Full wwPDB X-ray Structure Validation Report ⓘ

May 29, 2020 – 02:12 am BST

PDB ID	:	1EKU
Title	:	CRYSTAL STRUCTURE OF A BIOLOGICALLY ACTIVE SINGLE CHAIN MUTANT OF HUMAN IFN-GAMMA
Authors	:	Landar, A.; Curry, B.; Parker, M.H.; DiGiacomo, R.; Indelicato, S.R.; Walter, M.R.
Deposited on	:	2000-03-09
Resolution	:	2.90 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
https://www.wwpdb.org/validation/2017/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:

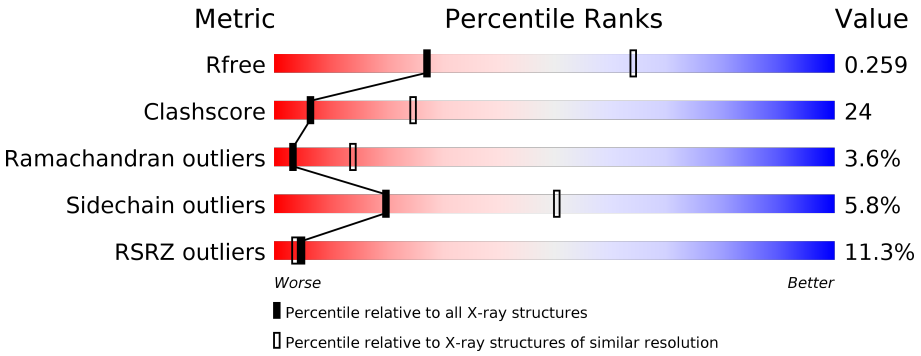
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

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 2.90 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}	130704	1957 (2.90-2.90)
Clashscore	141614	2172 (2.90-2.90)
Ramachandran outliers	138981	2115 (2.90-2.90)
Sidechain outliers	138945	2117 (2.90-2.90)
RSRZ outliers	127900	1906 (2.90-2.90)

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 respectively. 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	265	12% 50% 38% 6% • 5%
1	B	265	9% 52% 39% • • •

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 4232 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.

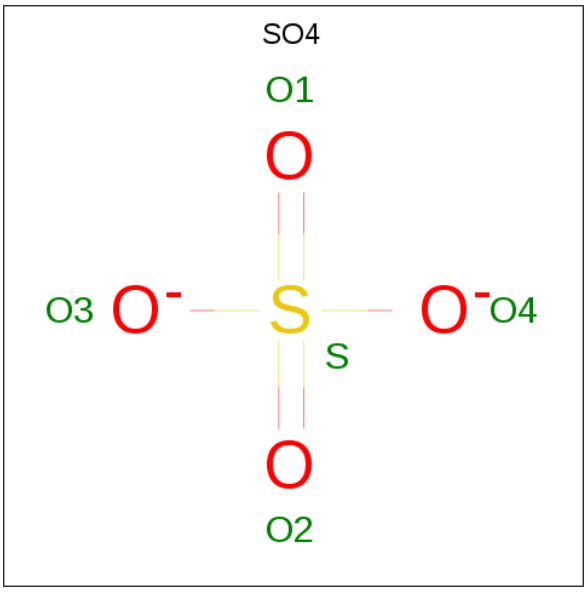
- Molecule 1 is a protein called Interferon gamma.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	252	Total	C	N	O	S	0	0	0
			2089	1331	347	404	7			
1	B	254	Total	C	N	O	S	0	0	0
			2106	1339	352	407	8			

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	MET	-	initiating methionine	UNP P01579
A	111	ASP	HIS	engineered mutation	UNP P01579
A	120	PHE	LEU	engineered mutation	UNP P01579
A	122A	THR	-	linker	UNP P01579
A	122B	GLU	-	linker	UNP P01579
A	122C	GLU	-	linker	UNP P01579
A	122D	GLN	-	linker	UNP P01579
A	122E	GLN	-	linker	UNP P01579
A	122F	GLU	-	linker	UNP P01579
A	122G	GLY	-	linker	UNP P01579
B	0	MET	-	initiating methionine	UNP P01579
B	111	ASP	HIS	engineered mutation	UNP P01579
B	120	PHE	LEU	engineered mutation	UNP P01579
B	122A	THR	-	linker	UNP P01579
B	122B	GLU	-	linker	UNP P01579
B	122C	GLU	-	linker	UNP P01579
B	122D	GLN	-	linker	UNP P01579
B	122E	GLN	-	linker	UNP P01579
B	122F	GLU	-	linker	UNP P01579
B	122G	GLY	-	linker	UNP P01579

