



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 13, 2017 – 01:16 am GMT

PDB ID : 1NNT
Title : STRUCTURAL EVIDENCE FOR A PH-SENSITIVE DI-LYSINE TRIGGER IN THE HEN OVOTRANSFERRIN N-LOBE: IMPLICATIONS FOR TRANSFERRIN IRON RELEASE
Authors : Dewan, J.C.; Mikami, B.; Sacchettini, J.C.
Deposited on : 1993-09-15
Resolution : 2.30 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 : 1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix) : 1.9-1692
EDS : trunk28620
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
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) : recalc28949

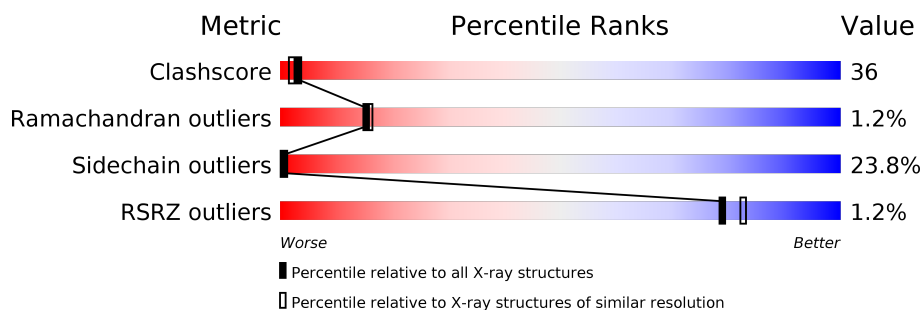
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	112137	4751 (2.30-2.30)
Ramachandran outliers	110173	4705 (2.30-2.30)
Sidechain outliers	110143	4704 (2.30-2.30)
RSRZ outliers	101464	4156 (2.30-2.30)

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	328	<div> <div></div> <div> <div></div> <div>37%</div> <div>43%</div> <div>18%</div> <div>.</div> </div> </div>

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 2646 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.

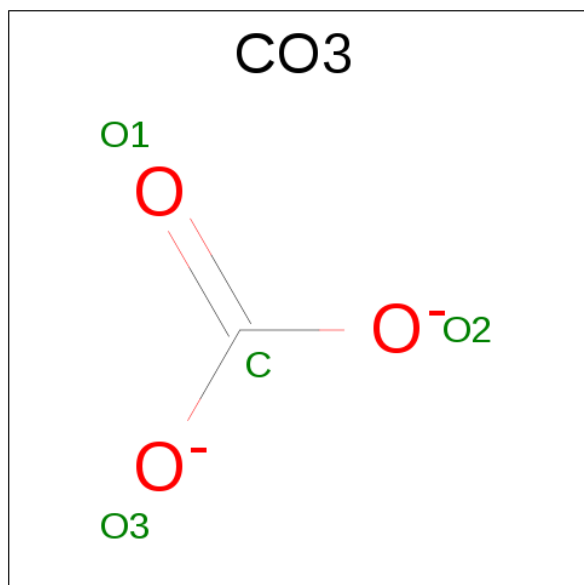
- Molecule 1 is a protein called OVOTRANSFERRIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	328	Total	C	N	O	S	0	0	0
			2533	1592	435	491	15			

- Molecule 2 is FE (III) ION (three-letter code: FE) (formula: Fe).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Fe	0	0
			1	1		

- Molecule 3 is CARBONATE ION (three-letter code: CO3) (formula: CO₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			4	1	3		

