	-3.40	112.99	118.75
2	Q	0	NAD	C4A-C5A-N7A	-2.56	106.94	109.41
2	Q	0	NAD	PN-O3-PA	-2.41	124.53	132.63
2	O	0	NAD	PN-O3-PA	-2.37	124.68	132.63
2	R	0	NAD	O3D-C3D-C4D	-2.27	104.48	111.06

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	O	0	NAD	O3D-C3D-C4D	-2.09	105.00	111.06
2	R	0	NAD	O3B-C3B-C4B	-2.06	105.10	111.06
2	R	0	NAD	C5B-C4B-C3B	-2.02	107.70	115.29
2	R	0	NAD	C4D-O4D-C1D	2.05	111.96	109.83
2	O	0	NAD	C4D-O4D-C1D	2.05	111.97	109.83
2	O	0	NAD	C2N-C3N-C4N	2.27	120.88	118.26
2	O	0	NAD	C4A-C5A-N7A	2.34	111.67	109.41
2	P	0	NAD	O2N-PN-O1N	2.51	124.91	112.14
2	R	0	NAD	C3N-C2N-N1N	2.55	122.96	120.41
2	P	0	NAD	C4B-O4B-C1B	2.63	112.57	109.83
2	O	0	NAD	N6A-C6A-N1A	3.11	125.02	118.57
2	R	0	NAD	C3N-C7N-N7N	5.44	124.08	117.76
2	O	0	NAD	C1B-N9A-C4A	9.56	143.16	126.64

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	O	0	NAD	2	0
2	Q	0	NAD	1	0
2	R	0	NAD	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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	O	334/336 (99%)	-0.00	8 (2%) 59 56	19, 27, 45, 57	0
1	P	334/336 (99%)	0.19	10 (2%) 50 48	19, 30, 50, 60	0
1	Q	334/336 (99%)	0.53	30 (8%) 9 8	19, 37, 64, 77	0
1	R	334/336 (99%)	-0.04	6 (1%) 68 66	18, 26, 42, 53	0
All	All	1336/1344 (99%)	0.17	54 (4%) 38 36	18, 29, 53, 77	0

All (54) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	Q	1	MET	6.2
1	Q	2	ALA	4.4
1	R	1	MET	3.9
1	Q	89	ASN	3.7
1	Q	88	LEU	3.6
1	Q	69	GLY	3.5
1	Q	13	ILE	3.4
1	Q	94	LEU	3.4
1	P	69	GLY	3.4
1	Q	7	ILE	3.3
1	Q	99	PHE	3.2
1	Q	55	THR	3.1
1	Q	304	ASP	3.1
1	P	94	LEU	2.9
1	Q	96	CYS	2.9
1	R	304	ASP	2.9
1	Q	87	ASP	2.8
1	Q	265	ASN	2.8
1	P	13	ILE	2.8
1	Q	102	ASP	2.7
1	Q	105	LYS	2.7

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Mol	Chain	Res	Type	RSRZ
1	Q	101	THR	2.7
1	P	192	ARG	2.6
1	Q	210	SER	2.6
1	R	7	ILE	2.6
1	Q	10	PHE	2.6
1	P	126	ASP	2.5
1	O	243	THR	2.5
1	Q	3	VAL	2.4
1	O	55	THR	2.4
1	P	333	GLU	2.4
1	Q	90	ILE	2.4
1	O	1	MET	2.3
1	Q	222	PRO	2.3
1	Q	108	ALA	2.3
1	R	94	LEU	2.2
1	O	25	GLU	2.2
1	Q	26	GLY	2.2
1	Q	218	GLY	2.2
1	P	62	ASP	2.2
1	Q	111	GLU	2.2
1	Q	63	GLY	2.2
1	P	193	LYS	2.1
1	Q	93	VAL	2.1
1	O	333	GLU	2.1
1	Q	192	ARG	2.1
1	P	57	GLU	2.1
1	P	321	THR	2.1
1	Q	79	ASP	2.1
1	O	7	ILE	2.1
1	R	66	ARG	2.1
1	O	68	ASN	2.1
1	O	177	ILE	2.1
1	R	57	GLU	2.1

## 6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

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

## 6.3 Carbohydrates ⓘ

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. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
2	NAD	O	0	44/44	0.94	0.13	15,20,28,32	0
2	NAD	P	0	44/44	0.95	0.11	15,19,24,25	0
2	NAD	Q	0	44/44	0.95	0.10	21,28,31,33	0
2	NAD	R	0	44/44	0.98	0.09	15,19,22,24	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.