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O_4S).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total O S 5 4 1	0	0
2	A	1	Total O S 5 4 1	0	0
2	B	1	Total O S 5 4 1	0	0
2	B	1	Total O S 5 4 1	0	0
2	B	1	Total O S 5 4 1	0	0
2	B	1	Total O S 5 4 1	0	0
2	B	1	Total O S 5 4 1	0	0

- Molecule 3 is water.

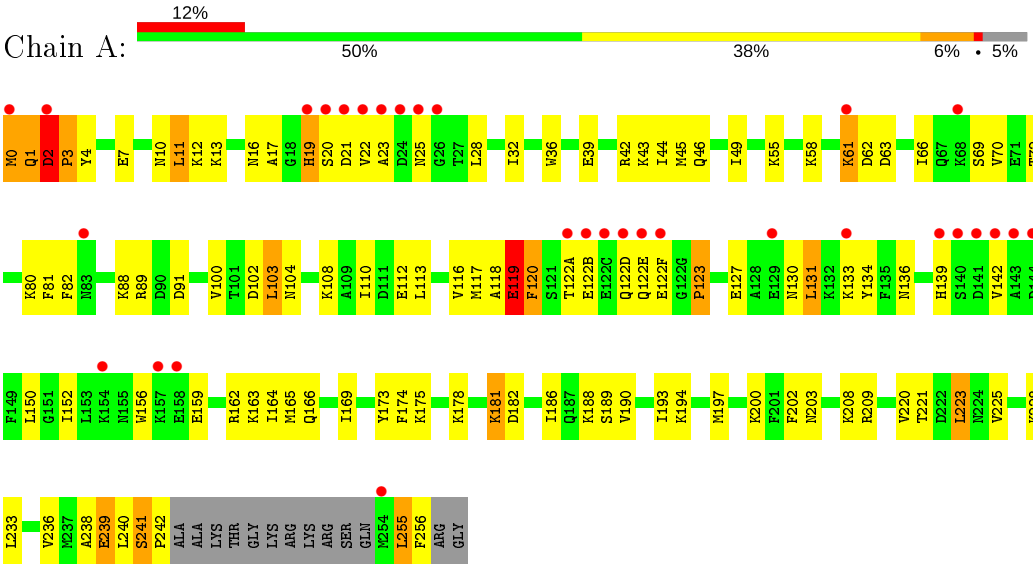
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	B	2	Total O 2 2	0	0

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.

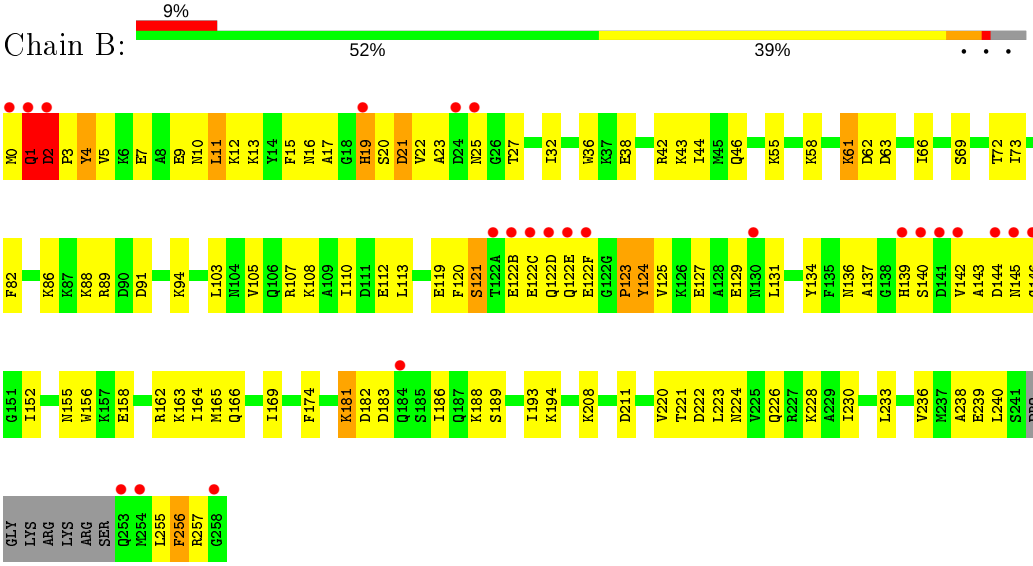
- Molecule 1: Interferon gamma

Chain A:



- Molecule 1: Interferon gamma

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	H 3 2	Depositor
Cell constants a, b, c, α, β, γ	111.38Å 111.38Å 311.96Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	20.00 – 2.90 19.51 – 2.91	Depositor EDS
% Data completeness (in resolution range)	95.9 (20.00-2.90) 96.4 (19.51-2.91)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	5.19 (at 2.93Å)	Xtriage
Refinement program	CNS 0.4	Depositor
R, R_{free}	0.246 , 0.265 0.236 , 0.259	Depositor DCC
R_{free} test set	808 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å^2)	72.0	Xtriage
Anisotropy	0.036	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.32 , 59.1	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	4232	wwPDB-VP
Average B, all atoms (Å^2)	71.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.55% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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: SO4

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	0.42	0/2125	0.59	0/2843
1	B	0.44	0/2141	0.63	0/2860
All	All	0.43	0/4266	0.61	0/5703

There are no bond length outliers.

There are no bond angle outliers.

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	2089	0	2066	97	0
1	B	2106	0	2084	107	0
2	A	10	0	0	1	0
2	B	25	0	0	1	0
3	B	2	0	0	1	0
All	All	4232	0	4150	200	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 24.

All (200) 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:42:ARG:NH2	1:A:239:GLU:HB3	1.86	0.90
1:A:81:PHE:HD1	1:A:240:LEU:HD11	1.36	0.90
1:A:110:ILE:HD12	1:A:131:LEU:HD12	1.56	0.85
1:A:81:PHE:HB2	1:A:240:LEU:HD21	1.62	0.81
1:A:39:GLU:OE1	1:A:242:PRO:HB2	1.79	0.81
1:A:122(F):GLU:O	1:A:123:PRO:HD2	1.80	0.81
1:B:110:ILE:HD12	1:B:131:LEU:HD12	1.63	0.80
1:B:240:LEU:O	1:B:240:LEU:HD23	1.82	0.80
1:B:189:SER:O	1:B:193:ILE:HG13	1.83	0.79
1:B:0:MET:HE3	1:B:3:PRO:HD2	1.65	0.78
1:B:121:SER:OG	1:B:122(D):GLN:HB2	1.84	0.77
1:B:0:MET:HG2	1:B:1:GLN:H	1.51	0.75
1:B:43:LYS:NZ	1:B:46:GLN:HE22	1.85	0.73
1:B:11:LEU:HD12	1:B:230:ILE:HD12	1.69	0.73
1:B:43:LYS:HD2	1:B:164:ILE:HD11	1.70	0.73
1:B:0:MET:HG2	1:B:1:GLN:N	2.05	0.72
1:B:127:GLU:HB3	1:B:189:SER:HB3	1.72	0.70
1:B:1:GLN:HG2	1:B:5:VAL:HG21	1.71	0.70
1:A:42:ARG:HH22	1:A:239:GLU:HB3	1.54	0.70
1:B:131:LEU:HD22	1:B:186:ILE:HD11	1.73	0.69
1:B:94:LYS:HD2	1:B:152:ILE:HD11	1.76	0.68
1:B:2:ASP:HB3	1:B:3:PRO:CD	2.23	0.67
1:A:43:LYS:NZ	1:A:46:GLN:HE22	1.93	0.67
1:B:12:LYS:HG3	1:B:17:ALA:HB3	1.77	0.67
1:A:81:PHE:CD1	1:A:240:LEU:HD11	2.24	0.66
1:B:163:LYS:NZ	1:B:166:GLN:HE22	1.95	0.65