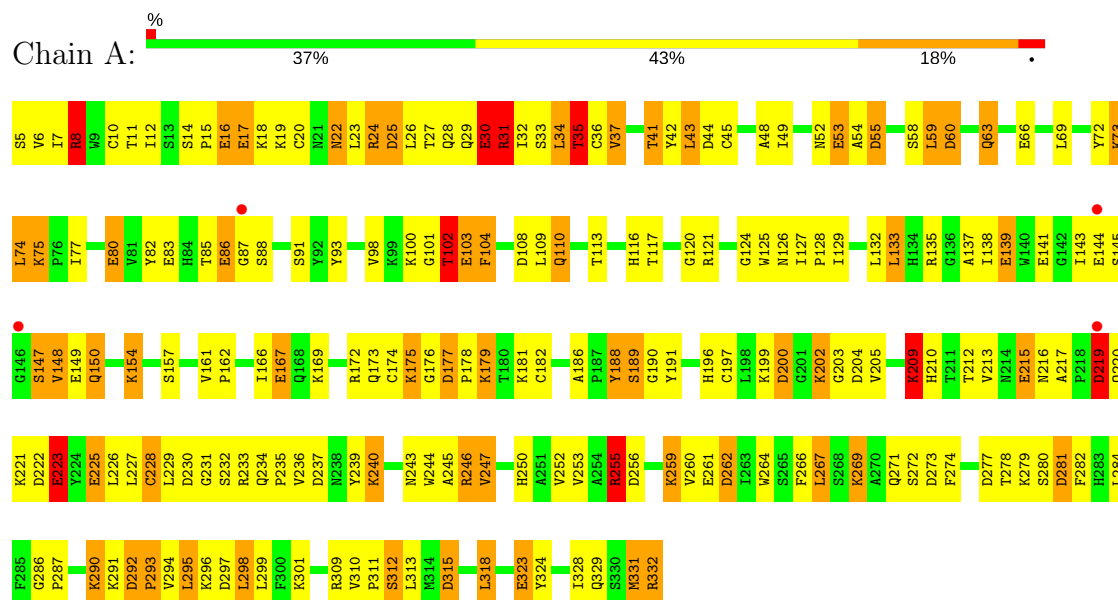
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	108	Total 108	O 108	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 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: OVOTRANSFERRIN



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	46.94Å 91.79Å 75.82Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	(Not available) – 2.30 28.37 – 1.92	Depositor EDS
% Data completeness (in resolution range)	(Not available) ((Not available)-2.30) 54.0 (28.37-1.92)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.26 (at 1.92Å)	Xtriage
Refinement program	TNT, X-PLOR	Depositor
R, R_{free}	0.160 , (Not available) (Not available) , (Not available)	Depositor DCC
R_{free} test set	NotAvailable	DCC
Wilson B-factor (Å ²)	21.5	Xtriage
Anisotropy	0.168	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.25 , 76.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	2646	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 5.33% 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, 0.333 respectively for untwinned datasets, and 0.375, 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: CO3, FE

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	1.10	19/2586 (0.7%)	1.39	40/3497 (1.1%)

All (19) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	144	GLU	CD-OE2	9.68	1.36	1.25
1	A	261	GLU	CD-OE2	7.63	1.34	1.25
1	A	323	GLU	CD-OE1	7.31	1.33	1.25
1	A	103	GLU	CD-OE2	7.23	1.33	1.25
1	A	149	GLU	CD-OE1	6.84	1.33	1.25
1	A	139	GLU	CD-OE2	6.61	1.32	1.25
1	A	86	GLU	CD-OE1	6.42	1.32	1.25
1	A	141	GLU	CD-OE2	6.26	1.32	1.25
1	A	80	GLU	CD-OE1	-6.13	1.19	1.25
1	A	167	GLU	CD-OE2	5.94	1.32	1.25
1	A	53	GLU	CD-OE2	5.88	1.32	1.25
1	A	223	GLU	CD-OE1	5.86	1.32	1.25
1	A	225	GLU	CD-OE1	5.63	1.31	1.25
1	A	66	GLU	CD-OE1	5.50	1.31	1.25
1	A	17	GLU	CD-OE1	5.40	1.31	1.25
1	A	16	GLU	CD-OE1	5.33	1.31	1.25
1	A	215	GLU	CD-OE2	5.28	1.31	1.25
1	A	30	GLU	CD-OE2	5.22	1.31	1.25
1	A	83	GLU	CD-OE1	5.19	1.31	1.25