1:A:127:GLU:HB3	1:A:189:SER:HB3	1.78	0.65
1:A:11:LEU:HD12	1:A:230:ILE:HD12	1.77	0.65
1:B:2:ASP:HB3	1:B:3:PRO:HD3	1.78	0.65
1:A:189:SER:O	1:A:193:ILE:HG13	1.98	0.64
1:B:155:ASN:HD22	1:B:155:ASN:N	1.93	0.64
1:A:17:ALA:O	1:A:22:VAL:HG21	1.99	0.63
1:B:0:MET:HB3	1:B:80:LYS:HE3	1.80	0.62
1:A:11:LEU:HD22	1:A:66:ILE:HD11	1.81	0.62
1:B:42:ARG:NH2	1:B:239:GLU:HB3	2.15	0.62
1:A:28:LEU:HG	1:A:228:LYS:HD2	1.82	0.61
1:A:131:LEU:HD22	1:A:186:ILE:HD11	1.82	0.61
1:A:43:LYS:HZ2	1:A:46:GLN:HE22	1.48	0.60
1:A:117:MET:O	1:A:120:PHE:HB2	2.02	0.59
1:B:20:SER:O	1:B:23:ALA:N	2.35	0.59
1:B:43:LYS:HZ2	1:B:46:GLN:HE22	1.49	0.59
1:B:122(F):GLU:HG2	1:B:125:VAL:HG21	1.85	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:181:LYS:HD2	1:A:182:ASP:N	2.19	0.58
1:A:122(D):GLN:OE1	1:A:200:LYS:HE2	2.04	0.58
1:A:256:PHE:HA	1:B:134:TYR:CD2	2.39	0.57
1:B:17:ALA:O	1:B:22:VAL:HG21	2.05	0.56
1:B:163:LYS:HZ3	1:B:166:GLN:HE22	1.52	0.56
1:B:44:ILE:HD11	1:B:163:LYS:HD2	1.87	0.56
1:A:113:LEU:HD13	1:A:173:TYR:CE2	2.41	0.55
1:B:121:SER:CB	1:B:122(D):GLN:HB2	2.37	0.55
1:A:55:LYS:HD2	1:A:220:VAL:HG21	1.89	0.55
1:A:232:GLU:O	1:A:236:VAL:HG23	2.07	0.54
1:A:139:HIS:O	1:A:142:VAL:HG22	2.08	0.54
1:B:61:LYS:HD2	1:B:62:ASP:N	2.23	0.53
1:B:82:PHE:CE2	1:B:89:ARG:HA	2.43	0.53
1:A:119:GLU:CD	1:A:162:ARG:HH22	2.12	0.53
1:B:144:ASP:CG	1:B:145:ASN:H	2.11	0.53
1:A:165:MET:O	1:A:169:ILE:HG13	2.07	0.53
1:A:186:ILE:O	1:A:190:VAL:HG23	2.09	0.53
1:A:25:ASN:HB2	1:A:228:LYS:NZ	2.24	0.53
1:B:0:MET:CE	1:B:3:PRO:HD2	2.36	0.53
1:B:27:THR:HG23	2:B:505:SO4:O2	2.09	0.53
1:B:43:LYS:HZ1	1:B:46:GLN:HE22	1.56	0.53
1:A:255:LEU:O	1:A:256:PHE:HB2	2.08	0.52
1:B:134:TYR:CE1	1:B:186:ILE:HB	2.43	0.52
1:A:113:LEU:HD21	1:A:193:ILE:HG21	1.91	0.52
1:A:61:LYS:HD2	1:A:62:ASP:N	2.24	0.52
1:A:7:GLU:HB3	1:A:69:SER:HB3	1.91	0.52
1:A:58:LYS:O	1:A:61:LYS:HG3	2.10	0.52
1:A:103:LEU:HD21	1:A:256:PHE:CE1	2.45	0.52
1:A:122(A):THR:HG23	1:A:159:GLU:CD	2.30	0.52
1:A:36:TRP:CZ2	1:A:208:LYS:HA	2.45	0.52
1:B:155:ASN:ND2	1:B:155:ASN:N	2.57	0.52
1:B:165:MET:O	1:B:169:ILE:HG13	2.10	0.52
1:B:139:HIS:ND1	1:B:140:SER:N	2.58	0.51
1:A:241:SER:H	1:A:242:PRO:HA	1.75	0.51
1:A:69:SER:O	1:A:73:ILE:HG13	2.11	0.51
1:B:137:ALA:C	1:B:142:VAL:HG21	2.31	0.51
1:B:3:PRO:HG2	1:B:4:TYR:H	1.75	0.51
1:B:158:GLU:O	1:B:162:ARG:HG3	2.11	0.51
1:A:223:LEU:HD21	1:B:256:PHE:CZ	2.46	0.51
1:A:134:TYR:O	1:A:255:LEU:HB3	2.11	0.50
1:A:45:MET:O	1:A:49:ILE:HG13	2.10	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:58:LYS:O	1:B:61:LYS:HG3	2.10	0.50
1:B:88:LYS:HA	1:B:156:TRP:CZ2	2.46	0.50
1:A:3:PRO:HG2	1:A:4:TYR:H	1.75	0.50
1:A:44:ILE:HD11	1:A:163:LYS:HD2	1.94	0.50
1:A:112:GLU:O	1:A:116:VAL:HG23	2.11	0.50
1:A:119:GLU:HB3	1:A:162:ARG:HH22	1.77	0.50
1:A:88:LYS:HA	1:A:156:TRP:CZ2	2.47	0.50
1:A:42:ARG:HH21	1:A:239:GLU:HB3	1.71	0.50
1:A:43:LYS:HD2	1:A:164:ILE:HD11	1.93	0.50
1:B:43:LYS:HZ2	1:B:46:GLN:NE2	2.10	0.50
1:B:73:ILE:HG21	1:B:233:LEU:HD21	1.94	0.50
1:A:118:ALA:C	1:A:120:PHE:H	2.16	0.49
1:B:255:LEU:O	1:B:256:PHE:HB2	2.12	0.49
1:A:120:PHE:HE1	1:A:197:MET:HG3	1.78	0.49
1:A:17:ALA:HB1	1:A:231:HIS:HB2	1.94	0.49
1:B:38:GLU:HG2	3:B:401:HOH:O	2.12	0.49
1:B:122(F):GLU:CG	1:B:125:VAL:HG21	2.42	0.49
1:B:19:HIS:CG	1:B:20:SER:H	2.31	0.49
1:A:255:LEU:O	1:A:256:PHE:CB	2.60	0.49
1:B:122(F):GLU:HG2	1:B:125:VAL:CG2	2.43	0.49
1:A:163:LYS:NZ	1:A:166:GLN:HE22	2.11	0.48
1:B:142:VAL:HG23	1:B:143:ALA:N	2.28	0.48
1:A:122(D):GLN:HE22	1:A:200:LYS:HD3	1.79	0.48
1:B:5:VAL:O	1:B:9:GLU:HG2	2.14	0.48
1:A:4:TYR:O	1:A:7:GLU:N	2.46	0.48
1:A:190:VAL:O	1:A:194:LYS:HB2	2.13	0.48
1:B:112:GLU:OE2	1:B:150:LEU:HG	2.13	0.48
1:B:15:PHE:CE2	1:B:256:PHE:HE2	2.32	0.48
1:B:36:TRP:CZ2	1:B:208:LYS:HA	2.49	0.48
1:B:7:GLU:HB3	1:B:69:SER:HB3	1.95	0.47
1:A:82:PHE:CE2	1:A:89:ARG:HA	2.49	0.47
1:A:20:SER:O	1:A:23:ALA:N	2.48	0.47
1:A:91:ASP:OD1	1:A:152:ILE:HG23	2.15	0.47
1:A:100:VAL:HG21	1:A:175:LYS:HD2	1.96	0.47
1:A:73:ILE:HG21	1:A:233:LEU:HD21	1.97	0.47
1:B:0:MET:HB3	1:B:80:LYS:CE	2.44	0.47
1:A:10:ASN:O	1:A:13:LYS:HG2	2.15	0.47
1:A:12:LYS:HG3	1:A:17:ALA:HB3	1.98	0.46
1:B:131:LEU:HD22	1:B:186:ILE:CD1	2.43	0.46
1:B:42:ARG:HH22	1:B:239:GLU:HB3	1.79	0.46
1:B:10:ASN:O	1:B:13:LYS:HG2	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:256:PHE:O	1:B:257:ARG:HB3	2.15	0.46
1:A:119:GLU:CD	1:A:162:ARG:NH2	2.70	0.46
1:B:122(F):GLU:HG3	1:B:125:VAL:HG11	1.97	0.46
1:A:203:ASN:ND2	2:A:502:SO4:O4	2.45	0.46
1:B:11:LEU:HD22	1:B:66:ILE:HD11	1.98	0.45
1:A:103:LEU:HD21	1:A:256:PHE:CZ	2.51	0.45
1:A:76:ASP:OD2	1:A:80:LYS:NZ	2.48	0.45
1:B:122(B):GLU:HG3	1:B:122(C):GLU:N	2.31	0.45
1:B:91:ASP:HB3	1:B:152:ILE:HG23	1.98	0.45
1:B:32:ILE:HG23	1:B:211:ASP:HB3	1.97	0.45
1:B:63:ASP:HB3	1:B:66:ILE:HG22	1.98	0.45
1:A:130:ASN:O	1:A:133:LYS:HG2	2.17	0.45
1:B:105:VAL:HG13	1:B:148:LEU:HD21	1.98	0.45
1:B:43:LYS:HD2	1:B:164:ILE:CD1	2.42	0.45
1:B:76:ASP:OD2	1:B:80:LYS:NZ	2.49	0.45
1:B:122(F):GLU:O	1:B:123:PRO:HD2	2.17	0.44
1:A:42:ARG:HH22	1:A:239:GLU:CD	2.21	0.44
1:A:63:ASP:HB3	1:A:66:ILE:HG22	1.99	0.44
1:B:113:LEU:HD21	1:B:193:ILE:HG21	1.98	0.44
1:B:125:VAL:O	1:B:129:GLU:HG2	2.17	0.44