All (40) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	297	ASP	CB-CG-OD1	-9.83	109.45	118.30
1	A	277	ASP	CB-CG-OD1	-8.14	110.97	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	297	ASP	CB-CG-OD2	7.72	125.25	118.30
1	A	60	ASP	CB-CG-OD2	-7.71	111.36	118.30
1	A	200	ASP	CB-CG-OD1	7.65	125.19	118.30
1	A	121	ARG	NE-CZ-NH2	-7.60	116.50	120.30
1	A	315	ASP	CB-CG-OD1	7.51	125.06	118.30
1	A	60	ASP	CB-CG-OD1	7.44	125.00	118.30
1	A	25	ASP	CB-CG-OD1	-7.37	111.67	118.30
1	A	315	ASP	CB-CG-OD2	-7.33	111.71	118.30
1	A	177	ASP	CB-CG-OD2	-7.24	111.79	118.30
1	A	204	ASP	CB-CG-OD1	-6.83	112.15	118.30
1	A	277	ASP	CB-CG-OD2	6.74	124.37	118.30
1	A	200	ASP	CB-CG-OD2	-6.64	112.32	118.30
1	A	292	ASP	CB-CG-OD1	6.49	124.14	118.30
1	A	8	ARG	NE-CZ-NH1	6.45	123.53	120.30
1	A	292	ASP	CB-CG-OD2	-6.37	112.57	118.30
1	A	219	ASP	CB-CG-OD2	6.36	124.02	118.30
1	A	219	ASP	CB-CG-OD1	-6.30	112.63	118.30
1	A	262	ASP	CB-CG-OD1	6.15	123.83	118.30
1	A	262	ASP	CB-CG-OD2	-6.13	112.79	118.30
1	A	255	ARG	NE-CZ-NH1	6.09	123.34	120.30
1	A	209	LYS	CB-CA-C	-5.99	98.42	110.40
1	A	55	ASP	CB-CG-OD1	-5.93	112.96	118.30
1	A	222	ASP	CB-CG-OD1	-5.87	113.02	118.30
1	A	273	ASP	CB-CG-OD1	-5.84	113.04	118.30
1	A	44	ASP	CB-CG-OD2	-5.81	113.07	118.30
1	A	35	THR	N-CA-CB	5.58	120.89	110.30
1	A	177	ASP	CB-CG-OD1	5.50	123.25	118.30
1	A	281	ASP	CB-CG-OD1	-5.49	113.36	118.30
1	A	246	ARG	NE-CZ-NH1	5.46	123.03	120.30
1	A	256	ASP	CB-CG-OD1	5.34	123.11	118.30
1	A	222	ASP	CB-CG-OD2	5.32	123.09	118.30
1	A	256	ASP	CB-CG-OD2	-5.26	113.57	118.30
1	A	196	HIS	CA-CB-CG	-5.25	104.67	113.60
1	A	31	ARG	NE-CZ-NH2	-5.25	117.68	120.30
1	A	55	ASP	CB-CG-OD2	5.25	123.02	118.30
1	A	273	ASP	CB-CG-OD2	5.17	122.96	118.30
1	A	25	ASP	CB-CG-OD2	5.17	122.95	118.30
1	A	237	ASP	CB-CG-OD2	5.09	122.88	118.30

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	A	2533	0	2470	182	0
2	A	1	0	0	0	0
3	A	4	0	0	0	0
4	A	108	0	0	7	0
All	All	2646	0	2470	182	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 36.