1:A:91:ASP:CG	1:A:152:ILE:HG23	2.38	0.44
1:A:70:VAL:O	1:A:74:LYS:HB2	2.17	0.43
1:B:121:SER:C	1:B:122(B):GLU:H	2.21	0.43
1:B:257:ARG:HG3	1:B:257:ARG:O	2.18	0.43
1:B:222:ASP:OD1	1:B:224:ASN:HB2	2.18	0.43
1:B:25:ASN:HB2	1:B:228:LYS:NZ	2.33	0.43
1:B:55:LYS:HD2	1:B:220:VAL:HG21	2.00	0.43
1:A:0:MET:HB3	1:A:80:LYS:NZ	2.34	0.43
1:B:1:GLN:HE21	1:B:1:GLN:HB3	1.64	0.43
1:B:86:LYS:HE3	1:B:86:LYS:HB2	1.72	0.43
1:A:221:THR:HG22	1:B:221:THR:HG22	1.99	0.43
1:A:188:LYS:HD3	1:A:188:LYS:C	2.39	0.43
1:B:140:SER:O	1:B:144:ASP:HB3	2.19	0.43
1:B:236:VAL:O	1:B:240:LEU:HB2	2.18	0.43
1:B:119:GLU:O	1:B:162:ARG:NH2	2.52	0.43
1:B:120:PHE:HE1	1:B:166:GLN:HG2	1.84	0.42
1:B:124:TYR:CD1	1:B:125:VAL:N	2.87	0.42
1:A:256:PHE:HA	1:B:134:TYR:CE2	2.54	0.42
1:B:123:PRO:HG2	1:B:124:TYR:H	1.85	0.42
1:B:4:TYR:C	1:B:4:TYR:CD1	2.93	0.42
1:A:108:LYS:HD2	1:A:148:LEU:HG	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:11:LEU:HD22	1:A:66:ILE:CD1	2.50	0.42
1:B:183:ASP:HB3	1:B:186:ILE:HG22	2.00	0.42
1:A:202:PHE:CE2	1:A:209:ARG:HA	2.55	0.42
1:A:7:GLU:HG3	1:A:72:THR:HB	2.01	0.42
1:B:107:ARG:HB3	1:B:142:VAL:HG11	2.00	0.42
1:A:131:LEU:HD22	1:A:186:ILE:CD1	2.49	0.42
1:A:127:GLU:HB3	1:A:189:SER:CB	2.49	0.42
1:A:152:ILE:O	1:A:156:TRP:HD1	2.02	0.42
1:B:181:LYS:HD2	1:B:182:ASP:N	2.35	0.42
1:A:43:LYS:HZ2	1:A:46:GLN:NE2	2.16	0.42
1:A:238:ALA:C	1:A:240:LEU:H	2.23	0.41
1:B:69:SER:O	1:B:73:ILE:HG13	2.20	0.41
1:B:7:GLU:HG3	1:B:72:THR:HB	2.02	0.41
1:A:1:GLN:O	1:A:2:ASP:OD1	2.38	0.41
1:A:178:LYS:O	1:A:181:LYS:HG3	2.21	0.41
1:B:131:LEU:HD22	1:B:186:ILE:CG1	2.50	0.41
1:A:131:LEU:HD22	1:A:186:ILE:CG1	2.51	0.41
1:A:28:LEU:HD21	1:A:225:VAL:HG13	2.03	0.41
1:A:32:ILE:O	1:A:36:TRP:HD1	2.04	0.41
1:B:127:GLU:HB3	1:B:189:SER:CB	2.46	0.41
1:B:188:LYS:HD3	1:B:188:LYS:C	2.41	0.41
1:A:112:GLU:OE2	1:A:150:LEU:HG	2.21	0.41
1:B:238:ALA:C	1:B:240:LEU:H	2.23	0.41
1:A:174:PHE:CD1	1:A:194:LYS:HE3	2.56	0.41
1:B:91:ASP:CG	1:B:152:ILE:HG23	2.41	0.41
1:B:174:PHE:CD1	1:B:194:LYS:HE3	2.56	0.41
1:B:11:LEU:HD22	1:B:66:ILE:CG1	2.52	0.40
1:A:4:TYR:HE2	1:A:80:LYS:NZ	2.19	0.40
1:B:108:LYS:HD2	1:B:148:LEU:HG	2.04	0.40
1:B:226:GLN:O	1:B:230:ILE:HG12	2.22	0.40
1:A:102:ASP:OD1	1:A:104:ASN:HB2	2.22	0.40
1:A:25:ASN:HB2	1:A:228:LYS:HZ1	1.84	0.40
1:A:19:HIS:CG	1:A:20:SER:H	2.39	0.40
1:B:22:VAL:O	1:B:228:LYS:HG3	2.21	0.40
1:B:43:LYS:HD2	1:B:164:ILE:CG1	2.52	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	248/265 (94%)	215 (87%)	25 (10%)	8 (3%)	4 16
1	B	250/265 (94%)	219 (88%)	21 (8%)	10 (4%)	3 11
All	All	498/530 (94%)	434 (87%)	46 (9%)	18 (4%)	3 14