All (182) 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:220:GLN:HB2	1:A:223:GLU:HG3	1.38	1.04
1:A:143:ILE:H	1:A:143:ILE:HD12	1.25	1.00
1:A:59:LEU:HG	1:A:63:GLN:HB2	1.52	0.91
1:A:191:TYR:CE1	1:A:209:LYS:HG3	2.12	0.85
1:A:93:TYR:H	1:A:210:HIS:HD2	1.23	0.83
1:A:229:LEU:HD11	1:A:244:TRP:HA	1.60	0.81
1:A:209:LYS:NZ	1:A:301:LYS:NZ	2.29	0.81
1:A:332:ARG:HG3	1:A:332:ARG:HH11	1.45	0.81
1:A:173:GLN:HB3	1:A:202:LYS:HB3	1.64	0.80
1:A:41:THR:HG23	1:A:43:LEU:H	1.47	0.79
1:A:11:THR:HB	1:A:16:GLU:HG2	1.64	0.79
1:A:209:LYS:HZ3	1:A:301:LYS:NZ	1.81	0.77
1:A:169:LYS:HG3	1:A:172:ARG:NH1	1.99	0.77
1:A:324:TYR:CZ	1:A:328:ILE:HD11	2.20	0.76
1:A:41:THR:HG23	1:A:43:LEU:N	2.01	0.76
1:A:74:LEU:HB3	1:A:253:VAL:CG1	2.16	0.75
1:A:267:LEU:O	1:A:271:GLN:HG2	1.87	0.75
1:A:77:ILE:HG13	1:A:260:VAL:HG13	1.68	0.74
1:A:6:VAL:HG12	1:A:33:SER:OG	1.87	0.73
1:A:30:GLU:OE1	1:A:269:LYS:HE3	1.87	0.73
1:A:32:ILE:HD13	1:A:262:ASP:O	1.88	0.73
1:A:324:TYR:O	1:A:328:ILE:HD12	1.89	0.73
1:A:175:LYS:HG3	1:A:176:GLY:N	2.05	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:24:ARG:O	1:A:27:THR:HG22	1.89	0.71
1:A:143:ILE:CD1	1:A:143:ILE:H	1.98	0.71
1:A:229:LEU:HD21	1:A:244:TRP:CD2	2.25	0.71
1:A:24:ARG:HH11	1:A:24:ARG:HG2	1.55	0.71
1:A:24:ARG:NH1	1:A:24:ARG:HG2	2.07	0.69
1:A:191:TYR:CD1	1:A:209:LYS:HG3	2.27	0.69
1:A:75:LYS:HE3	1:A:312:SER:O	1.92	0.69
1:A:45:CYS:O	1:A:49:ILE:HG13	1.93	0.68
1:A:324:TYR:CE1	1:A:328:ILE:HD11	2.29	0.68
1:A:234:GLN:HB3	1:A:235:PRO:HD2	1.74	0.68
1:A:221:LYS:N	4:A:521:HOH:O	2.28	0.67
1:A:209:LYS:NZ	1:A:301:LYS:HZ1	1.92	0.66
1:A:166:ILE:O	1:A:167:GLU:HG2	1.95	0.66
1:A:86:GLU:N	1:A:86:GLU:OE1	2.29	0.66
1:A:293:PRO:HA	1:A:296:LYS:HG3	1.78	0.66
1:A:116:HIS:CD2	1:A:161:VAL:HG22	2.31	0.66
1:A:74:LEU:HB3	1:A:253:VAL:HG13	1.77	0.65
1:A:14:SER:HB2	1:A:15:PRO:HD3	1.79	0.65
1:A:93:TYR:H	1:A:210:HIS:CD2	2.09	0.64
1:A:23:LEU:HB2	1:A:282:PHE:CZ	2.33	0.64
1:A:14:SER:O	1:A:17:GLU:HB3	1.99	0.63
1:A:213:VAL:HG21	1:A:236:VAL:CG2	2.29	0.62
1:A:73:LYS:HB3	1:A:73:LYS:NZ	2.14	0.62
1:A:125:TRP:C	1:A:128:PRO:HD2	2.20	0.62
1:A:169:LYS:HG3	1:A:172:ARG:HH12	1.64	0.61
1:A:24:ARG:HA	1:A:27:THR:HG22	1.82	0.61
1:A:274:PHE:HA	1:A:278:THR:HB	1.81	0.61
1:A:255:ARG:HB2	1:A:255:ARG:NH1	2.15	0.61
1:A:229:LEU:CD1	1:A:244:TRP:HA	2.30	0.61
1:A:55:ASP:OD2	1:A:259:LYS:NZ	2.35	0.60
1:A:209:LYS:HZ3	1:A:301:LYS:CE	2.12	0.60
1:A:98:VAL:HG13	1:A:205:VAL:HG12	1.83	0.60
1:A:49:ILE:O	1:A:255:ARG:HD3	2.01	0.60
1:A:12:ILE:HG13	1:A:16:GLU:OE2	2.02	0.60
1:A:295:LEU:HA	1:A:298:LEU:HD21	1.83	0.60
1:A:226:LEU:O	1:A:233:ARG:HA	2.02	0.60
1:A:17:GLU:OE2	1:A:36:CYS:HB2	2.02	0.59
1:A:24:ARG:HB2	1:A:34:LEU:HB3	1.85	0.59