All (18) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	123	PRO
1	B	122(E)	GLN
1	B	123	PRO
1	A	3	PRO
1	B	2	ASP
1	B	146	GLY
1	A	2	ASP
1	A	19	HIS
1	A	119	GLU
1	A	241	SER
1	B	19	HIS
1	B	124	TYR
1	B	256	PHE
1	A	122(B)	GLU
1	B	21	ASP
1	B	121	SER
1	B	1	GLN
1	A	239	GLU

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	234/244 (96%)	218 (93%)	16 (7%)	16 42
1	B	235/244 (96%)	224 (95%)	11 (5%)	26 59
All	All	469/488 (96%)	442 (94%)	27 (6%)	20 50

All (27) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	0	MET
1	A	1	GLN
1	A	2	ASP
1	A	11	LEU
1	A	16	ASN
1	A	21	ASP
1	A	61	LYS
1	A	103	LEU
1	A	119	GLU
1	A	120	PHE
1	A	122(E)	GLN
1	A	131	LEU
1	A	136	ASN
1	A	181	LYS
1	A	223	LEU
1	A	255	LEU
1	B	1	GLN
1	B	2	ASP
1	B	4	TYR
1	B	11	LEU
1	B	16	ASN
1	B	21	ASP
1	B	61	LYS
1	B	103	LEU
1	B	136	ASN
1	B	181	LYS
1	B	223	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (29) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	1	GLN

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Mol	Chain	Res	Type
1	A	10	ASN
1	A	35	ASN
1	A	46	GLN
1	A	48	GLN
1	A	67	GLN
1	A	122(D)	GLN
1	A	122(E)	GLN
1	A	130	ASN
1	A	136	ASN
1	A	139	HIS
1	A	155	ASN
1	A	166	GLN
1	A	168	GLN
1	A	187	GLN
1	B	1	GLN
1	B	10	ASN
1	B	35	ASN
1	B	46	GLN
1	B	48	GLN
1	B	67	GLN
1	B	106	GLN
1	B	122(D)	GLN
1	B	130	ASN
1	B	136	ASN
1	B	155	ASN
1	B	166	GLN
1	B	168	GLN
1	B	187	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 (i)

7 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	SO4	A	502	-	4,4,4	0.28	0	6,6,6	0.10	0
2	SO4	B	501	-	4,4,4	0.28	0	6,6,6	0.10	0
2	SO4	B	503	-	4,4,4	0.27	0	6,6,6	0.10	0
2	SO4	B	507	-	4,4,4	0.31	0	6,6,6	0.18	0
2	SO4	A	506	-	4,4,4	0.30	0	6,6,6	0.10	0
2	SO4	B	504	-	4,4,4	0.27	0	6,6,6	0.12	0
2	SO4	B	505	-	4,4,4	0.29	0	6,6,6	0.16	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.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	502	SO4	1	0
2	B	505	SO4	1	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^{th} 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	252/265 (95%)	0.40	33 (13%) 3 2	39, 72, 119, 131	0
1	B	254/265 (95%)	0.32	24 (9%) 8 6	27, 64, 118, 137	0
All	All	506/530 (95%)	0.36	57 (11%) 5 4	27, 68, 119, 137	0

All (57) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	122(B)	GLU	10.4
1	B	253	GLN	9.3
1	A	20	SER	7.7
1	A	0	MET	7.0
1	B	0	MET	6.5
1	A	145	ASN	6.2
1	B	122(C)	GLU	5.9
1	B	122(D)	GLN	5.9
1	A	254	MET	5.7
1	A	21	ASP	5.7
1	A	23	ALA	5.4
1	A	141	ASP	5.3
1	A	140	SER	4.9
1	A	122(E)	GLN	4.8
1	B	25	ASN	4.7
1	B	122(E)	GLN	4.6
1	A	122(D)	GLN	4.4
1	A	24	ASP	4.4
1	A	19	HIS	4.3
1	A	2	ASP	4.2
1	B	141	ASP	4.0
1	B	1	GLN	4.0
1	A	158	GLU	3.9
1	A	122(A)	THR	3.9

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Mol	Chain	Res	Type	RSRZ
1	A	122(C)	GLU	3.8
1	A	144	ASP	3.6
1	A	122(B)	GLU	3.4
1	B	142	VAL	3.3
1	B	2	ASP	3.3
1	B	258	GLY	3.2
1	B	122(A)	THR	2.8
1	A	22	VAL	2.8
1	A	139	HIS	2.8
1	A	61	LYS	2.8
1	B	144	ASP	2.8
1	A	122(F)	GLU	2.8
1	B	146	GLY	2.7
1	B	24	ASP	2.7
1	B	139	HIS	2.6
1	A	143	ALA	2.6
1	B	19	HIS	2.6
1	B	184	GLN	2.5
1	A	26	GLY	2.5
1	A	133	LYS	2.4
1	A	25	ASN	2.4
1	A	68	LYS	2.3
1	A	142	VAL	2.3
1	B	145	ASN	2.2
1	B	122(F)	GLU	2.2
1	A	129	GLU	2.1
1	A	157	LYS	2.1
1	A	83	ASN	2.1
1	B	130	ASN	2.1
1	A	146	GLY	2.1
1	A	154	LYS	2.1
1	B	140	SER	2.0
1	B	254	MET	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

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^{th} 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(Å^2)	Q<0.9
2	SO4	B	507	5/5	0.79	0.34	115,115,119,119	0
2	SO4	B	503	5/5	0.81	0.31	126,127,128,129	0
2	SO4	B	505	5/5	0.86	0.34	100,102,103,103	0
2	SO4	B	504	5/5	0.93	0.23	119,120,121,121	0
2	SO4	A	502	5/5	0.94	0.16	43,43,51,51	5
2	SO4	A	506	5/5	0.94	0.25	108,108,110,111	0
2	SO4	B	501	5/5	0.98	0.12	19,29,30,30	5

6.5 Other polymers

There are no such residues in this entry.