1:A:296:LYS:O	1:A:298:LEU:HD13	2.03	0.59
1:A:73:LYS:HB3	1:A:73:LYS:HZ2	1.67	0.59
1:A:150:GLN:O	1:A:154:LYS:HG3	2.02	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:295:LEU:O	1:A:298:LEU:HD22	2.04	0.58
1:A:17:GLU:O	1:A:20:CYS:HB3	2.03	0.58
1:A:216:ASN:O	1:A:290:LYS:HG2	2.04	0.57
1:A:162:PRO:HG2	1:A:189:SER:HA	1.86	0.57
1:A:209:LYS:NZ	1:A:301:LYS:HZ3	2.02	0.56
1:A:126:ASN:HA	1:A:331:MET:HE1	1.88	0.56
1:A:174:CYS:O	1:A:181:LYS:HD2	2.06	0.56
1:A:32:ILE:HG21	1:A:266:PHE:HB2	1.87	0.56
1:A:178:PRO:HA	1:A:181:LYS:HG2	1.88	0.56
1:A:48:ALA:HB1	1:A:53:GLU:HB2	1.87	0.56
1:A:209:LYS:HZ2	1:A:301:LYS:NZ	2.03	0.55
1:A:98:VAL:CG1	1:A:205:VAL:HG12	2.36	0.55
1:A:132:LEU:HB3	1:A:138:ILE:HD12	1.88	0.55
1:A:240:LYS:O	1:A:240:LYS:HD2	2.07	0.55
1:A:217:ALA:HB1	1:A:220:GLN:HG2	1.90	0.54
1:A:7:ILE:HD11	1:A:34:LEU:CD2	2.38	0.54
1:A:117:THR:HG22	1:A:190:GLY:C	2.29	0.54
1:A:239:TYR:O	1:A:243:ASN:HB3	2.08	0.53
1:A:24:ARG:HH11	1:A:24:ARG:CG	2.22	0.53
1:A:188:TYR:CZ	1:A:197:CYS:HA	2.44	0.53
1:A:10:CYS:HA	1:A:37:VAL:O	2.09	0.53
1:A:147:SER:OG	1:A:148:VAL:N	2.40	0.52
1:A:173:GLN:NE2	1:A:202:LYS:O	2.39	0.52
1:A:24:ARG:CA	1:A:27:THR:HG22	2.39	0.52
1:A:24:ARG:HA	1:A:27:THR:CG2	2.39	0.52
1:A:332:ARG:CG	1:A:332:ARG:HH11	2.19	0.52
1:A:225:GLU:HB2	1:A:234:GLN:O	2.10	0.52
1:A:103:GLU:O	1:A:104:PHE:HB3	2.09	0.52
1:A:264:TRP:HA	1:A:264:TRP:CE3	2.44	0.52
1:A:291:LYS:HD3	1:A:295:LEU:HB2	1.91	0.52
1:A:213:VAL:HG21	1:A:236:VAL:HG21	1.90	0.52
1:A:213:VAL:HG21	1:A:236:VAL:HG22	1.92	0.52
1:A:229:LEU:HD21	1:A:244:TRP:CE2	2.45	0.51
1:A:210:HIS:HB2	1:A:239:TYR:CG	2.46	0.51
1:A:116:HIS:HD2	1:A:161:VAL:HG22	1.73	0.51
1:A:104:PHE:CD2	1:A:233:ARG:NH2	2.79	0.51
1:A:324:TYR:CE2	1:A:328:ILE:HD11	2.46	0.51
1:A:91:SER:HB2	1:A:247:VAL:O	2.10	0.51
1:A:102:THR:OG1	1:A:102:THR:O	2.29	0.51
1:A:177:ASP:O	1:A:181:LYS:N	2.43	0.51
1:A:104:PHE:CE2	1:A:233:ARG:NH2	2.79	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:209:LYS:HB2	1:A:212:THR:OG1	2.12	0.50
1:A:101:GLY:O	1:A:103:GLU:N	2.45	0.50
1:A:309:ARG:HG2	1:A:310:VAL:N	2.27	0.50
1:A:19:LYS:HG2	1:A:299:LEU:HG	1.93	0.49
1:A:127:ILE:HD12	1:A:245:ALA:CB	2.42	0.49
1:A:117:THR:HG22	1:A:191:TYR:HA	1.94	0.49
1:A:24:ARG:C	1:A:27:THR:HG22	2.32	0.49
1:A:244:TRP:O	1:A:245:ALA:HB2	2.13	0.48
1:A:125:TRP:HD1	1:A:126:ASN:OD1	1.95	0.48
1:A:41:THR:HA	4:A:522:HOH:O	2.13	0.48
1:A:292:ASP:O	1:A:295:LEU:N	2.38	0.48
1:A:72:TYR:C	1:A:73:LYS:HG3	2.34	0.48
1:A:186:ALA:HB1	4:A:356:HOH:O	2.13	0.48
1:A:113:THR:OG1	1:A:203:GLY:HA2	2.14	0.48
1:A:286:GLY:HA3	1:A:287:PRO:HA	1.49	0.47
1:A:132:LEU:O	1:A:137:ALA:HB3	2.14	0.47
1:A:228:CYS:SG	1:A:234:GLN:HG3	2.55	0.47
1:A:177:ASP:OD1	1:A:178:PRO:HD2	2.15	0.47
1:A:230:ASP:OD1	1:A:231:GLY:N	2.48	0.47
1:A:234:GLN:HB3	1:A:235:PRO:CD	2.42	0.47
1:A:255:ARG:HB2	1:A:255:ARG:CZ	2.45	0.47
1:A:310:VAL:HG13	1:A:311:PRO:HD2	1.97	0.47
1:A:301:LYS:HB3	4:A:509:HOH:O	2.15	0.47
1:A:133:LEU:O	1:A:135:ARG:O	2.32	0.46
1:A:23:LEU:O	1:A:27:THR:HB	2.14	0.46
1:A:69:LEU:CD1	1:A:69:LEU:N	2.79	0.46
1:A:24:ARG:NH1	1:A:25:ASP:OD1	2.48	0.45
1:A:7:ILE:HD11	1:A:34:LEU:HD21	1.99	0.45
1:A:12:ILE:HD12	1:A:12:ILE:C	2.37	0.45
1:A:240:LYS:C	1:A:240:LYS:HD2	2.36	0.45
1:A:6:VAL:HG12	1:A:33:SER:HG	1.79	0.45
1:A:116:HIS:HB3	1:A:124:GLY:O	2.17	0.45
1:A:58:SER:HA	1:A:252:VAL:HA	1.98	0.44
1:A:117:THR:HG22	1:A:191:TYR:N	2.33	0.44
1:A:110:GLN:HE21	1:A:110:GLN:HB3	1.61	0.44
1:A:332:ARG:CG	1:A:332:ARG:NH1	2.79	0.44
1:A:127:ILE:HB	1:A:128:PRO:HD3	1.99	0.44
1:A:98:VAL:HG21	1:A:227:LEU:HD13	2.00	0.44
1:A:80:GLU:OE1	1:A:82:TYR:OH	2.22	0.44
1:A:120:GLY:HA2	1:A:125:TRP:CD1	2.53	0.44
1:A:191:TYR:CE2	1:A:301:LYS:HE3	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:229:LEU:HD11	1:A:244:TRP:CA	2.40	0.43
1:A:315:ASP:OD1	1:A:318:LEU:HD22	2.17	0.43
1:A:31:ARG:HG2	1:A:32:ILE:HG13	2.01	0.43
1:A:109:LEU:HA	1:A:109:LEU:HD23	1.81	0.43
1:A:177:ASP:OD1	1:A:179:LYS:HB2	2.18	0.43
1:A:77:ILE:HG13	1:A:260:VAL:CG1	2.44	0.43
1:A:135:ARG:C	1:A:137:ALA:H	2.23	0.43
1:A:169:LYS:HG3	1:A:172:ARG:CZ	2.49	0.43
1:A:219:ASP:OD1	1:A:290:LYS:HD2	2.19	0.43
1:A:27:THR:HG23	1:A:28:GLN:OE1	2.19	0.42
1:A:42:TYR:CE2	1:A:43:LEU:HD12	2.54	0.42
1:A:87:GLY:O	1:A:88:SER:HB3	2.19	0.42
1:A:298:LEU:O	1:A:299:LEU:HB2	2.20	0.42
1:A:20:CYS:SG	1:A:34:LEU:HD11	2.60	0.42
1:A:74:LEU:HB3	1:A:253:VAL:HG12	1.98	0.42
1:A:75:LYS:HD3	4:A:343:HOH:O	2.18	0.42
1:A:60:ASP:HA	1:A:250:HIS:CD2	2.55	0.42
1:A:34:LEU:HD22	1:A:35:THR:H	1.85	0.42
1:A:245:ALA:HA	4:A:365:HOH:O	2.20	0.41
1:A:188:TYR:OH	1:A:200:ASP:HB2	2.20	0.41
1:A:209:LYS:HZ3	1:A:301:LYS:HE2	1.82	0.41
1:A:117:THR:CG2	1:A:191:TYR:HA	2.49	0.41
1:A:77:ILE:N	1:A:252:VAL:O	2.52	0.41
1:A:8:ARG:HG3	1:A:54:ALA:HA	2.03	0.41
1:A:117:THR:OG1	1:A:124:GLY:HA3	2.20	0.41
1:A:34:LEU:O	1:A:35:THR:HG23	2.20	0.41
1:A:177:ASP:HA	1:A:178:PRO:HD3	1.96	0.41
1:A:292:ASP:OD1	1:A:294:VAL:HB	2.20	0.41
1:A:24:ARG:CG	1:A:25:ASP:N	2.79	0.41
1:A:173:GLN:HG3	1:A:202:LYS:O	2.21	0.40
1:A:34:LEU:HD23	1:A:34:LEU:HA	1.75	0.40
1:A:284:LEU:HD12	1:A:284:LEU:HA	1.81	0.40
1:A:291:LYS:NZ	4:A:529:HOH:O	2.55	0.40
1:A:54:ALA:O	1:A:55:ASP:OD1	2.39	0.40
1:A:22:ASN:HA	1:A:22:ASN:HD22	1.58	0.40
1:A:280:SER:OG	1:A:281:ASP:N	2.54	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	326/328 (99%)	286 (88%)	36 (11%)	4 (1%)	15 16

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	102	THR
1	A	104	PHE
1	A	35	THR
1	A	293	PRO

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	273/273 (100%)	208 (76%)	65 (24%)	1 0

All (65) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	5	SER
1	A	8	ARG
1	A	18	LYS
1	A	22	ASN
1	A	24	ARG
1	A	26	LEU
1	A	29	GLN

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Mol	Chain	Res	Type
1	A	30	GLU
1	A	31	ARG
1	A	34	LEU
1	A	37	VAL
1	A	41	THR
1	A	43	LEU
1	A	52	ASN
1	A	59	LEU
1	A	63	GLN
1	A	73	LYS
1	A	74	LEU
1	A	75	LYS
1	A	85	THR
1	A	100	LYS
1	A	102	THR
1	A	108	ASP
1	A	110	GLN
1	A	129	ILE
1	A	133	LEU
1	A	139	GLU
1	A	145	SER
1	A	147	SER
1	A	148	VAL
1	A	150	GLN
1	A	154	LYS
1	A	157	SER
1	A	175	LYS
1	A	179	LYS
1	A	182	CYS
1	A	188	TYR
1	A	189	SER
1	A	199	LYS
1	A	202	LYS
1	A	209	LYS
1	A	215	GLU
1	A	219	ASP
1	A	223	GLU
1	A	228	CYS
1	A	232	SER
1	A	240	LYS
1	A	246	ARG
1	A	247	VAL

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Mol	Chain	Res	Type
1	A	255	ARG
1	A	259	LYS
1	A	267	LEU
1	A	269	LYS
1	A	272	SER
1	A	279	LYS
1	A	290	LYS
1	A	295	LEU
1	A	298	LEU
1	A	312	SER
1	A	313	LEU
1	A	318	LEU
1	A	323	GLU
1	A	329	GLN
1	A	331	MET
1	A	332	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	22	ASN
1	A	63	GLN
1	A	110	GLN
1	A	210	HIS
1	A	283	HIS
1	A	329	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](#)

Of 2 ligands modelled in this entry, 1 is monoatomic - leaving 1 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
3	CO3	A	334	2	0,3,3	0.00	-	0,3,3	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
3	CO3	A	334	2	-	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.

No monomer is involved in short contacts.

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	328/328 (100%)	-0.21	4 (1%) 79 82	3, 25, 50, 70	0

All (4) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	146	GLY	2.7
1	A	87	GLY	2.6
1	A	219	ASP	2.3
1	A	144	GLU	2.3

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
3	CO3	A	334	4/4	0.97	0.15	0.28	4,6,6,6	0
2	FE	A	333	1/1	0.99	0.09	-2.41	12,12,12,12	0

6.5 Other polymers [i](#)

There are no such residues in this entry.